

CTAGTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA TCCGAACCCG CTGACCCnAC 360
CnGCGTGCAA AGCAGGCGCT CTACCCAGCT TGAGCTAAGG 400

(2) INFORMATION FOR SEQ ID NO: 3943:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3943:

CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTGAAACCC CCGCGAGCCG 60
TTAAGCCCCCT GTCGGTTTC AAGACCGATC CCTT@GCCG GACTTGGGT@ TTCCCTCCAAA 120
ATTATATGG@ CCTTGAGGA CTCGAACCTG CGACCGAACG GTTATGGAGC CGTTAGCTCT 180
GAACCAA@TG AGCTAAAGGT CCTAAATATA ATTTACAAC TAATAAATAG TGGCGGTGGA 240
GGGGATCGAA CCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 300
CGCCTTATAT AGTTTGTA@A TnAnnATGGT GGGAGACTAG CGGGGTTCGA ACCGCTGGAC 360
CTCCTGCGTG CCAAAGCAGG CGGCTTCTAC CCAGCTGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3944:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 406 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3944:

CACAAATTGC ACCTTGTG@ TTATTGGAA AATCAATATn GnTAGGGGGT ATAAGATGCA 60
CCTACTTAA CTGTCGCCAA CATGCCGCA ATCATTCAA AACTACGTT@ TGTAAACAAG 120
GCAACCCGTT GACCATTGCC CACACCATT@ GATAGGAGCA TGTGCGCAAT GGCATCCACA 180
TAGTTGCGTA ATGTTTCATA CGTCATTGTC AAATCATTCA TGACTAGCGC AACATGATTA 240
CCTTGTGCGTG AGAAACTTCA TTAAAGTAAC TTATGATAGA TTTATTTCCC GGGACATTAA 300
GCATTCGATC GTTAACATGC GTATTGACCC AATTAGAAG TTCCTCCGTG CCGTTGGTA 360
TATCACAAAT TTGTAGTGTA wCtTG@TGCT TCmAAATAtC AATCAn 406

(2) INFORMATION FOR SEQ ID NO: 3945:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3945:

CAATGACAAC AGCAACTGAG ACAGTGTCAA ACGCTTAATA ATAATGATGT AGTGTG T AATACCGCAT TAAATGTACC AACTAAAACA AATGAAAATG GTTCAGGAGG ACATCTAACT	60
TTAAAGGAAA TTCAAGAAGA TGTCGTCAT TCTTCAAATA AACCAAGAGCT AGTTGCAATT GCTGGAACCA GCATCTGAAT AGACCGAAAA AGAGAAGTTA GACGTGCGGC ACCGGCAGAT	120
CCTGAATGCC AACTCCAGCA GATCCAGCGG CTGCAGCGGT TAGGAAACGG TGGTGCACCA GTTGCAATT CAGGCCATA TACGCCAACAA ACTGATCCTA ATGCCATGAn GCCAGGACAA	180
ATGGCACCTA ACGAnGCTTG TTCATTTGAT GGACAnGGTA	240
	300
	360
	400

(2) INFORMATION FOR SEQ ID NO: 3946:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3946:

CTCGCTGCGA TAAAGTACCA GTTCATAGCA AC G TTGTnT TAATAGGnTC TGAAACGATA CGTGTGCGG GTTCTGTAAA TGAATAGACC AAAGCATCTT GCATACCAAC AACTATATTT	60
GCTGCAAATC CTCCAACAGC GGAAnATATG CCATCGTTAG TCCAGCGATA GGGTGATAGC CAATTTAAT AAAAACGATT GCTGCAACGG CCGGCAAGAT AATTGTCGCA GCATCGC G	120
CTGTACTACC TAAAATACCA ATTAATATAA TAGTCGGTAA AATTAAGAAA CGTGGTGCGC GATTCACAAC AGAAATCATT AACTTATCGA AGTATCCTGT TTTCTCTGCA ACACCAATAC	180
CAATCATCAC TGCTAGGTAC TAAGCCTAAT GCTGGGnACT	240
	300
	360
	400

(2) INFORMATION FOR SEQ ID NO: 3947:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3947:

GCCGGCCAGA GGACTTGGAA CCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT	60
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GAGCTAGGCC	GGCAATATGT	AAGAATAAAAT	GGTGGAGAAT	GACGGGTTCG	AACCGCCGAC	120
CCTCTGCTTG	TAAGGCAGAT	GCTCTCCCAG	CTGAGCTAAT	TCTCCGATT	AAAACGTGCT	180
GGCAACGTTTC	TACTCTAGCG	GAAnTAATTC	GnACTACCAT	CGACGCTAAG	GAGCTTAACT	240
TCTGTGTTCG	GCATGGGAAC	AGGTGTGACC	TCCTTGCTAT	AGTCACCAGA	CATATGAATG	300
TAATTTATAC	ATTCAAAACT	AGATAGTAAG	TAAAAGTGAT	TTTGCnTTCG	CAAAACATTT	360
A						361

(2) INFORMATION FOR SEQ ID NO: 3948:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3948:

TTCCGTCAGA	CCCTGACATG	GTTCATGGGT	TCATATTGCA	TAGGACCGAA	ATCTTCAAAC	60
ACTACGTGCT	TTGGGCAGAC	TCGCAAAAAA	TACGGCCTCA	ACAAAGGAAT	TAAGCCTCGC	120
ATAAAGCGGA	TTTCGAGTAC	AGGGAACCGC	TACCTCCCCA	CCTAGCACGG	CAAGATATAT	180
ATTACTATAT	TTTAATAGTT	AATTGCAAGT	ATAAATCATT	TATATCATTG	TTTACTTTAT	240
ACGACGTCTT	GAGAAGTCAT	TAATTAAAT	TCATTTGCAA	GATGTTTGA	AATATTATAT	300
TGAAACGGCA	TTGTATTTTC	TAAATACACA	nTACTTCGAA	CTGTTGCnGA	ATAGGCCACC	360
GATACATCAC	CAACAATTGG	nA				382

(2) INFORMATION FOR SEQ ID NO: 3949:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3949:

GCCAAGCCAT	TTTTCTTTGT	GTTTACTTTT	TATTTGACG	TTTTAGACAT	AAAAAAAAGA	60
GACCTTGCAG	TCTCAATGCG	GCTCATCGCA	TCCATTTTT	GCCTGGCAAC	GTTCTACTCT	120
AGCGGAACGT	AAGTTGGCTA	CCATCGACGC	TAAGAACCTT	TCTTGACTTG	TGACAATGC	180
TTGCTTCTTT	CCTCTTCTTC	GGCTCTCGCT	TACTCATT	GCTCTACTAA	ACTCGTTGCG	240
CTCTTTCTC	GTTCGTCAG	ATTCAAACGT	TTTCACTTCG	CCAAGCCATT	TTTCTTTGTG	300
TTTGCTTTT	AnTTTGACGT	TTTAGACATA	AAAAAAAGAG	ACCTTGCAGn	CTCAATGnGG	360

GCTCATCGCA TCCAATTTT GGCCTGGCAA CGGTTCTACT 400

(2) INFORMATION FOR SEQ ID NO: 3950:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3950:

ACTCGGTTT GCTTGAAAAA TCTATATTAA CTTACTTATC TAGTTTCAA TGTACAATT	60
CTTTTAGTC AAGCGCTCGC ATACTGCTTT ATTTCATAA GCAATATCAC TTTAACCAA	120
AAATATTGA ATGTTAAATA AACATTAAA ACTAAATACA ATATGTCACG TTATTCCGCA	180
TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC	240
CGATACGGCT ACCTTGTAC GACTTCACCC CAATCATTG TCCCACCTTC GACGGCTAGC	300
TCCTAAAAGG nTACnCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT GACGGGC	360
GTTACAAGA CCCGGGAACG nATTCAACCG	389

(2) INFORMATION FOR SEQ ID NO: 3951:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3951:

AAAGCTCGAC TTGTTTACGA TGTTGAAAAA CAAGATTATG TACCTGTATC GCAACCACAA	60
TTACCAATT TAAATGAATT TAATAAAGAC TTAGTGCATA ACCTTGATAC CATATTCAAT	120
GCGCAAGACG AnCGGGACTA TTTTATGGG AGACATTACG TAATAATTTC TATTACTCTG	180
CTATCAATGT ACCTAAAGCT ACCGATGATT TCCGAGACAT AGACCGTGCG CTTGTCTGGG	240
GGTCAACTG GAAACTTGGT CCATTCAAT TATGGGATGC AATGGGATAC GAACGTGTTA	300
AAACAnTGAT GGGAGACGA ACTTGGGAGA CTTACACAA TGGGATTAGT GAnTTAGATG	360
GTTGGCTTTAT AAACAAG	377

(2) INFORMATION FOR SEQ ID NO: 3952:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3952:

CAAAGGGCAG CGAAACCGCG AGTCCAGAGC AAATCCCATA AAGTTGTTCT CAGTCGGAT	60
TGTAGTCTGC AACTCGACTA CATGAAGCTG GAATCGCTAG TAATCGTAGA TCAGATGCT	120
ACGGTGAATA CGTTCCCGGG TCTTGTACAC ACCGCCGTC ACACCACGAG AGTTTGTAAAC	180
ACCCGAAGCC GGTGGAGTAA CCTTTAGGA GCTAGCCGTC GAAGTGGGAC AAATGATTGG	240
GGTGAAGTCG TAACAAGGTA GCCGTATCGG AAGGTGCGGC TGGGATCACC TCCTTCTGA	300
AGGATATATT CGGAAACATC TTCTTCAGAA GAGCGGAAAT AACGTGACAT ATTGTATTCA	360
GnTTTGAAT GTTTnnTTAA CATTnCAAAA AAATGGGGCC	400

(2) INFORMATION FOR SEQ ID NO: 3953:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3953:

TGATTTGAC GTTTAGACA TAAAAAAAAG AGACCTTGCG GTCTCAAATG CGGCTCATCG	60
CATCCATTTC TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAATTGGCT ACCATCGACG	120
CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTTCTT CGGCTCTCGC	180
TTACTCATT AGCTCTACTA AACTCGTTGC GCTCTTTCT CGTTTGTCA GATTCAAACG	240
TTTCACTTC GCCAAGCCAT TTTCTTTGT GTTGCTTT TATTTGACG TTTTAGAAT	300
AAAAAAAAGA GACCTTGCAG TCTCAATGCG GGCTCATCGC ATCCATTTT TGCCTGGCAA	360
CGTTCTACTC nAGCGGGAAG TGAAGnCGGA CTGACCAAGC	400

(2) INFORMATION FOR SEQ ID NO: 3954:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3954:

AAACTACATA ATGAAAATGC CGTTTTAACG GGTAAATTAA ATATGGATGA GTTGCAATG	60
GGTGGTTCAA CAGAAACATC TTATTCAAA AAAACAGTTA ACCCATTTGA CCATAAAGCA	120

GTGCCAGGTG GTTCATCAGG TGGATCTGCA GCAGCAGTTG CAGCTGGCTT AGTACCATT	180
AGCTTAGGTT CAGACACAGG TGGTTCAATT AGACAACCGG CTGCATATTG TGGCGTTGTC	240
GGTATGAAAC CAACATACGG TCGTGTATCT CGATTGGAT TAGTGCTTTG CATCTTCATA	300
GACCAAATTG GGCCATGACT CGAATGTAAA GTAATGCCAT CGTATTAGAA GCTATTCTGG	360
TGCAGATGnT AATGACTCTA CCAGTGCACC AGTGATGAGG	400

(2) INFORMATION FOR SEQ ID NO: 3955:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3955:

TCGATTGGCA TTTCTCCGCT ACCCTCAGTT CATCCGCTCA CTTTCAACG TAACGGTTC	60
GGTCCTCCAT TCAGTGTAC CTGAACCTCA ACCTGACCAA GGGTAGATCA CCTGGTTTCG	120
GGTCTACGAC AAATACTAAA CGCCCTATTC AGACTCGCTT TCGCTACGGC TCCACATTAA	180
CTGCTTAACC TTGCATCAAA TCGTAACTCG CCGGTTCAATT CTACAAAAGG CACGCCATCA	240
CCCATTAACG GGCTCTGACT ACTTGTAAGC ACACGGTTTC AGGTTCTATT TCACTCCCCT	300
TCCGGGGGTG CTTTCACTT TTCnCTTCAA GGTATGGGTT CACTATCGGT nACTAGAGAG	360
TAATTAGCTT AGGnGATGGT CCTCCCAGAT TCGGAAGGGA	400

(2) INFORMATION FOR SEQ ID NO: 3956:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3956:

GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG AACCGGTAGT	60
GGnTnCACTC ACCGCAGATT TTAAGTCCTG TGCGTCTGCC AGTTCCGCCA CCCCGGCACT	120
ATAAAAAATGG AGCAGAACGAC GGGATTGAA CCCGCGACCC CAACCTGGC AAGGTTGTAT	180
TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGGTAAG	240
CTTAGGGATCC TAAGTCTAGT GCGTCTGCCA ATTCCGCCAC ACCCGCAAAT GGTGAGCCAT	300
AGAGGATTG AACCTCTGGA CCCTCTGGAT TAAAAGTCAG ATGCTCTACC AACTGGAGCT	360

AATGGCTCTT TCCATGGTGC CGGGCCAGAG GACTTGAAAn

400

(2) INFORMATION FOR SEQ ID NO: 3957:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3957:

CAGACATGTG TTATACGGGA AATTGGCGA ACCGCAACTA TTATACATTG ATTTACACCT	60
TATACATGAA GTTACTTCTC CTCAAGCATT TGAAGGACTT AGGCTTCAAA ACAGAAAATT	120
AAGACGCCA GATTTAACAT TTGCAACACT CGATCACAAT GTTCCTACTA TTGATATATT	180
CAATATTAAA GATGAAATTG CAAACAAACA ATCACAACA TTACAAAAAA ACGCCATAGA	240
TTTGGGGTG CATATTTTG ATATGGGTTG TGATGAACAA GGTATTGTTG ACATGGTAGG	300
ACCTGAGACA GGACTTACAC AGCCTGGChA GACCATCCGT nTGTGGGTGA CTCTCACACA	360
GCCACACATG GnGCCTTT	379

(2) INFORMATION FOR SEQ ID NO: 3958:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3958:

TGTTAAAATA CGGTACATCT AAATTAATGT TAACTGATTT TCAAAAAGAG AATTAAATAA	60
ATATATTCAA GGTCAGAnAC AACGCGTGAT ATTTGAAAAT GGCCATTTG TCTAATTGAT	120
AGTGAATATA ATTAGAGTAA GAGGCTGGGA CATAAATCCC TAAAAAACAG CAGTAAGATA	180
ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTA TACAATACTT CGTATTGAAT	240
GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT GCTCCCTCAG	300
GGGTCTCGCC ATTAATACTA CGTATTAACA TGTAATTTA CTTTGGAAAT ACTnTAAAAA	360
AATAAGACAT TTGnCCAAct TGACACTACC ATTAAAAACT	400

(2) INFORMATION FOR SEQ ID NO: 3959:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3959:

GAGCCGCAGT GGAATGAGGC CCAAGCGACT GTTTATCAAA AACACAGGTC TCTGCTAAC	60
CGTAAGGATG TGTTATAGGG GCTGACGGCT GCCCGGTGCT GGAAGGTTAA GAGGAGTGGT	120
TAGCTTCTGC GACGTACrGA ATCGAAGCCC CAGTAAACGG CGGCCGTAAC TATAACGGTC	180
CTAAGGTAGC GAAATTCCCTT GTCGGGTAAG TTCCGACCCG CACGAAAGGC GTAACGATT	240
GGGCACGTGTC TCAACCGAGAG ACTCGGTGAA AATCATAGTA CCTGTGAAGA TGCAGGTTAC	300
CCCGGTACAG GACGGAAAGn CCCCTGGAGC TTTACTGTAG CCTGATATTG AAATnCGGCA	360
CAGTTTGTAC AGGATAGGTT AGGAGCCTTG GAAACGTGTG	400

(2) INFORMATION FOR SEQ ID NO: 3960:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3960:

TGGTCCAAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTAA ACGCGCCCGA	60
TAGGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG	120
GGCGCATATG TTTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTGAnTnC	180
ACTCACCGCA GATTTAAGT CCTGTGCGTC TGCCAGTTCC GCCACCCCGG CACTATAAAA	240
ATGGAGCAGA AGACGGGATT CGAACCCCGCG ACCCCAACCT TGGCAAGTTG TTATTCTTAC	300
CGCTGGAACT ACTTCTGGCA TATGCGGTT GAAGGGGAGT CGAACCCCCA CGCCTAGGC	360
TTAAGATTCC TGAAGTCTAG TGCCTCTGGC CAATTCCGG	400

(2) INFORMATION FOR SEQ ID NO: 3961:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3961:

TTTGATACA TAATCTAAAT TTCTCAAAGC GCCAATAACA GAGGACCATC TCCTAAGGCT	60
,AAATACTCTC TAGTGACCGA TAGTGAACCA GTACCGTGAG GGAAAGGTGA AAAGCACCCC	120

GGAAGGGAGT GAAATAGAAC CTGAAACCGT GTGCTTACAA GTAGTCAGAG CCCGTTAATG	180
GGTGATGGCG TGCCTTTGT AGAATGAACC GGCGAGTTAC GATTTGATGC AAGGTTAACG	240
AGTAAATGTG GAGCCGTAGC GAAAGCGAnG TCTGAATAGG GCGTTAGTA TTTGGTCGTA	300
GACCGGAAAC CAGGTGATCT ACCCTGGTC AGTTGAAGT TCAGGTAACA CTGAATGGAG	360
GACCGAACCG ACTTACGTTG AAAAGTGAGC GGATGAACTG	400

(2) INFORMATION FOR SEQ ID NO: 3962:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3962:

TAATAATTAC AGTATATCGG GAAGACAGGA TTGAAACCTn CGACCCCTTG GTCCCAAACC	60
AAGTGCTCTA CCAAGCTGAG CTACTTCCCG TATAAnTTAAC GCGCCCGATA GAGTCGAAC	120
CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTG	180
TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA	240
TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCGGCA CTATAnAAAT GGATCAGAAG	300
ACGGGATTCTG AACCCGCGAC CCCAACCTTG GCAAGGTTGT ATTCTACCGC TGAACTACTT	360
C	361

(2) INFORMATION FOR SEQ ID NO: 3963:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3963:

CGCGAAATAT CATTGGAGG AATTCTAACAA GAAGTTTTA TTGGTAGTGT AAGTTGGGCA	60
AAGTGTCTTA TTTTTTAAA GTATTCAA GTAAAATTAC ATGTTAACAC GTAGATTAAT	120
GGCGAGACTC CTGAGGGAGC AGTGCCAGTC GAAGCCGTAG GCTGAGACGG CACCTAGGA	180
AAGCGAACCA TTCAATACGA AGATnTnATn AAATAGAGAA CAGCAGTAAG ATATTTCTA	240
ATTGAAAATT ATCTTACTGC TGTTTTTAG GGATTTATGT CCCAGCCTCT TA T CTAATT	300
ATATTCACTA TCAATTAGAC AAAATGGCCA TTTCAAATA TCACGCGTTG GTTTCTGACC	360
TTGGAATATA TTTAT	375

(2) INFORMATION FOR SEQ ID NO: 3964:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3964:

AAAATGGCCT	TGATAGACTT	GCTCAATGCA	GGGTTGCCAC	AAACCAATGA	TGCACTTACA	60
ATTTTAAATA	GATTTTAAG	ACCTTGTGG	TTTGTACAA	TTAATGTGAC	ATGACTAGGT	120
CTTGCACGTT	TATATGCATC	TTCATTACTG	AGTTTTTGT	TGATTCGTT	ATGATTTAAT	180
ACGCCTAATT	CTTTCATTTG	TTGAACCATT	TTTATGAAAA	TGTAAGCTGT	TGCTTCTGTA	240
TCATAAAATGG	CACGGTGATG	TTGCGTTAAT	TCTACGCCAT	ATTTTTAGC	CAAGAAATTC	300
AAACCATGTT	TACCATATTC	AGTATTAATC	GTACGAGGAT	AATTCTAAAG	TATCGATAAAC	360
ACCATTGTT	GGATGGTCCA	AACCCAAGAC	GTTCATATCC			400

(2) INFORMATION FOR SEQ ID NO: 3965:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3965:

ACTTTTAATT	TTGTCATGAT	GTGCCTCCTT	ACCGTATGAT	GTTATTCAAAGTAAATTGCT	60	
TTGCCTGATT	TTGCAGACTG	ATAAATCGCT	TCAAGAATT	TTGTAACTAC	CATTGCTTGT	120
TCCGGTTTCA	CAACTGGTTC	AGTATCATT	ACAAC TGCA	CAATCCAAGC	TTTGCTTCT	180
TCTTCAGCTT	CATCCACTTC	ATTACCTTCA	TAAAAGTCGA	CGCCTTGTT	TTCCAATTCA	240
ACGTGTTGG	TATAAAGTGT	ACCCATGTCT	TCACCATGAA	TACGTAGACC	ATCTTCATA	300
TCAGCACCTG	CTTTAGGTTTC	CTGATAATGA	ACATTTGGC	CTCATCCACT	TCTAAAnGAA	360
TTAATCGCCC	AAGnGGGATT	CCAAAAAGGA	n			391

(2) INFORMATION FOR SEQ ID NO: 396:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3966:

CGCTATCAGG TATTGTTCA ACAATTCA	TAAACATATCG TGAAATATCA	TTTGAGGGA	60
TTCTAACAGA AGTTTCTATT GGTAGTGTAG TTGGGCATG	TTATAATTT TATACATAAG		120
GCACCTCGTT AATTTAGTTT AGTGGTATT ATTAAATTAT	AAGAAGGGAC CCAACACAGA		180
AAATTCAATT TATTGAATT TACATTTATG TGCAAGTTGG	GCAAAGTGTC TATTTTTA		240
AAAGTATTTC AAAGTAAAAT TACATGTTAA TACGTAtATA	ATGGcGAGAC TCCTGAGGGA		300
GCAGTGCCAG TCGAAGC _n CAA GGCTGAGACG	GCACCCtAGG AAAGCGAc _n C ATTcAATACG		360
AAGATTGTAT AAATAGAGAA CAGCAGTAAG ATATTTTC			398

(2) INFORMATION FOR SEQ ID NO: 3967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3967:

GCTATAGAAA AAATAAAATC ACAAGTTACG ATTAGCGTAC	TTGATGGGGA GTGAAAATAA	60
TGAGAGTAAC AGAGTTATTA ACAAAAGATA CAATAGCAAT	GGATTTAATG GCAAATGACA	120
AAAATGGTGT TATTGATGAG TTAGTAAATC AATTAGACAA	AGCAGGTAAA TTAAGTGATG	180
TCGCGTCATT TAAGGAAGCG ATTCAAAATC GAGAATCACA	AAGTACAACG GGTATCGGCG	240
AGGTATTGCC ATTCCACATG CCAAAGTGGC CGCAGTTGAA	GTCACCAGCT ATTGCCTTG	300
GTAAATCTAA AGCAGGCGTG GATTATCAAn TTTGGnTATG	CAACCAGCAC ACTTnTTCTT	360
TGTGGTTGGC AGCG		374

(2) INFORMATION FOR SEQ ID NO: 3968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3968:

ACCCCGGCAC TATAAAAATG GAGCAGAAGA CGGGATTGCA	ACCCGCGACC CCAACCTTGG	60
CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG	GGTGAAGGGA GTCGAACCCC	120
CACGCCGTAA nCTGAGGATC CTAAGTCTAG TGCGTCTGCC	AATTCCGCCA CACCCGCAAA	180

TGGTGAGCCA TAGAGGATTC GAACCTCTGG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC	240
AACTGAGCTG AATGGCTCTT CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTGACT	300
GGATTACAAG TCAGTTGCTC TACCAATTGA GCTAAGGCCG GGCAATATGT AAGAATAAAT	360
GGTGGAGAAT GACGGGTTTC GAAAnCGCCGA CCCTCTGCTT	400

(2) INFORMATION FOR SEQ ID NO: 3969:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3969:

GCGAGTTGGG GTGTGGGCC CAACATAGAG AAATTGGATT CCCAATTCT ACAGACAATG	60
CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC ATTAnCAATA ATGTGCAAGT	120
TGGCGGGGCC CCAACACAGA AGCTGACGAA AAGTCATTAn CAATAATGTGCAAGTTGGCG	180
GGGCCCCAAC ACAGAAGCTG GCGGAAAGTC AGCTTACAAT AATGTGCAAG TTGGGGTGGG	240
ACAACGATAA AGTAATACTT TTTCTATAGA AATTAGTATT TCTTATGCAT GAGTTTACT	300
CATGTATTCC TATTTTAAG TACACATTAG CTGTGGCTAA TGTTTAAGAC CCACTACATA	360
ATAAAATCATT AGTGGCTCTn TATCATTCT GTCCCCACTCC	400

(2) INFORMATION FOR SEQ ID NO: 3970:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 419 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3970:

GATAAGATCA GCCGAAAATG GATGGTGT TA AGAGCGTTAC TTGGTTGGC GGTATGCTTA	60
TTTTTAATGG CATTGTGTAC GACACCATT A CAGTTGTAC TTGTGAGGTT ATTGCAGGG	120
CTATTTGGTG GTGTTGTTGA TGCAT&AGT GCGTTGCGA GTGCAGAGGC GCCACTGAKA	180
GATCGTGGAA AGtATTAGGA gACTGCAAAT TCAGTCAGCG CAGGtCTCTT GTGGGGCCAT	240
TAATTGGCGG TGTTACAGCT TCGATATTAG GTTTAGTGC GTTACTGATG AGTATTGCCG	300
TTATTACTTT TATTGTCTGT ATTTCGGTG CATTAAAATg ATTGAAACGA &CATATGCC	360
AAaATCACAA ACACCAAATA TTAATAAAGG TnTTCGCCGT TCCAnTTnCA ATGTCTAAT	419

(2) INFORMATION FOR SEQ ID NO: 3971:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3971:

AAACTTGGGA GACTTCATA ACAGATTTAG GTTATCTAA AAATCAGGCA TATAATTCT	60
TAATTACATC TAGTCAAAGA TGGGGCCTTA ATCAAGGGAT AAATGCAAAT GGCTGGATGA	120
GAACTGACTT GAAAGGTTCA GAGTTACTT TTACACCAGA AGCGCCAAAA ACAATAACAG	180
AATTAGAAAA AAAAGTTGAA GAGATTCCAT TCAAGAAAGA ACGTAAATT AATCCGGATT	240
TAGCACCAGG GACAGAAAAA GTAACAAGAG AAGGACAAAA AGGTGAGAAG ACAATAACGA	300
CACCAACACT AAAAATCCA TTAACTGGAG TAATTATTAG TAAAGGTGAA CCnnAAGGAG	360
GGGTTTCCAn AGTCCGTTAT G	381

(2) INFORMATION FOR SEQ ID NO: 3972:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3972:

GGGTTTCAGAA CGTCGTGAGA CAGTTCGGTC CCTATCCGTC GTGGGCGTAG GAAATTTGAG	60
AGGAGCTGTC CTTAGTACGA GAGGACCGGG ATGGACATAC CTCTGGTGA CCAGTTGTGCG	120
TGCCAACGGC ATAGCTGGGT AGCTATGTGT GGACGGGATA AGTGCTGAAA GCATCTAAC	180
ATGAAGCCCC CCTCAAGATG AGATTTCCA ACTTCGGTTA TAAGATCCCT CAAAGATGAT	240
GAngTTAATA GGTCGAGGT GGAAGCATGG TGACATGTGG AGCTGACGAA TACTAATCGn	300
TCGAnGACTT AATCAAAATA AATGTTTGC GACCAAATCA CTTTACTTAC TATCTAGTT	360
GAATGATAAA TACATCATAT GCTGGnGCCA TACCAAGGGG	400

(2) INFORMATION FOR SEQ ID NO: 3973:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3973:

TCTTTAATT ACGTAATGGC TTACCAAGTTT TTAACATATG TGCAATTCTT TCATATGATT	60
TTTAGATTT TAGTAAGTCA ATAAGCCAA TTTCTCCAA CGATTGAATG TAACGTTGAT	120
TGATAAAATGT ATTTCTGGT AAATCACAC CCGCTAAAAT TGTGGCGATA TTTAAGGCAA	180
TATGATAATC ATGGTCGCTA ATAAAATGAC CCCGTCTTG CGCATCTAAT TGCCTTGGA	240
TCAATGCTT GAAGTCTTCA CCTAAAGCGA TATATTGATG TCTAGGATTGGAATATAGT	300
TTGTTCTGC TTCATATTTC GCACGTGTGA GCGCAACTTC GACACGnTGG TGCCTGGATT	360
nGAAAATAAA CCGGAnCCnG GGATCCACGG GAAATAACCC	400

(2) INFORMATION FOR SEQ ID NO: 3974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3974:

TGCCATGTT ACCTTGTAA AAATCAAGGT TTGTAATGTT TCCTTGTGTC ACGATAATAG	60
GCGTAATATC ACTCTTGCA TGATTGCGGA TGTAGTCTAA ATCAAAGTTG ATTAATAAAAT	120
CACCTGTTT AACTCTTGA CCTTCCTCAA CATGTAAAGT AAAGCCTTCT CCGTTAATT	180
TAACAGTGTCA TAAACCGATG TGGATTAATA GTTCTAAACC ACTATCTGAA TACAAGACCA	240
ATTGCATGTT TTGTTGGAA AATCAATTGT TACTTTACCG TTGAAATGGT GCACGAAACT	300
TCACCTTGTG AnGTTTTGG ATAGCGATAC CGTCACCCCCA TCCATTGTTT TTCGCTGAAA	360
CACTTGGATC AnGGCACTTC TGAATAAAATG GTGGTTAACT	400

(2) INFORMATION FOR SEQ ID NO: 3975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3975:

CCTTGCAGC GCCTCCGTTA CCTTTAGGA GGCGACCGCC CCAGTAAAC TGCCCGCCTG	60
ACACTGTCTC CCACCACGAT AAGnGCGGGn GTTAGAAAG CCAACACAGC TAGGGTAGTA	120
TCCCACCAGC GCCTCCACGT AAGCTAGCGC TCACGTTCA AAGGCTCCTA CCTATCCTGT	180

ACAAGCTGTG CCGAATTCA ATATCAGGCT ACAGTAAAGC TCCACGGGT CTTCCGTCC	240
TGTCGCGGGT AACCTGCATC TTCACAGGTA CTATGATTC ACCGAGTCTC TCGTTGAGAC	300
AGTGCCCCAA TCGTTAACGC CTTCGTGCG GGTCGGAACT TACCCGACAA GGAnTTTCCGC	360
TAACCTAGGA CC	372

(2) INFORMATION FOR SEQ ID NO: 3976:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3976:

AGGGAATCGA ATTTCTTTC TCTCCTnCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT	60
GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC	120
CCCATTGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA	180
GTAACGTCCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCT AAATAACTTA	240
ATCTATGTTT CCACCATTAA TATAAGTCAA ACGCTCACAT ACGGCTTCGT TTTCATTATT	300
TTAAAGCTCA TTTACATAAG TAAACTCTGC TTTAAATGAT TTAACTCATT GTCTGCTAAA	360
ACGGTTTnTT TTATGAAAAG GTTTGAAACG GGTTn	395

(2) INFORMATION FOR SEQ ID NO: 3977:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3977:

TTGGTCCCAA ACCAAGTGCT CTACCAAGCT GAGCTACTTC CCGTATAATT AACGCGCCCG	60
ATAGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG	120
GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTnnTTCA	180
CTCACGCAGA TTTTAAGTCC TGTGTCTG CCAGTTCCGC CACCCGGCA CTATAAAAT	240
GGAGCAGAAG ACGGGATTG AACCCGCGAC CCCAACCTTG GCAAGTTGTT ATTCTACCGC	300
TGAACTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA GGCTTAGATC	360
CTTAAGTCTA AGTGCCTCTG GCCAATTCC GCCAnACCCG	400

(2) INFORMATION FOR SEQ ID NO: 3978:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3978:

AAGTGGTTAA ATATTATAGA AAACATCAAA GGATGTTAAG AAATACAATT TATTACCCAG	60
CATTTAATAA TGGTGCTATA GAAGGAATTAA ATAATAAGAT AAAATTAATC AAGTGAATT	120
CTTTGGTTA CAGAAATTTC AACAACTTTA AAGCACGTAT AATGATGATT TTCAGCTTGT	180
ACAAAGGAGA AAAAAAGAAG ACAACCAAGC CCAATAATGG ACTGGCCGCC TAATAATAAA	240
AGCTCTAAAA GTTGTATTTT AAAAATAGTT CTTAAATTA TATAACCCACC ACATTTGGTG	300
GAGGAACCTA AAAAAAAGCA CTTCCCAAAA ATGGGAAAGT GCAGTrAGTG GAGCCATAGA	360
GGATTCCGAA CCTCGGACCC TCnGArT	387

(2) INFORMATION FOR SEQ ID NO: 3979:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3979:

TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCAACCTT GGCAAGGTTG TATTCTACCG	60
CTGAACTACT TCTGCATATG CGGGTGAAGG GAGTCGAACC CCCACGCCGT AAnTTAGCAT	120
CCTAAGTCTA GTGCGTCTGC CAATTCCGCC ACACCCGCAA ATGGT@GCC ATAGAGGATT	180
CGAACCTCTG GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTT	240
CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTT CAGTTGCTCT	300
ACCAATTGAG CTAGGCCGGn CAATATGTA GAATAAAATGG TGGAGAATGA CGGGTTTCGA	360
ACCGCCGAAC CCTCTGCTTG TnAAGGGCAG ATGGCTCnTC	400

(2) INFORMATION FOR SEQ ID NO: 3980:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3980:

TTACCACGTA TTTAGGTTTC TTTGGTGGCT CTAGATTGT CCCTATTGTC ACAGCATTG	60
CCGCAATCTT TTTAGGTGTA TTGATGTTT TCATTTGGCC AAGCATACAA GCCGGCATT	120
ATCATGTTGG TGGATTGTA AGAAAACAG GTGCCATCGG TACTTTGTT TATGGCTTCA	180
TCTTAAGATT GTTAGGTCCA CTCGGTTAC ACCATATTT TTACTTACCG TTTGGCAGA	240
CGGCACCTGG TGTTACTTTA GAAGTCAAAG GGCACCTAGT TCAAGGTACG CAGAACATCT	300
TCTTGCTCA ACTTGGTGAT CCAGATGTGA CGAnTATTAT TCCAGGTGG TCACGCTTTA	360
nGTCAGCCGT TTTAATACGA GGATGTTCGG CTAnGTGGTG	400

(2) INFORMATION FOR SEQ ID NO: 3981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3981:

CGACATACGC TGATAAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC	60
GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG	120
CTGGAACTAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GATACAATT	180
AAGTTGTTGC AACGCAAGGG AAGCGGAGAG ACAGTGTAGT GGATGGAGCA ACCTATAGTT	240
GGATTTCACCA GTTGTGACAC CACAACCGAA CCAAGCGACT GACTGAAGAT TTGGCAAAAT	300
GGnCATATTG ATATCACGCC TAATGAnTCC ATTCAAGGACA TTTAATTAAT CCAACTCAAG	360
CAATGGATAT TGCTTGACAC TGAAAAATGG GTAAAnTGGTG	400

(2) INFORMATION FOR SEQ ID NO: 3982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3982:

TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA	60
TAATGTTCAT ACAATTCTG GACAAGGTAC GCTTGCTAAA GAAAGCTAG AACAAAGCAAA	120
GTCTGACAAT GTTAACTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATT	180
AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG AAAATTATAG GTGTTGAACC	240

TTCAGTGCAA GTAGTATGTA TGAATCTGTT GTGGTAAATA ATCAGGTAGT CACATTGCCT	300
AATATCGATA AATTTGTGGG ACGGTGCATC TGTAGCTAGA GTTGGCGATA TTACATTGGA	360
AATTGCCAAA GAAAAGTAGA GGATTACGTT CCAGTAGAGn	400

(2) INFORMATION FOR SEQ ID NO: 3983:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3983:

CCACCATTAT TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT TTACCAAGCA	60
AAACCGAGTG AATAAAGAGT TTTAAATAAG CTTGAATTCA TAAGAAATAA TCGCTAGTGT	120
TCGAAAGAcG CGACAAGATT AATAACGCGT TTAAATCTT TTATAAAAGA AAACGTTAG	180
CAGACAATGA GTTAAATTAT TTTAAAGCAG AGTTTACTTA TGTAATGAG CATTAAAAT	240
AATGAAAACG AGGCCGTATG TGGAGCGTTT GACTTATnAA AAATG@GGGG AAACATAGAT	300
TCAAGTTATT GAAGGGCGCA CGGTGGGATG CCTTGGGCAC TAGnAAGCCG nTGGAAAGGAC	360
GTTACTAACG ACGATATGCC TTGGGGGAGC	390

(2) INFORMATION FOR SEQ ID NO: 3984:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3984:

GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTTGC CTTGTATCTG CAAATGTTT	60
GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTGACC ACAAAATTCAA ATGTATCAGG	120
CGTTTCTTT ATCCATTCA ATATATTCT TTCCGGTTGT ATCGCATAGT ATGTCGCATC	180
TAATTCGACA ACCGGAAAAT GTCCAGCATA TGTTTAAGT TTATCGGTTT GGCGTTCTAA	240
ATCTTCATAT AATGAATAGT G@TCACCCCCA ACCTGTTAAT CCGATGTTTT ATCATATATA	300
TCACCAATGT CATCATACCA TATAACTTT ATCATnATCA TTTCAGCGAA CTTTAGGTTT	360
GnAGGTTTT TGGCCTGGAT TAAAnATCTT TCGGGCGGAT	400

(2) INFORMATION FOR SEQ ID NO: 3985:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3985:

GCATTTGCTT ATATCTTAA AAAAGATTT GAAGATATTG AAGAAAAAC TAAAGAAATT	60
ATTCTGATA TTGAAAGTAA AAATAACTAA TAACATTTAG AGGCTGGAC ATAAATCCCT	120
AAAAAnCAGC AGTAAGATAA TTTCAATTA GAAAATATCT TACTGCTGTT CTCTATTTAT	180
ACAATACTTC GTATTGAAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTTGGTCTTC	240
GACTGGCACT GCTCCCTCAG GAGTCTCGCC ATTGAATACT ACGTATTAAC ATGTnAATT	300
TACTTGGAA ATACTTTAA AAAATAAGAC ACTTGGCCA ACTTGGCACA TAAATGTTAA	360
AATnCAATGA AATGAATTCT GTGTGTTGGG TCCCCTnCTA	400

(2) INFORMATION FOR SEQ ID NO: 3986:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3986:

TTCGTTCAAA GTCATCTAGG TCACATTATT CTATTGGGA TTCTTAGTGC TGTTCTTATT	60
TGCGGCTTTA ACGTCATCTA TTTCTTATT AGCAATTAAA TGTTTCTAAC TTCACGAAGA	120
ATGACAATAC AAAACGTAAA AAAGTCGCAG TGATCGGTAG TATTTAGTA TTTATCATTA	180
GTATTCCAGC AACCTTATCT TTTGGTATCT TAAAAGATGT AAGATCGGT GCGGGAACGA	240
TTTTGATAA TATGGATTTC ATCGTTCGA ATGTATTGAT GCCATTAGGC GCATTAGGTA	300
CTACGCTTGT CGTAGGnCAA TTATTAGnTA AAAAATTATT ACAnCAATAT TTTGGTAAAG	360
AnCGATTTAG GATTATTCAG TGGTTGGTAT TACTTAATTA	400

(2) INFORMATION FOR SEQ ID NO: 3987:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3987:

GGATTGAAAC	CCCCGCGAGC	CGTTAAGCCC	CTGTCGGTTT	TCAAGACCGA	TCCCTTCAGC	60
CGGACTTGGG	TATTCCTCCA	AAATTATATG	GACCTTGCAG	GACTCGAAC	TGCGACCGAA	120
CGGTTATGAG	CCGTTAGCTC	TAACCAA	ACTG	AGCTAAAGGT	CCTAAATATA	180
TAATAAAATAG	TGGCGGTGGA	GGGGATCGAA	CCCCCGACCT	CACGGGTATG	AACCGTACGC	240
TCTAGGCCAGC	TGAGCTACAC	CGCCTTATAT	AGTTTGAAA	TAATATGGTG	GGGACTAnCG	300
GGATCGGAAC	CGCTGGACCT	CCTGCGTGGC	AAAGCAGGCC	GCTCTCCCAG	CTGGAGCTAA	360
GnCCCCCATA	ATAATnACAG	TATATCnGGG	AAGACAGGAT			400

(2) INFORMATION FOR SEQ ID NO: 3988:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3988:

CAGCTGATAA	ACAAGTTGAT	CTGGTCCCGA	TTTGTGGGT	AAACGGTTGA	TTAATGnAAA	60
ATGTTCGCCG	AAGGATTCA	AATCCGAGAG	GTCTAATTCA	ACGTATCATT	AATCAAGATG	120
CGCCTATT	TCAATCTGAA	ACAAATTATC	ATTCGAAAGA	TCGCGGTAAG	TCTAAAATG	80
GTATTCAAAT	GGTGTATCAA	CATTTAATGA	ACGGTGTATC	GT	TTTATGGnT	240
TAGTTGGTGG	ACTCCTTATC	GCCATCGCGC	TGACTCCTAG	GCGGTGAACG	ACCATCCAAA	300
AGGATTAGTC	ATCCCAGATG	ATTCA	TTTG	GAAATCCATT	GAAAACCATG	360
CCTTTAAATT	AATGGTCCC	A	TACCA	GnCGG	GATAAACGCT	400

(2) INFORMATION FOR SEQ ID NO: 3989:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3989:

CCAGAGATT	CCGAATGGGG	GAAACCCAGC	CATGAGTTAT	GTCATGTTAT	CGATATGTGA	60
ATACATAGCA	TATCAGAAGG	CACACCCGGA	GAAC	TGAAAC	ATCTTAGTAC	120
GAAAGAAAAT	TCGATTCCCT	TAGTAGCGGC	GAGCAAACGG	GAGAGCCCA	AACCAACAAG	180
CTTGCTTnGn	GGTnTGTAGG	ACACTCTATA	CGGATTACAA	AGGACGACAT	TAGACGAATC	240

ATCTGGAAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT CGAAAATGTT GTCTCTCTTG	300
AGTGGATCCT GAGTACGACG GAGCACGTGG AAATTCCGTC GGAATCTGGG AGGACCATCT	360
CCT	363

(2) INFORMATION FOR SEQ ID NO: 3990:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3990:

TTTCCAAGAA CATGAGCCTG TACAGTTAAC ACCATGTnTG nTTCTTACTT CTTTATCGTG	60
GCTCCAACGT TCTCTGTACA TTTTTTCCCA TTCTCTACTT TTACTTTCTA GGATCGACCA	120
ATTCCCATT AATTTTCIG TTGGCTTAAA GAAATTCAAT CCAAATTTTC CCATATTTAT	180
ATCCTCCTAC GTATAAAAAT ACGATGTGTA GATGTCGTGT TTTAAATAC TTTAAAATGC	240
CCAAGACTAT TGCTTTAATT AGATTGTACA TTTTTTCACA AACATAAAAT ATTAGGGAAT	300
CACCTAATT A CTTAAGGnAT TCCCTATCAA TAACGGGATT TCATGAAAT AATACACAAT	360
CAGTAnGGTC AGCCTAATGC CAGGCTAAAT CGTTCAAATT	400

(2) INFORMATION FOR SEQ ID NO: 3991:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3991:

AAAGTGGTTA AATATTATAG AAAACATCAA AGGATGTTAA GAAATACAAT TTATTACCCA	60
GCATTTAATA ATGGTGCTAT AGAAGGAATT AATAATAAGA TAAAATTAAT CAAGTGAATT	120
TCTTTGGTT ACAGAAATT CAACAACTTT AAAGCAnGTA TAATGATGAT TTTCAGCTTG	180
TACAAAGGAG AAAAAAAGAA GACAACCAAG CCCAATAATG GACTGGCCGC CTAATAATnn	240
GAGCTCTAAA AGTTGTATTT TAAAAATAGT TCTTTAAATT ATATACCCAC CACATTTGGT	300
GGAGAACCTA AAAAAAAGCA CTTCCCAAAA ATGGAAAGTG CAAGTAGTGA GCCATAGAGG	360
ATTGGAACCT CTGACCCTCT GATTAAAAGT CAGATGCTCT	400

(2) INFORMATION FOR SEQ ID NO: 3992:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3992:

AGTGTATGGT TATCAAAGAT TTGATACGAC GGTCAATT ATTACCGTTA TTGTATTAGT	60
CATTATTGTC CAAGTGATTC AAACGCTAGG GAATGTTCTAGCTAGATTCA TACGTnGACA	120
TTAATGATAT ATAGTGAAGA TTTTGAAAGG AATTGATAGA ATGAAAAGAT TGATTGGTT	180
AGTTATCGTA GCACTTGTAT TAATTAGCAG CGTGTGGTGG TAACAATGAT AAAAAAGTAA	240
CAATTGGTGT CGCATCAAAT GACACTAAGG CTTGGGGAGA AGGTTAAAAG AATTAGCTAA	300
AAAAAGATGG ATnTTGATGT GGGAGATTAA GCACCCCTC nGGATTACAA TTTACCGGAT	360
TAAAGCCTTn AAATGGATGG TGATATTGAT AATGAATGCC	400

(2) INFORMATION FOR SEQ ID NO: 3993:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3993:

AAGAATTTC GACATTATC TCGTAAAGAA AACTTACAAC AATTGGTTGA TAAGCAATGG	60
TTATCAGAAC AACAAATCGA CATTACTG AATCATCCAT TAATCGATGA AGAAGTAGCC	120
AATAGTTAA TTGAAAATGT CATCGCGCAA GGnGCATTAC CCGTTGGATT ATTACCGAAT	180
ATCATTGTGG ACGATAAGGC ATATGTTGTA CCTATGATGG TGGAAAGAGCC TTCAGTTGTC	240
GCTGCAGCTA GTTATGGTGC AAAGCTAGTG AATCAGACTG GGGATTAA AACGGTATCT	300
TCTGAACGTA TTATGATAGG TCAAATCGTC TTTGATGGCG TTGACGATAC TGAAAAnTnT	360
CCGCCGGCAT TGAGAGCCTT AGA	383

(2) INFORMATION FOR SEQ ID NO: 3994:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3994:

GGTACTATGA TTTCACCGAG TCTCTCGTG AGACAGTGCC CAAATCGTTA CGCCTTCGT	60
GCAGGTCGGA ACTTACCGA CAAGGAATT CGCTACCTTA GGACCGTTAT AGTTACGGCC	120
GCCTTACTG GGGCTCGAT TCGTAGCTTC GCAGnnAAC CnACTCCTCT TAACCTTCCA	180
GCACCGGGCA GGCACACCC TGATACATCA CCTTACGGTT TAGCAGAGAC CTGTGTTTT	240
GATAAACAGT CGCTTGGCC TATTCACTGC GGCTCTCTG GGCGTTAACCTGAAAGAGC	300
ACCCCTCTC CCGAATTACG GGGTCATTG CCGATTCTT AACGAGATTC GCTCGCTCAC	360
CTTAGA	366

(2) INFORMATION FOR SEQ ID NO: 3995:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3995:

AGATATTTA CATGTGAATC AAGTAGGTAT TCATGATAAT TTCTTGAAAT TAGGTGGCCA	60
TTCATTAAGA GCAACGTTAT GnTGAATCGG ATAGAGGCAT CTACTGGAA ACGATTACAA	120
ATTGGTGTATT TATTACAAAA GCCAACTGTA TTTGAACCTAG CACAAGCGAT TGCTAAGGTT	180
CAAGAACAAA ACTATGAAGT GATTCCAGAA ACTATAGTTA AAGATGATTA TGTGCTGAGC	240
TCTGCACAAA AGCGTATGTA TTTATTATGG AAATCAAACC ATAAAGATAC GGTGTATAAC	300
GTACCTTTT TATGGCGGTT ATnCATCAGA ACTTAATGTA GCTCAnTGCG ACAAGCATG	359

(2) INFORMATION FOR SEQ ID NO: 3996:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3996:

CAATTATTGG TATTCAACTT AAAGATCATG ATGATTTAAT ACAACTCAAA CAACGTTnAA	60
ATCATTTCGA TCCTTCCAAT ATTTATATTA ATGAAAATAA GATGTTATAT TCATTGTTAA	120
TTAACACAT AGTAAGAAAA ACAGTCATAA ATTGATTTCT AATTGAAATC ATCTTATGAC	180
TGCTTTTAT TATACTTTAC ATTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA	240
AGCCATCTT CTTTGTGTT GCTTTTATTT TGACGTTTAGACATAAAA AAGAGACCTT	300
GCGGTCTCAA ATGCGGCTCA TCGCATCCAC TTTTGCGCTG GGCAACGTT CACTCTAGGC	360

GGAAnGTAAG TGGGACTTAC CATCGACGGn TAAGGGGCTT 400

(2) INFORMATION FOR SEQ ID NO: 3997:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3997:

GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC TTATCGTGGT GGGAGACAGT	60
GTCAnGCAGG CAGTTGACT GGGGCGGTGCG CTCCTAAAAG GTAAACGGAGG CGCTCAAAGG	120
TTCCCTCAGA TGGTTGGAAA TCATTCTAG AGTGTAAGG CATAAGGGAG CTTGACTGCG	180
AGACCTACAA GTCGAGCAGG GTCGAAAnCG GACTTAGTGA TCCGGTGGTT CCCGATTGAA	240
GGGCCATCGC TCAACGGATA AAAGCTACCC CGGGGATAAAC AGGCTTATCT CCCCCAAGAG	300
TTCACACGAC GGGGAGGGTTT GGCACCTCGA TGTCGnCTCA TCGCATTCTG GGGCTGTA	358

(2) INFORMATION FOR SEQ ID NO: 3998:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3998:

TAGGAGGAAT TTATATGACA TTTGAAAAAG AAACGGTCTT AAAAACATTA TTTCCTGAAG	60
ATGTACTTAG TATTGCTAAA GGTTAACAG ACGGTGAGT CGAATTTTA CAACAAGTAG	120
ATTCAATTGCT AGAAAGTAAG TACCGTGGAAA ATATTAATCA ACATTGGATA GACGCTACTG	180
TACCCGAGGA CTATTTAAA GATCTGGGAG ArTTAAATTA TTTAACArT CCATTACTT	240
ACAAGGATCG TCCAAACGCC AAAATGCCTA GTCAAnCTATT TCAGTTTTC ATGTCTTACC	300
TACTCGCGCG ATTTGATATT TCCTTAGCTA CCCTACTCGG TGTTCACCAA GGTTAGGGCA	360
TAACACTTTC TATTCGGAG GTAGCAAAGA CAAATTGCGA	400

(2) INFORMATION FOR SEQ ID NO: 3999:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3999:

CGCCCCTTAG TGCTGCAcTA ACGCATTAAG CACTCCGsCT GGGGAGTACG ACCGCAAGTg	60
AAACTCAAAG GAATTGACGG GGACCCGCAC AAGnGTGGAG CATGTGGTTT AATTGAGGC	120
AACGGtAGAA CCTTACCAAA TCTTGACATC CTTGACAAC TCTAGAGATA GAGCTTCCC	180
CTTCGGGGAC CAAAGTGACA GGTGGTGCAT GGTTGTCGTC AGCTCGTGTc GTGAGATGTT	240
GGGTTAAGTC CCGCAACGAG CGCAACCCTT AAGCTTAGT GCCATCATTA AGTTGGGCAC	300
TCTAAGTTGA CTGCCGGTGA CAAACCCAGG AAGGTTGGGG ATGACGTCAA ATCATCATGC	360
CCCTTATGGn TTTGGGTTAC ACAAGTGGTT ACAATGGG	398

(2) INFORMATION FOR SEQ ID NO: 4000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4000:

TGTTCTTGCA ACGCTATTa GTATCAGGTT TAACAACAGG TGCGACAAAA GGTTAGTTT	60
AAATTAGGAG TGGGGCAGAA TTGATAAAGA ACCACTAATG ACGATAAAGA TTAAAAGGAG	120
GACGTTATGA TGACGATTAA AGTTGGAATC ATTGGGTGTG GTGGTATTGC GAATGGCAAG	180
CACATGCCAA GTTTACAAAA AGTTGAAAAT GTTGAAATGA TCGCATTTC TGACGTAGAC	240
ATTTCGAAAG CAGCCaGTGC GGCAGAAGCA TACGGAACTG ACAATGSCAA aGTTATGAT	300
GATTACmAAG CaTTGTTAAA AGATGACACG ATTGATGTTA TCCATGTTT GTACCCCCAA	360
TGGACCCCGC ATTGTGG	377

(2) INFORMATION FOR SEQ ID NO: 4001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4001:

TCGGGTTCTC AAATCATCGA ACATAACAAA AGAA&TAAG CAACATGTAG GCCGTTGTCA	60
CTTAACCTCT TGTTTTCCG ATGACAGCTT CTATTTAGAG AATGTCATGA TTATTTATA	120
TTCACTTCAA TGTTATCAAT ATTAGTGCCA TCTATGACAT CTGCCATGCG ATTTCTTGT	180

AATTTTTGT GCAATTCAAA CGTGTACTTT CCACCGTTT TCATTTAAT ACAATTAA	240
CCTGAACCAA CGTTACCGTA CAGATTATT TTTCAATAA GTGTTTCTC AATTTAAAAT	300
CAAGTTCTT CAAGGAAATC TGTTCTTAG TAATCTTGAA TTCTGAAACA TCATGGnGA	360
TTGTACCGTA TnATCTTnCC TAGTAAT	387

(2) INFORMATION FOR SEQ ID NO: 4002:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4002:

CTATTACGAT TGCTGCGAAA GAAGGTATTA AAAATATACA AATAGGCATG GCTCACCGTG	60
GACGTTAAA CGTTTAAACG CATGTCTTAG AAAAACCGTA CGAAATGATG ATTCAGAAT	120
TTATGCATAC AGATCCAATG AAATTCTTAC CTGAAGATGG TAGCTTGCAG TTAACTGCTG	180
GATGGACTGG TGATGTGAAA TATCACTTGG TGGGCATAA AACTACTGAT TCATACGGTA	240
CAATGCAGCG TATTGCACTG GCTAACAAATC CAAGTCACTT GGAAATTGTT GCACCTGTTG	300
TTGAGGGGCG TACGAGAGCA GCACAAGATG ATACACAACG AGCTGGGCT CCGACGACTG	360
TCCATCATAA AnGCAATGnC CATTGTTGAT ACATGGCGAT	400

(2) INFORMATION FOR SEQ ID NO: 4003:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQID NO: 4003:

AGAAATATAT GCATTCGGA TATCATGGTA AAGAGAATGG ATTAAGCGGT AAATCACGTG	60
ATGAAGTGCAG CGCAAATGA AACAAAATT AGATGTCATG CGAGACGATA ATCAAAGGGA	120
CGACAGGTGA TGGGGTTGAA AGTGTAACTGn GCTACACTGG TCATGATGCT GCTAAACTAC	180
GTGATTATAA TGAAACACAT CATGCTTGT CTGGATATGA AATGATTGAC GCAGCAAAGG	240
TGCCATTGCA ACAAAATGAAG TCAATGCTGC GATGGGTATT ATTTGTGCAC GCCAACAGCT	300
GGTCCTCGG GTACCATTCC CGGTGCACCTT TTTAAATTAG GAAAAAACAC ATGATTAAAC	360
AGAAGAGCAA ATGATTGAT TTCTTATTCA CTTCAGCAT	400

(2) INFORMATION FOR SEQ ID NO: 4004:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4004:

TGAAATAGAA CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC	60
GTGCCTTTG TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT	120
GGAGCCGTAG CGAAAGCGAG TCTGAATAGG GCGTTAGTA TTTGGTCGTA GACCGAAC	180
AGGTGATCTA CCCTTGGTCA GGTTGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA	240
CTTACGTTGA AAAAGTGAGC GGATGAACTG AGGGTAGCGG AGAAATTCCA ATCGACCTGG	300
AGGATAAnTGG TTCTCTCCGA ATAGTTAGG GCTAGCCTCA AGTGTGATTA TTGAGGTAGA	360
nACTGTTGA CGAGGGGCC CGTCGGGTAC CGAATTCAAGG	400

(2) INFORMATION FOR SEQ ID NO: 4005:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 415 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4005:

ATACTAAGGC GTTATTAGAC GaTTAGACAA TGGTGTGATT AAAGGTGCAG CACTTGATAC	60
GTATGAATT TGATCAAAC TTTTCCCAAG TGATCAAAGG GGCAAAACAC TGAACGATCC	120
ATTGTTAGAA TCGTTGATTG ACAGGGAAGA TGTCATTTA ACACCACATA TTGCGTTTA	180
TACTGAAGCT GCAGTTAAA ATCTAATTGT CGATGCATTA GATGCAACAT TAGATGTATT	240
GGCAGACTGG AGATACTAGG TTACGAGTAA ATTAAAATC GAACTGATGA GATAATTGG	300
ATTGTTGGGG ATTCTGCATC CAGTTGATT TTTTAATTG GGTGTTGGAT GACGTTGnAA	360
TGTTGCCTAA TTTAAACGAC ATCGTAAACC nTGGATCCTC CAATGGCGTC CTTnC	415

(2) INFORMATION FOR SEQ ID NO: 4006:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 444 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4006:

CTAACAGAAG CTAGTATAGG AAATCGGTAC TCGTTAAGGC TGATCTGTGA TGGGGAGAAG	60
ACATTGTGTC TTGAGTCGT TGATTCACA CTGCCGAGAA AAGCCTCTAG ATAGAAAATA	120
GGTGCCCGTA OCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG	180
AACTCTCGTT AAGGAACCTCG GCAAAATGAC CCCGTAACCT CGGGAGAAGG GGtGCTCTT	240
AGGGTTAACG CCCAGAAGAG CCGCAGTGAA TAGGCCAAG CGACTGTTA TCAAAAACAC	300
AGGTCTCTGC TAAACCCGTA AGTGATGTAT AGGGGCEAC GCTGCCCGT GCTGGAAAGT	360
TAAnGAGAGT GGGTTACTTC TTGCGACTTA nCGAAATCGA GnCCCCAGTA AACGGCGGGC	420
CGTAACATAA ACnGTCCTAA GGTAA	444

(2) INFORMATION FOR SEQ ID NO: 4007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4007:

TTTGAACCTCT ATCAAAGCAT CAGCAATCAA AACATACGTA TCTTTACAAC AGTAATATG	60
CATTCTATGA TGCTTCTAAC TGAATTAAAG CATCGAACAA TCGGAAGCAT ATTTCTAAAT	120
TATTTATTCA TTATAGTCTT AAACATAACA TGACCTAATA TATTACTAAC CTATTAAAAT	180
AAACCACGCA CATCTAAGTG ATATACGACA ATCACAGCAA TAATAATTGC TTTAGAAAGT	240
CGTGCCTAAC TGGAACCTAC AAGTCTAGTT CGAACACACA CTGATGTGAG TGGTTTCTT	300
TATTTTAAAC ATGAACAATC AGATAAGTTA CTAGCATTAG CAAATATTAT TAAATCAAGG	360
GCTTCGnTTC ATAAATTAA AACATGTTAA ATTAGACGTG	400

(2) INFORMATION FOR SEQ ID NO: 4008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4008:

TATACTTGTT TTTACAAACC ACAAAAAGCT CTAACATTA GTTTAAACCA ATGCTTAGAG	60
CTTTCTAATT ATTTTATGCT TTAAAAGATA CTGTGTTATC TACGATGACC TTACCGTCTT	120

TAATAACTTT TTCTGCGTGA TTGATACCAA AATGATATGG AATATATTCA TGATTTGGTG	180
CATCCCAAAT TACTAAATTA GCCTTATCAC CTGTGTTAAT TGTACCCGCG TTAATGTCAT	240
TTGCTTTAGA GCCATTGACC GTAACAGCAT TCCAAACTTC ATTAGGTGAT AGCTTTAATT	300
TCAAGGCTGC AATGCCATA ACAAGTTGTA AGTTGTTGT GGACACTACT ACCAGGGTTA	360
TAATCAGTTG GCTAATGCCA TCGGCACCGG TTAATGGTCC	400

(2) INFORMATION FOR SEQ ID NO: 4009:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4009:

ACAAACATTG AAATTAGAGG TATATAAAAA ATGCTTCTGC AATAGATGCA ATAAACATGC	60
AATACAATAT GGAGGCGAAG TAAATGAAAA GTATTACGTT TGAAGAACAT TATGTCATTG	120
AAGATATTCA AAAAGAACG ATGAATGCGA TATCAGCAGA TCCTAAAGGT GTACCGATGA	180
AAGTAATGTT AGAAGGCCTT GAAAAAAAGA CAGGTTTAC AAATGCCGAC GAATTATCAC	240
ATCATGATGA ACGTATCCAA TTTATGAATA ATCAAGACGT TCAAATTCAA GTCTTATCTT	300
ATGGAAATGG TTCTGCTTCA AATTTGGTTG GTCAGAAAGC CATTGAATTAA TGTCCAAAAG	360
GCAAATGATC CATTGGCAA ACTATATTGC ACCATATCCC	400

(2) INFORMATION FOR SEQ ID NO: 4010:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4010:

ACTAGAGAAG GTATGTTACG TGACAATGAA TTACTAAATG GTATTTATTC ATCGAGTTAC	60
ATCTATAGTT TATTAAAATC AGAATACGAC CAAAAATGAC AAATTAGACT TACAAAAGAG	120
TGATGACATT TAAAATGGCA GCGCTTTTT ATTAAATTT TGAAAATAAA AGGTTGTTGA	180
CAGTATTATT TTATAACAAT ATAATGATTT TGATAATTAT TATCAACTAG ATGATGTTA	240
TGGGAGGATG CTTAAAACA GCCGTTTAA GTGTAATGTA TTATTTAGC GTGTAGGGAT	300
GCGAAAATAT ATTTATAGGA CACATCTGG GGATAATnGA TTTCTATAAT GAGGTGTCAA	360
ATGGAAAAGT TACCACGCTA TTATTAGCCn CCACGTATT	400

(2) INFORMATION FOR SEQ ID NO: 4011:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4011:

TnTCAATTAG AAAATATCTT ACCGCTGnCT CTATTTATAc AATCCTCGTA TTGAATGGnT	60
CGCTTTCCTA GGGTGCCGTC TCAGCATCGG CTTCGACTGG CACTGCTCCC TCAGGAGTCT	120
CGCCATTAAT ACTACGTATT AACATGTAAT TTTACTTTGA AATACTTTAA AAAAATAGA	180
CACTTTGCCA AACTTACACT ACCAATAAAA ACTTCTGTTA GAATTCCCTCA AAATGATATT	240
TCGCGACATG TTAATGAAAT TGTTGAAACG ATACCTGATA GCAAATTCGA TGAATTAGA	300
CATCATCGTG GCGAACATC CTATCATCCA AAGATGATGT TAAAAATCAT CTTATATGCA	360
TATACTCAAT CTGTATTTTC TGGTCGTAGA ATAGAGAAAT TACTTCATGA CAGTATTAGA	420
ATGATGTGGT TAGCTCAGGT CCAAACAnCT TCTnATAAAAA CTATTAATCG TTTTGGGGTG	480
GAATCCnAAT ACTG	494

(2) INFORMATION FOR SEQ ID NO: 4012:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4012:

TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTACTTTTT ATTGACGT TTTAGACATA	60
AAAAAAAGAGA CCTCACGGTC CAACTTGCT GGCAACGTT TACTCTAGCG GAAGTAATTG	120
GCTACCATCG TCGCTAAAGA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCCTCTC	180
CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGCGCTCTT TCTCGTTG	240
TCAGATTCAA ACGTTTCAC TTCGCCAAGC CATTTTCTT TGTGTTACT TTTTATTTG	300
ACGTTTTAGG CATAAAAAAA AGAGACCTTG CGGTCCAAT GCAGGCTCAT CGCATCCATT	360
TTTGCCCTG GGCAACGTT TnATnCCAGC GGAAAnTnAAT	400

(2) INFORMATION FOR SEQ ID NO: 4013:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4013:

CGAACTGCCG AACCCGAAGA GCGGATTAC AGTCCGCCGC GTTTACCACT TCGCTACCCC	60
TCCAGCTTAT TCATATAATT TAATAATCAA AATGGTGGAG AATGACGGGT TCGAACCGCC	120
GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT AATTCTCCAA ATAATGACT	180
CCTACGGGAC TCGAACCGT GTTACCGCCG TGAA A GGCG GTGTCTTAAC CGCTTGACCA	240
AGGAGCCATG GCTCCACAGG TAGGACTCGA ACCTACGACC GATCGGTTAA CAGCCGATAG	300
CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTTA CTCTnAGCGG	360
AACGTGAATT CGACTTACCA TCGACGNtAA GGAGCTTnAC	400

(2) INFORMATION FOR SEQ ID NO: 4014:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4014:

ATTAGGACCT CAAGACGATA TTACTAAATT TGAATACTTA AAAAATCTT CTCAAAATAC	60
AGGTACTTCA TTATTGGTAT TCAACTTAAA GATCATGATG ATTTAATACA ACTCAAACAA	120
CGTGTGAAAT CATTTCGATC CTTCCAATAT TTATATTAAT GAAAATAAGA TGTTATATTC	180
ATTGTTAATT TAACACATAG TAAGAnAAAC AGTCATAAAT TGATTTCTAA TTGAAATCAT	240
CTTATGACTG CTTTACATT ATACTTTACA TTTCTCGTTT CGTCAGATTc AAACGTTTC	300
ACTTCGCCAA GCCATCTTC TTTGTGTTG CTTTATTTT GACGTTTAG ACATAAAAAA	360
nGnGACCTGC GGTCTCAATG CGGCTTCATC GCATCC A TT	400

(2) INFORMATION FOR SEQ ID NO: 4015:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4015:

GAATGAAAAG CTCTAAAAGT TGTATTTAA AAATAGTTCT TTAAATTATA TACCCACCAC	60
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ATTTGGGGAG GAACCTAAAA AAAAGCACTT CCCAAAAATG GAAAGTGC _A GTAGTGAGCC	120
ATAGAGGATT CGAACCTCTG ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGACT	180
AATGGCTCTG AATGGCTGGG CTAGCTGGAT TCGAACCAAC GAGTGACGGA GnAAAGGTCC	240
GTTGCCTTAC CGCTTGGCTA TAGCCAATA TATAGATGGT GGAGGGGGC AGATTGAAAC	300
TGCCGAACCC GAGGAGGC _G ATTTACAGTC CGCCGCGTTT AGCCCAC _T TC GnTACCCCTG	360
CCAGnTTATT CATATGA	377

(2) INFORMATION FOR SEQ ID NO: 4016:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4016:

CCCAGAGTTT TnCACGAATA TATGGATATT TGATTGAGG ACTGTATTCA TACCAAGAGA	60
ATGACGCACC TGACATCCTC TCGGTTCAT _A TTCAGGCATA TCCGGACCAC AACTGGATA	120
GTCAGTTGT TGATTTCCC AGGTAATCAC ACATTTTC ACAAA _T ACTT TCCAAGAAC _A	180
TGAGCCTGTA CAGTTAACAC CATGTGTTGT TTCTTACTTC TTTATCGTGG CTCCAACGTT	240
CTCTGTACAT TTTTCCC _A TCTCTACTTT TACTTTCTAG GATCGACCAA TTCCCATTGA	300
AATTTTCTG TTGGCTTAAA GAAATCAATC CAAATTTCCC ATATTTATAT CCTCCTAAG	360
GTGAAAAATA CGGTGTGTAG AnGTCGTGGT TTTTnAAATA	400

(2) INFORMATION FOR SEQ ID NO: 4017:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4017:

CTTGAGCGC CTCCGTTACC TTTTAGGAGG CGACCGTCCC AGTCAA _A CTG CCCGnCTGAC	60
ACTGnCTCCC ACCACGATAA GGGCGTGGGT TAGAAAGCCA ACACAGCTAG GGTAGTATCC	120
CACCAGCGnC TCCACGTAAG CTAGCGCTCA CGTTCAAAG GCTCCTACCT ATCCTGTACA	180
AGCTGTGCCG AATTCAATA TCAGGCTACA GTAAAGCTCC ACGGGGTCTT TCCGTCTGT	240
CGCGGGTAAC CTGCATCTTC ACAGGTACTA TGATTCACC GAGTCTCTCG TTGAGACAGT	300

GCCCCAAATCG TTACGTCTTT CGTTGCGGGT CGGA~~A~~TTAC CCGACAAGGA ATTCGTTAC 360
CTTAGGACCT TATAGTTACG GCCGnCTTA ATTGGGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4018:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4018:

TGTCGATTAA AGAGGCATGC TACGAGGAAT GATTGGTCAT CCGAAAAAAAG ATCGAGCGGC 60
ATATGAGGCA CGCCAAGCGA TTCCAAACAT TAATGAAAAC AGTCCGCCAA TATT~~A~~TTGT 120
ACATGGAGGG AAAGACCAGC AAGTTGGTAT TCATCATGCG TATTATTTAG CGGACCAACT 180
AGAGTTAAAA GGTGCCACGC ATGnAACAT TTTATCAAAT GGCAGAAGGA CATGTGCCAA 240
GACCACCAGC GATGGTTGAA ACATTGACTT ATATTAAAGA GTTTATGAAC CAAGTTGAGT 300
CGCATAGCTT AGTTATGGAA ACGTGGTGTG CGCATGGGA ACTATTCAAG CTTTGGAGGA 360
TGTGGTACTT ACATGCGTTG GAATTAGGGG TCCGGTTACT 400

(2) INFORMATION FOR SEQ ID NO: 4019:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4019:

GGAGGTTTGG CACCTCGATG TCGGCTCATC GC~~A~~TCCTGGG GCTGTAGTCG GTCCCAAGGG 60
TTGGGCTGTT CGCCCATTAA AGCGGTACCA ~~A~~CTGGGTTTC AGAACGTCGT GAGACAGTTC 120
GGTCCCTATC CGTCGTGGC GTAGGAAATT TGAGAGGAGC TGTCCTTAGT ACGAGAGGAC 180
CGGGATGGAC ATACCTCTGG TGTACCAGTT GTCGTGCCAA CGGCATTAGC TGGGTAGCTA 240
TGTGTGGACG GGATAAGTGC TTGAAACATC TTAAGCATGA AGCCCCCTC CAAGAT~~G~~AG 300
ATTTC~~C~~CAAC TTCGGTTnT AAGATCCCTC CAAAGnTGAT GGAGGTTAA TAGGTTTCGA 360
GGTGGGAAGC AnGGTGGACA GTTGGGAGCT GGACGAnTAC 400

(2) INFORMATION FOR SEQ ID NO: 4020:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4020:

GAAGATGTTGTCATTCTTC AAATAAACCA GAGCTAGTTG CAATTGCTGA ACCAGCATCT	60
AATAGACCGA AAAAGAGAAG TAGACGTGCG GCACCCGGCAG ATCCTAATGC AACTCCAGCA	120
GATCCAGCGG CTGCAGCGGT AGGAAACGGT GGTGCACCAG TTGCAATTAC AGGCCATAT	180
ACGCCAACAA CTGATCCTAA TGCCAATAAT GCAGGGACAAA ATGCACCTAA CCGAnTnTTG	240
TCATTTGAT GACAATGGTA TTAGACCAAG TACAAACCGT TCTGTGCCAA CAGTTAACG	300
TTTGTAAATA ACTTGCCGGG CTTCACACTA ATCAATGGTG GGCAAAGTAn GGGTGTAG	360
TCATGCAATG GGTAAGAACG AGCATGTTG GATTCAGGG	400

(2) INFORMATION FOR SEQ ID NO: 4021:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4021:

CTAAGTCATG AATGGGAAGT GGCTCGCGTT GAAGAAGGAC TGACTACTGC TGCACACAG	60
CTTGCTAAC AATTATCAGA ATTAGATTG GCGTCACATC CTTTGAT GTCAGAGCAG	120
TTTGCAAGTn TAAAAGATCG TCCATTTCAT CCATTAGCTA AAGAAAAAAG AGGATTAAGA	180
GAAGCGGATT ATCAAGTGTA TCAAGCTGAA TTAAATCAAT CATTCCCTT AATGGTGCA	240
GCAGTTAAAA AGACACATAT GATTGATGGC GATACTGCAA ATATCGATGA ATTAGAAAAT	300
TTGACAGTAC CTATAAAAGA ACAAGCGACA GACATGTTAA AATGATCCAA GGTTATCAnT	360
AGATGACTAT GTACCATTCC GGTACnTCCT GGCCAT	396

(2) INFORMATION FOR SEQ ID NO: 4022:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4022:

GATTGGTCTG nAAGAAGAAT TAATGGAAAA GCTACGTGAA AAATTAGAAG CGGCATTTGA	60
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TACGATTAC GAATTGTCTC AAAACCGAAA AATAGATATG AGACTTGCAG CATATATCAT	120
AGGTATTAAA CGTACAGCAG AAGCAGCTAG ATATCGTGGT TGGGCATAAT TAATTATCAT	180
ATGTGATTTA ACGAGCTTGG GACAGAAAAC AAAGCCCTAA GCTCGTTAAT TTTATTTAG	240
CAGTAGTTGA CTGTAAAACA ATGCCGTGT AAACGCTCTT TTCAAAAATA GTCGGGGCCC	300
CAACACAGAG GCTGGTGGGA AAGTCAGCCT ACAATAGnGT GCAAGTTGGC nGGGGCCCCA	360
ACACAGAGGC TGGCGG	376

(2) INFORMATION FOR SEQ ID NO: 4023:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4023:

CAAATGGTGG AGCCATAGGA GGATTCGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT	60
CTACCAACTG AGCTAATGGC TCTTCCATGG nGCnGCCAG AGGACTTGAA CCCCCAACCT	120
ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC GGCAATATGT AAGAATAAAT	180
GGTGGAGAGT GACGGGTTCG AACCGCCGAC CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG	240
CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTT TCCTCTAGCG GAAnTAATTC	300
GGACTACCCT CGACGCTAAA GGAGCTTAAC TTCTGTGTT CGGCATGGGA ACAGGTGTGA	360
CTCCTTGCTA TATCACCAGA C	381

(2) INFORMATION FOR SEQ ID NO: 4024:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 4024:

GCCCCTTATG ATTTGGGCTA CACACGTGCT ACAATGGACA ATACAAAGGG CAGCGAAACC	60
GCGAGTCGAA GCAAATCCA TAAAGTTGTT CTCAGTCGG ATTGTAGTCT GCAACTCGAC	120
TACATGAAGC TGGAATCGCT AGTAATCGTA GATCAGCATG CTACGGTGGA ATACGTTCCC	180
GGGTCTTGTG CACACCGCCC GTCACACCAC GAGAGTTGT AACACCCGAA GCCGGTGGGA	240
GTAACCTTT AAGGAGCTAG CCGTCGAAGG TGGGGACAAA TGGATTGGGG TGAAGTCGTG	300
AACAAGGTAG CCGTGATCGG AAGGTGCGGC TGGGATCACC TCCTTGCTG AAGGATGATG	360

ATTCGGnAA CATCnTTCTT CCAGAAGATG CC~~G~~TAATAAA 400

(2) INFORMATION FOR SEQ ID NO: 4025:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4025:

CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGGG TGAGAATCCC GTCCACCGAT	60
TGCTAAGGTT TCCAGAGGAA GGCTCGTCCG CTCTGGGTTA GTCGGGTCTT AAGCTGAGGC	120
CGACAnGTAn GGCGATGGAT AACAGGTTGA TATTCTGTA CCACCTATAA TC G TTTAAT	180
CGATGGGGGG ACGCATAGGn ATAGGCGAGG TGCGATTGGA TTGCACGTCT AAGCAGTAAG	240
GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT	300
GTGTCTTCGA GTCGTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AA	352

(2) INFORMATION FOR SEQ ID NO: 4026:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4026:

TGGGGCTCTT CCCGTTTCGC TCGCCGCTAC TAAGGGAATC GAATTTCTT TCTCTTCCTC	60
CGGGTACTAA GATGTTTCAG TTCTCCGGGT GTGCCCTCTG ATATGCTATG TATTCACATA	120
TCGATAACAT GACATAACTC ATGCTGGGTT TCCCCATTG GAAATCTCTG GATCAAAGCT	180
TAC TTACAGC TCCCCAAAGC ATATCGTCGT TAGTAACGTC CTTCATCGC TTCTAGTGCC	240
AAGGCATCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTAA TATAAGTCAA	300
AnGTTAACAT GAAGTTAGGT TCTTTATAA AAGGATTAAA nGGGTTATTA ATCTTGTGnG	360
TGTTCTTCG	370

(2) INFORMATION FOR SEQ ID NO: 4027:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4027:

TCATGTTTCG CTTGGTTAA TGCTGTTAAT GCGTTATCGA CACGATGTTT TTCATCTGAA	60
ATTGTTGTG CAGTTGCATC GCCATTGTCA ATAACACGTT GAGCTGCAGT TATTCAGTT	120
TCTGCTTCCG CTTCTTCGCA TTATAGTTAT CAATACTTG TTGCGTCATA CCAGCAGTTG	180
ATGGTACTTG GTTCACAGAA CTTTGTAAGT TATTTTAGA CGTTACTAAT TGGCTATTAT	240
CTTCTTTATT TTGAAGTAAT GCTTTACTTG GATCAATCTT AGTTGTGCG CACGAACTT	300
AGTTAGTGC G TGCA GAA ACT TGTTGTGGTG TTGCACGCTC ATTnATGAAG CACTGTTGGT	360
GCCTCCGTTT TCGCATAnTG GATTGTTGTT GGCATGAGG	400

(2) INFORMATION FOR SEQ ID NO: 4028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4028:

CTCATCGCAT CCATTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC	60
CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTC CTCTCCTTCG	120
GCTCTCGCTT ACTCATTAG CTCTACTAAA CTCGTTGCGC TCTTTCTCG TTCGTCAGA	180
TTCAAACGTT TTCACTTCGC CAAGCCATT TTCTTTGTGT TTACTTTTA TTTTGACGTT	240
TTAGACATAA AAAAAAGAGA CCTTGC GGTC TCAATGCGGC TCATCGC ATC CATT TTTGC	300
CTGGGCAACG TTCTACTCTA GC GGG AACGn AAGTTGGGCT TACCATCGAC GCTAAGAAC	360
TTTCTTGGAC TTGGTGGACA AACGGn GTGG CTGCTTTCC	400

(2) INFORMATION FOR SEQ ID NO: 4029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4029:

AGGACTTGAA CCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC	60
GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCG AACCGCCGAC CCTCTGCTTG	120
TAAGGCAGAT GCTCTCCCAG CTGAGCTAT TCTCCGATTT AAAACTGCCT GGCAACGTTC	180

TACTCTAGCG GAAAnTAATTC GGACTACCAC CGACGCTAAG GAGCTTAAC TCTGTGTTCG	240
GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG TAATTTGATA	300
CATTCAAAAC TAGATAGTnA AGTAAAAGT GATTTGGnT TCGAAAACC ATTGATTT	360
GATTGAAGTC CTTCGATCGA TTGAGTGATT CGTGCAGCTn	400

(2) INFORMATION FOR SEQ ID NO: 4030:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4030:

GATGATAAAAT CATGTTTTC ATACCAAGTC GCTGCCGGCA AAACAATGTC AGAATATAAC	60
GGTGTGCG TCATTCTGAA GTCTAAAGAG ACCACTAAAT CTAACCTTACC TGTTGTTCT	120
TCACGCCACG TAATTCTTC TGGCTTTCA TCTTCATTG GTGTAGCTAA TAACCCTGAT	180
TTTGTGCCAA GTAAATGCTT CATAAAAGTAT TCTTGACCTT TTGCAGAACT TGAAATTAAG	240
TTTGAACGCC ATATAAATAA TGATTTGGA TGATTCTTT CAAATCAGGA TCTTCTATTG	300
CAAATTGTGG TTTGTnTTGG ATTTCACnTC ATCAATTGCA CGTTGAAAAA TCGCTTCATG	360
TGAATCTATA CCCTGCATCT TGTAGCnTCC	390

(2) INFORMATION FOR SEQ ID NO: 4031:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4031:

TGGTTCGAAT CCAGCTAGCC CAGTTATTGG CGGCATAGCA AGTGGTAAGG CAGAGGTCTG	60
CAAAACCTT ATCACCGGTT CAAATCCGGT TGCCGCCTCC AGGTTTATGCGGGAGTAGTT	120
CAACTTTAG AACACGTTCC TTCCCGGAAn GAGGTATAGG TGCAAATCCT ATCTTCCGCT	180
CCATAATTAA ATAATAATGC GGGAGTATT CAACTCTTAG AATACATTCC TTCCTGGAAT	240
GAGGTATAGG TGTAAATCCT ATCTTCCGCT CCATAATTAA ATATTGCGG GGAGTAGTTC	300
CAACTTTAG AACACGTTCC TTCCCGGGAA GGAGGTATAn GTGTATCCTA TCTTCCGCnC	360
CATAATGCCT TCCAAAGGGG AATTTTTGG TTTnACCATT	400

(2) INFORMATION FOR SEQ ID NO: 4032:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4032:

GTATCGATGA GTTTCTTCGG TGCCTTCTCG ACAGCCATT TGACTTCGAC AAAATGCATC	60
ACATCGGGAT GACCATTAAT TGCATTAAAC GTGTCTTGT AATCTTTGA TGATTCAACG	120
TCATGAATTT CAACATTTT ACCACCAAAT ACAGCTGGTA AAGCTTATA ATCCCACATG	180
TGAATTCAT TATAAGGTTC ATACATGCCG TGAATAAGTC GTTCTACCGT rTrGCCGTCA	240
TTATTAATCA CCAATAATAC CGGGTTAATA TGCTGTCTAA TCATAGTTGG AATAGCTTG	300
AACAGTTAGT TGGCCATGAG CCATCACCCA TTTAATAATA AGTTACGACG GATCTTGTT	360
CTGCCAATTG GGGGAnCnCA ATGTTGCAGG GnAATGGTAT	400

(2) INFORMATION FOR SEQ ID NO: 4033:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4033:

CACGACGTTTC TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCTTgGG	60
ACCGACTACA GCCCCcAGGA TCGATGAGC CGACATCGAG GTGCCAAAct CCCCGTCGAT	120
GTGAACCTTT GGGGGAGATA AGCCTGTTAT CCCCGGGTA GCTTTATCC GTTGAGCGAT	180
GGCCCTTCCA TCGGAAACCA CCGGATCACT AAGTCCGTCT TTGACCCCTG CTCGACTTGT	240
AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTCC AACCAATTCTG	300
AGGGAACCTT GAAGCGCTCC GTACCTTTA AGAnGGCGAC CGGCCAGTC AACTGGCCG	360
CTGACACTGT CTTCCAACAC GATAAGTGGT GCGGGTTAGA	400

(2) INFORMATION FOR SEQ ID NO: 4034:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4034:

AATTCCATGT GTACGGTTGA AATGCGCAGA GATATGGAGG AACACCA&G nCGAAGCGAC	60
TTTCTGGTCT GTAACGTGACG CTGATGTGCG AAACGTGGGG ATCAAACAGG ATTAGATAACC	120
CTGGTAGTCC ACGCCGTAAA CGATGAGTGC TAAGTGTAG GGGGTTCCG CCCCTTAGTG	180
CTGCAGCTAA CGCATTAAAGC ACTCCGCCCTG GGGAGTACGA CCGCAAGTTG GAAACTCAAA	240
GGAATTGACG GGGACCCGCA CAAGCGTGGn AGCATGTGGT TTAnTCGAA CAACGCAGAG	300
AACCTTACCA AATCTTGACA TCCTTGACA ACTCTAGAGA TAAAGCCTCC CCTTCGGGGA	360
CAAATGACAG TGGTGCAnGT TGTCCCTCACT CGTGTGCGTGA	400

(2) INFORMATION FOR SEQ ID NO: 4035:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4035:

TTCGCTTTGC CCGTCTGTCA CATTACTGTA AAATTCTATA AATAGAATTT TTGATGACGG	60
GTCCCTTCCT AGGGTGCCGT CTCAGCCACC CCAACCGGCA CATTGTTGTA AGCTGACTAT	120
ATGTCACTTC TGTGTTGGGG CCCCTGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC	180
CATTAATACT ACGTATTAAC ATGTAATTTC ACTTTGAAAT ACATTAAGCCAAATTAAT	240
CAAAGCTTT CTGAACCAGA AACGAAAAAA ATCTATAGTC ATAGAAAAAT TTATGTAGAG	300
CCTGTTTTG GATTTATGAA GGCTATTGG GGTCACTCG AATGTCAGTT CGAGGAATAA	360
TnAAGTnAAC GAGAGCCAGG TTTGTAATTA TGGCACTnAT	400

(2) INFORMATION FOR SEQ ID NO: 4036:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4036:

TAAATGTTGA AAAAGCACGA TTAGATAGAA TTTGAAATAA CAATGAAATT CGTCAAATGA	60
TCACAGCATT TGGTACAGGA ATCGGTGGCG ACTTTGATCT AGCGAAAGCA AGATATCACA	120
AAATCGTCAT TATGACTGAT GCCGATGTGG ATGGAGCGCA TATTAGAACCA TTGTTATTAA	180

CATTCTTCTA TCGATTATG AGACCCTAA TTGAAGCAGG CTATGTGTAT ATTGCACAGC	240
CACCGTTGTA TAAACTGACA CAAGGTAAAC AAAAGTATTA TGTATACAAT GATAGGGGAC	300
TTGATAAACT TAAATCTGAA TTGAATCCAA CACCAAAATG GCTATTGCAC GTACAAAGGC	360
TTGGAGAATG AATGCAGTCC ATTTGGGAAC ACATGACCTG	400

(2) INFORMATION FOR SEQ ID NO: 4037:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4037:

TCGTCGCTAA AGACCTTCT TGACTTGTGA CAATCGCTTG CTTCTTCCT CTCCTTCGGC	60
TCTCGCTTAC TCATTTAGCT CTACTAAACT CGTTGCGCTC TTTTCTCGTT TCGTCAGATT	120
CAAACGTTTT CACTTCGCCA AGCCATTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT	180
AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA TTTTTGCCT	240
GGCAACGTTTC TACTCTAGCG GAAnTAAATT GGGCTACCAT CGACGCTAAG AACCTTCCTT	300
GACTTGTGAC AATCGCTTGC TTCTTCCTC TTCTTCGGCT CTCGCTTACn CATTAGCTC	360
TACnAAACTC GTTGCCTCT T	381

(2) INFORMATION FOR SEQ ID NO: 4038:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4038:

CTGTTTGCA TACTTCATAA ATCCTTTAAA TTCACCCATC GTATCTCCCC CTTTCCTTAA	60
TACACAAACGG CTGGTTTATG TTTAGCATCG ATTGTTTAC TGTCATCGTA AAATGCAGCT	120
AACATCGCTT CATCTTCATT GTCATGTAAT GATTGTGCA AATGAATTT TTGCATCATT	180
AATTGATAAT CTTTAGGAAT AACTTTAACG ACGACATCTT CAATGCGATC AAAATGTTT	240
AACACATGAA TCGCTCTCGT ACTATTCTG TGTGACACAT GTnCTTCCAG CATTGCTTA	300
ATGAATGCTT TTnCTTCTTG GTGTTAACG AAAGCGTATC TAGTGATAnG	360

(2) INFORMATION FOR SEQ ID NO: 4039:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4039:

AGTGCAGAAC	CATAACCTCT	TGATCCGTAG	TCAAACGCTC	TATCCAATTG	AGCTACGGGC	60
GCATATGTTT	TTATTGAAAA	TGGTGCCGAG	GACCGGAATC	GAACCGGTAG	TGA _n TGCACT	120
CACCGCAGAT	TTTAAGTCCT	GTGCGTCTGC	CAGTTCCGCC	ACCCCAGCAC	TATAAAAATG	180
GAGCAGAAGA	CGGGATTCTGA	ACC _n CGACC	CCAACCTTGG	CAAGGTTGTA	TTCTACCGCT	240
GAACACTACTTC	TGCATATGCG	GGTGAAGGGA	GTCGAACCCC	CACGCCGTAA	GCT _n AGGATC	300
CTAAGTCTAG	TGCGTCTGCC	AATTCCGCCA	CACCCGCAAA	TGGTGAGCCA	TAGAGGATTC	360
GAACCTCTGG	ACCCTCTGGA	TTAAAAAAGTC	AGATGCTCTA			400

(2) INFORMATION FOR SEQ ID NO: 4040:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4040:

CTTTCTTGAC	TTGTGACAAT	CGCTTGCTTC	TTTCCTCTCC	TTCGGCTCTC	GCTTACTCAT	60
TTAGCTCTAC	TAAACTCGTT	GCGCTCTTT	CTCGTTCGT	CAGATTCAAA	CGTTTCACT	120
TCGCCAAGCC	ATTTTCTTT	GTGTTTACTT	TTTATTTGA	CGTTTAGAC	ATAAAAAAAAG	180
AGACCTCACG	GTCTCAACTT	GCCTGGAAC	GTTCTACTCT	AGCGGAACGT	AAGTTGGCTA	240
CCATCGTCGC	TAAAGACCTT	TCTTGACTTG	TGACAATCGC	TTGCTTCTTT	CCTCTCCTTC	300
GGCTCTCGC _n	TACTCATT	GCTC _n ACTAA	ACTCGTTGCG	CTCTTGTCT	CGTTTCGGGC	360
AGATTCAAAC	GnTTGTCA					378

(2) INFORMATION FOR SEQ ID NO: 4041:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4041:

GTACCTAAC AATATCTGA AATGGACGAA CTAATTATG AACCGCATGA AAGGATACTT	60
GCGAATCATT TGAGCATGCT TGAATCATAA TATCACCATC GCTGTAATCG TCTATTAACT	120
GATCATTGG AAAATGCGGT AAATCTTAA AGGCATCGGG AATTTACTA GATAACCCAA	180
TTTCCTTCAT CAAAGACTTA CTAATCCCAA AGGTAATCGT TAACTTGCTT GCACCTAAC	240
CTATCGATTC ACCGGTATCT ACTGGTGGGC ATTAAAGGAT TGTTACTCGG GCTTGGCCAA	300
CTGTATCACCA ATCCATCATA CGATTCAAGCC ATAACGGTCC ACTTTTTAA ACATTGGCTT	360
TATTGGCACC CnAACCTTG GACTTCnAAT CTAACGGCCA	400

(2) INFORMATION FOR SEQ ID NO: 4042:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4042:

GACTTGCAAA CGTTGTGATG ACGGTCAAGA AAACCTGGTAA CACACCAGAC GGACGTAAAG	60
CTGGCGAACCTTTGCTCCA GGTGCAAACC CAATGCATGG CCGTGACCAA AAAGGTGCAT	120
TATCTTCATT AAGTTCTGTA GCTAAGATCC CTTACGATTG CTGTAAGAT GGTATTTCAA	180
ATACATTCACTATCGTACCA AAATCATTAG GTAAAGAACCC AGAAGATCAA AACCGTAAC	240
TAACTAGTAT GTTAGATGGT TACGCAATGC AATGTGGTCA CCACCTAAAT ATTAACGTAT	300
TTAACCGTGA AACATTAATA GATGCAATGG AACATCCAGA AGGAATAAC ACAGTTAAC	360
ATCCGTGTAT CTGGTTACGC TGTTAACTTC ATTAAATTAA	400

(2) INFORMATION FOR SEQ ID NO: 4043:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4043:

CTATTTATC TAAAGTTAAA CCTGACCCAC CTAGAATTGA CGCAAACCTCT GTGACATATA	60
AAGCAGGTCT TACAAACCAA GAATTAAAG TTAATAACGT ATTAAATAAC TCGTCAGTAA	120
AATTATTTAA AGCAGATAAT ACACCATTAA ATGTCACAAA TATTACTCAT GGTAGCGGTT	180
TTAGTTCGGT TGTGACAGTA AGTGACGCGT TACCAAATGG CGGAATTAAA GCAAATCTT	240
CAATTCAAT GAACAATGTG ACGTATACGA CGCAAGACGA ACATGGTCAA GTTGTACAG	300

TAACAAGAAA TGAATCTGTT GATCAAATG ACAGTGCACA GTAACAGTG GACACCACAA 360
TTGACAAGCC AACTACTGAA GGCGCnGTGn TTATTAAAAG 400

(2) INFORMATION FOR SEQ ID NO: 4044:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4044:

AAAATGGCTT GATTTGAAAA ACGACCAGCA TGCGCTACTG GnATAATAGC GAGGCTACCA 60
TGTGTTCA TCGTAGnCGC ATGTTAGTTA ATCCAGGGAT ACAACATCA TGATCAATAT 120
TAAAGCCATA TTCAAACAAT TGACCATAAG GTTCAATGTA AGCAGCGCCG GTGCACTTGC 180
ATTCCAGCTG AATTAGAGCG ACGTGCAGCA TAAGCCAAGT CTTCTTTGT AATATAGCCT 240
TCTTTGTTG ATGTGTTAC GGTCCATTGG GTGGATAATA CAAAGCGATT CGAAATTTG 300
ATGCCATTAG GTAAGTGGAT TGATTGTAAA AGTGGTTGT ATCGGTACAT ACTATGATTC 360
CnTTCCATT GCAAT 375

(2) INFORMATION FOR SEQ ID NO: 4045:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4045:

GTTCCAATGA AGATAGCTAG AAATGATATC CAAAACACAT GATGCATCAC TGGTGATGCT 60
CGACTAATTG TATTCCATGA TGCATTAATA ATAATGACCA ATACACATAA AATAAGCAGC 120
CATTTATCGT TTATTTAAA AATATAATGC AGCAAAAATC CCAAAATGAT TAATTGCACA 180
ACTGCTCGTA ATGTCGCAAC AATTAAATCT TTAATAATAT GTAAACCTTC TTTATATGAA 240
ATGATAATCG GAATGACTAA AAGCAATGCC GTCAATCCAA GTGCCnATT ACTCATGTnG 300
ATTCAACTCC TCTGTATTAG AAATTTGACC ATCAACAATT GTTATACGCT TTTTGnAAGT 360
GGTCGCATAC TTTGGGGCAT CGCTGTGGGG TAGGGGGnCn 400

(2) INFORMATION FOR SEQ ID NO: 4046:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4046:

CGAGTCTGAG TCGCTGTCTG AATCTGAATC GCTGTCTGAG TCCGAATCGC TATCTGAATC	60
TGAGTCGCTG TCTGAGTCTG AATCGCTATC TGAATCTGAG TCGCTATCTG AGTCTGAGTC	120
GCTGTCTGAG TCTGAGTCGC TGTCTGAGTC TGAATCGCTA TCTGAATCTG AGTCGCTGTC	180
TGAGTCTGAG TCGCTATCTG AGTCTGAGTC GCTGTCTGAA TCTGGAGTCG CTGTCTGAAT	240
CTGGAATCGC TGTCTGGAGT CTAATCGCT ATCTGAGTCT GGAATCGCTA TCTGAGTCTG	300
AATCACTGGT CTGGAGTCCG AGTCACTGTC TGAATCTGAC TGCACAnACn GGATTCTGAG	360
TCGCTAACnG GAATC	375

(2) INFORMATION FOR SEQ ID NO: 4047:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4047:

ATGGGTAAAA AGGCATTAGA GTCAATCATT GATAACGCTG AAAAAACAAC TCAAGAGCGT	60
TTACGTTCAAG GATATGAAGA TGCTGTAGAT TATAACCGTT ATGTCGGTAA TATTTATACT	120
GGATCATTAT ATTTAAGCCT AATATCATT A CTTGAAAATC GAGATTACAGA AGCTGGTGAA	180
ACAATCGGTT TATTCAGTTA TGGCTCAGGT TCAGTTGGTG AATTTATAG TGCGACATT	240
GTTGAAGGCT ACAAAAGATCA TTTAGATCAA GCTGCACATA AAGCATTATT AAATAACCGT	300
ACTGAnGTAT CTGTTGGATG GCATATGGAA ACATTCTTCC AACAGTTTG GATGACGGTG	360
GAATTTGACG GnGGACCAAG ATGCnTGTTC CAGGAGGTCC	400

(2) INFORMATION FOR SEQ ID NO: 4048:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4048:

CAAACCATCT GACATAATAT ACACCTGGAT GTTAGATAAG GGTTTGCCAA TTGGAATCGT	60
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CTCAGGTATC AATCACCA CA ATGATGTGAC CAATACGATG TGATGACTGT TGACTCAGAT 120
GGTCCATAGG CATTGAAATA CGTGCCACAA TGCTTCTCAA TATATTTAAC AAAGGATGCC 180
GTACTAGTTG CCCCGCCTGT AATCAACTTT TCAATATAAA AGTTCGCAT AACACTACAC 240
ATCTGTAACG GAATCGACGC AACCGTCACA CGATGCTTAT TAATGAGTTG TTGTAACTGT 300
TCTGGATTAA CACGnTCCTC TCTATCTGGA nTCACAAGCG TATGACCATT AACAAACAAAC 360
AATAAAATCTC CATAACTGnT GCATCAAAAAA CATATTGCAT 400

(2) INFORMATION FOR SEQ ID NO: 4049:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4049:

TCTGCATGTT CTCGAGATCC ACCAAATGTT AAATGGGTAT GTGCATCTAC TAATGCTGGG 60
GACACTACCT TCCCCTAGC ATCAATCGTC TCAGTCGCAT CGTAGTCATC TGTATGTGTT 120
CCAGCATATA CAATTTGGC CATCTTAAT GACAACGTGTA CCATTTTCA CAACATTTGA 180
ATTCACTCAA TTCCTTACCC TTCAAAGGTT TATCTGTTGA TCTCGGTAAA ATTAATTGCT 240
GCTATATGAT TAATTTAAA TCATTCACTA CTATCACCTG CTTATCAATC ATGGAATAGA 300
ATACCTTTTC nTTAGCGTTT GAATAGCGAG TCATAGCCAG CATCAACATG TCGGGCAACA 360
CCCATACCGG GGTCACTCGTC CAATACACGT TCCAAAnCTnC 400

(2) INFORMATION FOR SEQ ID NO: 4050:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4050:

ATCACCCATG TTCTGACTCC CAAGTTAAAT TAATTGGCAT TCGGAGTTG TCTGAATTG 60
GTAACCCGAG AGGGGCCCCCT CGTCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG 120
GCTAGCCCTA AAGCTATTTC GGAGAGAACCC AGCTATTCC AGGTTCGATT GGAATTCTC 80
CGCTACCCCTC AGTCATCCG CTCACTTTTC AACGTAAGTC GGTTCGGTCC TCCATTCACT 240
GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACAAATA 300

CTAAACGCCT ATTCAAGCTCG nTTCGTACGG CTCCACATTT ACTGCTAAnC TTGCATCAAT 360
CGTACTCGCG GTCAATCTAC AAAAGnACGC ATCACCAAnTA 400

(2) INFORMATION FOR SEQ ID NO: 4051:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4051:

AGTGAAAATG ACTTTATCGG GCTGTTCAAC GCGACTAGGT 60
AACAAATGTCA AAGAACGTAC TGCTTTAAC TCTAAAGTCA TGTTAATCT TGACGACTTA 120
CCATTGTTTC ACAGTGACAT GGAAATTGAT ATGTTAGGTG AECATATGA ATTCTAATC 180
GGCGCCTTG CGGCGACAGC GGGTAAAAAA GCAGGCGAGT TCTATACACC ACAACAAGTA 240
TCTAAGATAAC TGGCGAAGTT GTCACAGACG GTAAAGATnA ATTACGTCAC GTGTAACGAC 300
CCAACATGTG GGnTCCGGTT CATTGTGGTA ACGTGTGGT AAAGAACGCA AGTGTATCGT 360
TAATTGGAC nAAGAACGTA ACAATACTAC nTACGACTTA 400

(2) INFORMATION FOR SEQ ID NO: 4052:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4052:

TCCTACAAACC CCAACAAAGCA AGCTTGTGGT GTTGGGCTCT TCCCCTTCG CTCGCCGCTA 60
CTAAGGGAAT CGAATTTCCT TTCTCTTCCT CCAGGTACTA AGATGTTCA GTTCTCCGGG 120
TGTGCCTTCT GATATGCTAT GTATTCACAT ATCGATAACA TGACATAACT CATGCTGGGT 180
TTCCCCATTC GGAAATCTCT GGATCAAAGC TTACTTACAG CTCCCCAAAG CATATCGTCG 240
TTAGTAACGT CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGGC CCTTAATAAC 300
TTAATCnATG TTTTCCACCA TTTTTTATAA GTnCAAAGGC TTCATACG GCTTCGGTTT 360
TTCATTAATT TTAAATGGCn CAATTAAACA 390

(2) INFORMATION FOR SEQ ID NO: 4053:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4053:

AACATACCGA TGTATATAAT CTATACACAA AGGATAATT A CTTATGC AAA GGC GGAGG AA	60
TCACATGTCT ATTACTGAAA AACAAACGTCA GCAACAAGCT GAATTACATA AAAAATTATG	120
GTCGATTGCG AATGATTAA GAGGGAACAT GGATGCGAGT GAATTCCGTA ATTACATT TT	180
AGGCTTGATT TTCTATCGCT TCTTATCTGA AAAAGCCGAA CAAGAATATG CAGATGCCTT	240
GTCAGGTGAA GACATCACGT ATCAAGAAC GC ATGGGCAGAT GAAGAATATC GTGAAGACTT	300
AAAAGCAGAA TTAATTGATC AAAGTCGGTT ACTTCATTGA GCCACAAGAT TTATTCAGTG	360
CGATGATCGT GAAATTGAnA CGCAnGATT T CCGATATAGA	400

(2) INFORMATION FOR SEQ ID NO: 4054:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4054:

GTAAGACCAT CGTACTTGAG TCTTCAAGTG TTC TTGATAA AACGGAACGA GAGACTTG GT	60
ATTTTCGAA CAAATCTTC ATTAACACAC CGACCATAATAATTACAATC GAAGCAACAC	120
CTGCAGCGAA TACAAGCGCA ATACAACAAA TAACAGTAAT ACATATTAAA CTT CCTACAG	180
AATGGATGCC TTTAGAAATA GTAGTTAATA AGACTTCTAA ACATCCTGCT TTTCTACAA	240
TACCTGCAA TGCATATCCG CAAAATATCG TTACTAATAT TTGGGnCATA CTCATCATAC	300
CACCTGTTCA TAACAAGCTT TCACACTGGA TGAATATGAG nTGATGTATC ATTGATCGTT	360
AAACCTAAT GTGCTTGAA CCATCGTCAT TTGAATGTGA	400

(2) INFORMATION FOR SEQ ID NO: 4055:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4055:

CGTCTACAAG TTCAAAATTC AAGTCTCCA TAATTGGTTT AACAAATCACT TCTACTTG TT	60
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CTGTAATTT ACTCATACAG GCCTCCCTT TTGGCAAATA GAAAAGAGCG GGAATCTCCC	120
ACTCTTCTGC CTGAGTCAC TAATTTTAA GCAACTTAAT TATAGCATAA GTTTATGCTT	180
GAAACAAATG ACTTCACTAT TAATCAGAGA TTCTGTAAA AGTTGTTCC TTTATTCAC	240
CATTACATTT GAATAGACTC GTAAGACATT GAAAAGAAAT AGGGCATAA TTTGTGTCC	300
AGCAGCAATT TTGTATTTCT TTGACTACGG CATA CGGATT AAATAAATAC CTTGATTATT	360
TCATTTACA TATCAAATAT CGGAAGTTGA GCTTTATCTG	400

(2) INFORMATION FOR SEQ ID NO: 4056:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4056:

ATTTGGTTT ACTTCATGTT GAGTTTAGA CATTAAACC ATCTCCAATA TAAAAATAAA	60
TTAAATTAAA TTCTCAGGGA CTTGCATGAC GCCACCTGTA TTTGCCTAG TTACTAGGGC	120
AGTATAACGA GCTAGATAAC CTGTTTTAC TTTCGCTTTA AATGGTGTAA AAGATTCTCG	180
GCGACGCGCT AGAACATCTT CAGGCTGGTT TACGTTTAAT GTACGATTTG TTAAATCAAT	240
AGTAATCTCA TCACCATCTT CAATTA _n G _c AATTGGTCCA CCAGATGCAG CTTCAGGGGA	300
AATATGaCCA ACTG _c AATAC CTCTTG _G ACCCG _t AAAA ACGCCCATCA GT _k AATTAAT	360
GC _a ACATCTT TACCTAAGCC GCGaCCAACA ATAGAGGAAG TAGGTGCTAA CATTTCAGG	420
nCATACCTGG GTCCACCTTT TAGGTGCCTT TCA _n TATCT _n ATG _a CAACG AC _c GTGGGCCT	480
G	481

(2) INFORMATION FOR SEQ ID NO: 4057:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4057:

TTTTGCCTG GCAACGTTCT ACTCTAGCGG AACGTAAGTT GGCTACCATC GTCGCTAAAG	60
ACCTTTCTTG ACTTGTGACA ATCGCTTGCT TCTTCCTCT CCTTCGGCTC TCGCTTACTC	120
ATTTAGCTCT ACTAAACTCG TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTCA	180
CTTCGCCAAG CCATTTTCT TTGTGTTAC TTTTATTT GGACGTTTA GACATAAAA	240

AAAGAGACCT TGCAGGCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCCTG GCAACGTTCT 300
ACTCTAGCGG AAGTAAATTG GGCTACCAnC GACGCTAAGA ACCTTTCTTG GACTGTGACA 360
ATCGGCTGCn TCTGTnCCT 379

(2) INFORMATION FOR SEQ ID NO: 4058:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4058:

CTGCATCACT GCCATAAAAAA CTACCGTCAG CAGCGATAGn CGGCCAATCA TACCAGGAAC 60
AAGACCGGGC TTGTCAGCGA TACTAACAGC GATATATCCAGCTAGTATTG GAACCATAAA 120
TTTAAAGGCT AAACTACCAA TGTTTCAAT GGATTTCCAA AATGAATCAT CTGGGATGAC 180
TAATCCTTTT GATGTCGTTT CACCGCCTAG AGTCAGCGCG ATGGCGATAA GGAGTCCACC 240
AACTACGATA AAAGGAACCA TAAACGATAC ACCGTTCATT AAATGTTGAT ACACCATTG 300
AATACCATT TAGACTnACC GCGATCTTC GAATGATAAT TTGTTTCAGA TGGTTAAATA 360
GGCGCATTG ATTTAATGAT ACGTGGATTG GGACCCTCGG 400

(2) INFORMATION FOR SEQ ID NO: 4059:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4059:

TTAAAAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAAC TA AGTnGAnCTA CCATCGACGC 60
TAAGGAGCTT AACTTCGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC 120
CAGACATATG AATGTAATT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTGCT 180
TCGCAAAACA TTTATTTGG ATTAAGTCTT CGATCGATTA GTATTGTCA GCTCCACATG 240
TCACCATGCT TCCACCTCGG AACCTATTAA CCTCATCATC TTGGAGGGGA TCTTATAAAC 300
CGAAATTGGG GAAATCTCAT CTTGAGGGGG GCTTnCATGC TTAGATGCTT TCCAGCACTT 360
ATCCCCT 367

(2) INFORMATION FOR SEQ ID NO: 4060:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4060:

TTCCGnACTC ACATAGCGAC TCAGGATTCA GACAGCGCAT TCAGATTAG ACACCGCATT	60
CAGATTCAAGC ATAGCGATTC AGCATTCCGC ACAGTGACTC AGnATTCCGA CAGTGACTCG	120
GATTCAAGATA GCGATTCAAGA TTCCGACAGT GACTCAGATT CCGACAGTGA CTCAGACTCA	180
GACAGTGATT CGGATTCAAGC GAGTGATTAG GATTCAAGATA GTGATTCCGA CTCCGACAGT	240
GACTCGGATT CAGATAGCGA CTCAGACTCG GATAGCGACT CGGATTCAAGA TAGCGATTAG	300
GACTCAGATA GCGATTCAAGA ATCAGACAGC GATTCAAGATT CAGACAGCGA CTCAGACAGT	360
GACTCAGATT CAGA	374

(2) INFORMATION FOR SEQ ID NO: 4061:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4061:

AAAATCATAA TATTTGGCAA TTTTTCAAC TTGACTCTG TCCTTCTGCA TAATGCCGT	60
AAATAATTCA CCTTCATCAC ACGCTGTACC TACCAATAAT CCCTCACGAT ATTCACTCAA	120
CAATGAACGT GGAATTGAG GTGTACGGTA GAAATACTTC ACCAATGATG CACTTACAAT	180
TTTAAATAGA TTTTTAAGAC CTTGTTGGTT TTGTACAATT AATGTGACAT GACTAGGTCT	240
TGCACGTTA TATGCATCTT CATTACTGAG TTTTGTtG ATTCGTTAT GATTTAATAC	300
GCCTAAwTCy TTCATTGTT GAACCATTG TATGAAAATG TAAGCTGTTG CTTCTGTATC	360
ATAAATGGCA CGGTGATGTT GCGTTAACAT TACGCCATAT TTTTAGCCA AGAAATTCAA	420
ACCATGTTA CC	432

(2) INFORMATION FOR SEQ ID NO: 4062:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4062:

TATCTTCGTT	CTCAATAGAA	TGATTAAAC	CTTCGATTC	TTTATCTAAA	TGACTACCAA	60
TTAAATCTAT	TTCTTCTATT	GTTAAATCGC	TATCTCCATC	TTCTTTATC	TCTGGTATTA	120
TTTTTCTTC	AACTAAGTCA	CGATATAATG	TTTTGAATTTCGTTCAAT	TTCGATTCGT		180
GATTTGAAT	ACTTTCTTC	CACACAAATG	TATACCTATT	GGCATTAGCT	TCTACTTTG	240
TACCATCAAT	AAGATTTGC	TTAACACATT	GACTATGAAA	CTGGGATAAA	TAAAGAnTCA	300
ATTAACGCAT	CAGTATTAGG	GAAnTCACTCT	AATACGATTA	ATAGTTTTA	TAAGAAGGTG	60
nTTGGATTTG	GAGCTAACCA	CATCCA				386

(2) INFORMATION FOR SEQ ID NO: 4063:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4063:

TAGGAGAGCG	TTCTAAGGGC	GTAGCATGAT	CGTAAGGACA	TGTGGAGCGC	TTAGGAGAAT	60
GCCGGTGTGA	GTAGCGAAAG	ACGGGTGAGA	ATCCCCTCCA	CCGATTGACT	AAGGTTCCA	120
GAGGAAGGCT	CGTCCGCTCT	GGGTTAGTCG	GGTCCTAACGC	TGAGGCCGAC	ACGTAGGGCG	180
ATGGATAACA	GGTGATATT	CCTGTACCAAC	CTATGAATCG	TTTAATCGA	TGGGGGGACG	240
CATAGGTATA	GGCGAGGTGA	CGATTGGGAT	TGCACGTCTT	AAGCAGTAAG	GCTGAGTATT	300
AGGCAAATCC	GGTACTCGTT	nAAGGCTTGA	GCTGTGGATG	GGAGAAGAC	ATnGAGTCTT	360
CGAGTTCGTT	GGnTTTCACA	ATGGCC				386

(2) INFORMATION FOR SEQ ID NO: 4064:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4064:

TAAGGCAGAT	GCTCTCCCAG	CTGAGCTAAT	TCTCCGATTT	AAAActGCCT	GGCAACGTT	60
TACTCTAGCG	GAACGTAAGT	TGGAGCTACC	ATCGACGCTA	AGGAGCTTAA	CTTCTGTGTT	120
CGGCATGGGA	ACAGGTGTGA	CCTCCTTGCT	ATAGTCACCA	GACATATGAA	TGTAATTTAT	180

ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTGCTTC GCAAACATT ATTGATTA	240
AGTCTTCGAT CGAnTAGTAT TCGTCAGCTC CACATGTCAC CATGCTTCCA CCTCGAACCT	300
ATTAACCTCA TCATCTTGA GGGGATCTTA TAACCGAAGT TGGGGAAATC TTCAnCTTGn	360
AGGGGGGGCT TCATGCCTT AGAATG	386

(2) INFORMATION FOR SEQ ID NO: 4065:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4065:

AATTCTTCG CTACTTGAAT GACAACACTT TGTTTACGC CTGAAATGGC TTCTTGCCAA	60
GCAGGTGTAT ATTTGATTC TGCATCGTCG TATCCTTGT ATTCTAATTG ATGATCAAAA	120
CGACGCACGC CATATTGACT TGCCATTAAG TCAAAAATTG TAGCAATACG GACTTTGTCA	180
CCATTTGCTA AAGTGACTTG TCGAGTTGGA ATTGGACGAT TGAATATCCC ATCTCCATCA	240
CTATCAAAGT ATGGGAATTG AATTGTTCT AATTCGTATC CACCTTCTGT CATTGATAAT	300
GTAGGGTTAA TTTAGAACCT ATCTTCTGTT TCTAGTTTA AGTTCCACTT CTTACCTTCT	360
TCCCAACGTG GACCCATGGT GCCATTAnGn ACTACTAAAC	400

(2) INFORMATION FOR SEQ ID NO: 4066:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4066:

ATTTGAAAT TGAGAAAACA ACTTATTGAA AAACATAATC TTTACGGTAA CATGGGTTCA	60
GGAACAATCG TTATTAAAAT GAAAAACGGT GGGAAATATA CGTTTGAATT ACACAAAAAA	120
CTGCAGAGCA TCGTATGGCA GACGTCATAG ATGGCACTAA TATTGATAAC ATTGAAGTGA	180
ATATAAAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA TCGGAAAAAC AAGAAGTTAA	240
GTGACAACGG TTTACATGTT GCTTAGCTTC TTTTATTATGCGTAATGATG TAAAAAGACG	300
nATATTCACT TGTTGTAAA AGTGGCATTG TATGTCTTAA AGTGACGnAA CTTCCAATGT	360
GCCCCAGTGTT TGATTCACAT CAAATCCATT TTTATTAAAC	400

(2) INFORMATION FOR SEQ ID NO: 4067:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4067:

CCTCATTCCA GGAAGGAATG TATTCTAAGA GTTCAAATAC TCCCGCATTAA TTATTAATT	60
ATGGAGCGGA AGATAGGATT TGCACCTATA CCTCGTTCCG GGAAGGAACG TGTTCTAAAA	120
GTTGAACCTAC TCCCGCATAA ACCTGGAGGC GGCAACCGGA TTTGAACCGG TGATAAAGGT	180
TTTGCAGACC TCTGCCTTAC CACTGGCTA TGCCGCCAAT AACTGGGCTA GCTGGATTG	240
AACCAACGAG TGACGGAGTC AAAGTCCGTT GCCTTACCGC TTGGCTATAG CCCATTAATA	300
ATAAGGGCGG CTGAAGGGGA TCGAACCCCTC GAATGTCGGA ACCACAATCC GATGTGTTAA	360
CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC	400

(2) INFORMATION FOR SEQ ID NO: 4068:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4068:

TATCTAATAG TTTTACTTTA AGTCCAGCAT TCACAAAAG TGCTGCCAGT TGAGCGCCCA	60
TTGTGCCTGC GCCAAGAACG GTTACTTTAT TAATTGTCAT AGTGATTCTT CCAATTAGT	120
TGAGGATAAG ATAACCATTAA AGATAATTGG AATAACGTTG CTATTTATA AAATTAATTAA	180
AGTATCTTG ACAGTCATCT TAGCCTCTTA TTTAAGGAAA AAGCTTTATG CTTAAAATAA	240
GTCTTTTTA GTGAAATTAA TGCATCTCAT ATAATTATTT GCTATTTATA CGAAAGCAGA	300
ATCTCCAGTC AAAGCGCGTC CAATCTAAG GCATTAATTAA CATGTGTACC TCGTACGTGT	360
AAATCGnTTC TGCATCAGnG AGGAAACGTG CAATATCATA	400

(2) INFORMATION FOR SEQ ID NO: 4069:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4069:

CAAAGGACCA ATTGCATTTG AGTATAACACA TATTAATAAC AATACCGAAC GTGGTTGGTT	60
AAAAAGAAGA ATTGAAACGC CATATAAAGT AACGTTAAAT AATAACGAAA AAAGGGCACT	120
ATTCAAACAA TTAGCGTATG TTGAAGGGTT TGAAAAATAT CTTCATAAAA ACTTCGTTGG	180
TGCAAAGCGT TTTTCAATTc nCGGGGTAGA CGCACTTGA CCGATGTTAC AACGTACTAT	240
TACGATTGCT GCGAAAGAAG GTATTAAAAA TATACAAATA GGCAATGGCTC ACCGTGGAC	300
GTAAACGT TTTAACGCA TGTnCTTAGA AAAAACCGTA CGAAATGATG ATTTCn	356

(2) INFORMATION FOR SEQ ID NO: 4070:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4070:

AAACGTTAG GGAAAATTAT CACACAGATA CAACAATACA CAGATATTGA TTACCCGAA	60
GCGATTGTCT TTCAAGCATC GTGTTTAAC GAGTTGTTG TTAAGGGCG TTAAAGTAAT	120
ATTATTCAA AATTGCAACA CTATTCAATT GAGGCACAAAC CAGGTATATG TATTATAGGG	180
GAAGTTGTTG ATTATACTGA AAACACTCCT AAATCATATG ATCCTATGAA GCAATTTAT	240
GTAGTAAGTG GTTCTAAACA TGACGCCCTT ATGCTCTGTG AACATTATAT GACGAAGGTT	300
ATGGCTGTTG CTAAACCCA ATGATACATC GAATGGGCAC CATTATCCAn TCGTCGCAAT	360
AATGGATTAC CCAAGGATGC CATTAnTTA AGCCnGCCAn	400

(2) INFORMATION FOR SEQ ID NO: 4071:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4071:

CCTCTGGAAA CCTTAGTCAA TCGGTGGACG GGATTCAC CCGTCTTCG CTACTCACAC	60
CGGCATTCTC ACTTCTAACGC GCTCCACATG TCCTTACGAT CATGCTCAA CGCCCTTAGA	120
ACGCTCTCCT ACCATTGTCC AAAGGnATnC CCACAGCTTC GGTAATATGT TTAGCCCCGG	180
TACATTTCG GCGCATGTGC ACTCGACTAG TGAGCTATTA CGCACTCTT AAATGGATGG	240
CTGCTTCTAA GCCAACATCC TAGTTGTCTG GGnAACGCCA CATCCTTTTC CACTAACAT	300

ATATTTGGG GACCTTGAGC TGGTGGTCTG GGGCTGTTTC GGGAACGGAA CACGGGACCT 360
T 361

(2) INFORMATION FOR SEQ ID NO: 4072:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4072:

ATGGTGACAA AAACATCGCA TTATTACTAG GTGTCGGCAC AGGCGTTGT GGTGCTGCTG 60
CTATTGCCGC AGTCGCTCCA ATATTCAAAT CACGTGAAAA GGATACAGCT ATTAGTATCG 120
GTATCATCGC ATTGATTGGT ACGATATTT CACTTATATA TACAGCTATC TACGCTATCT 180
TTTCAATGAC GACAAATGTT TATGGCGCTT GGTCTGGGT TAGTCTTCAT GAAATTGnCA 240
CACGTTGTCT TAGCTGGTGG CTTTGGTGGT AGTGATGCAC TTAAAATTGC ACTTCTTGGT 300
AAACTTGGTA GGAGTATTCT TACTGGATTC CCATTAACCA TCGTACTTAA TTTTAAATAT 360
GCGGTTnCCG TTnCATCAGG AnTCATCTAG GCAAGGGGTC 400

(2) INFORMATION FOR SEQ ID NO: 4073:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQID NO: 4073:

GCGACGATCA TTTAGAACAT CGCTTGGCG ATTAAATTCTT TAGAAGTGG A TGAGGCAAAA 60
TGTTCAATTAT CAGGAACCAA AGCAGGTGCT GATATGAAAG ATGGTCTACG TATTCACTGGT 120
GAAGACATGG GTACACTTA TACCAAACAC GTTGAATTGG AAAACAAAGG CGTCGACTTT 180
TATGAAGGTA ATGAAGTGG A TGAAGCTGAA GAAGAAGCAA AAGCTTGGAT TGATGCAGTT 240
GTAAATGATA CTGAACCAGT TGTGAACCGG AACAAAGCAAT GGTAGTTACC AnAATTCTTG 300
AAGCGATTAA TCCGTCTGCC AAATCCAGGC CAAAGCCATT TACTTGGAA TAACATCnTA 360
CCGGTAAGGG GGChCATCCT GGACCAAATT TAAAAGTTG 400

(2) INFORMATION FOR SEQ ID NO: 4074:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4074:

TCTTCCTAAT ACCTTCCAC GATCTTCAGC TGGCGCCTCT GCACTCGCAA ACGCACTTGA	60
TGCATCAACA ACACCACCAA ATAGTCCCTG CAATAACCTC ACAAGTACAA ACTGTAATGG	120
TGTCGTACAC AATGCCATTA AAAATAAGCA TACCGCCAAA CCAAGTAACG CTCTTAACQ	180
CATCCATTCT CGGCTGATCT TATCACCTAG CTTCCCCAT ATCGGCGGAG TTATGCATCG	240
TCGTTACAGC TGGAGCAGCA ATCGCTATAC CACTCCACAn CTGTATTTCT ACGGACTGAT	300
AGGATTTGT AGTGATGnCC ATGATGAAAT GGGCAATAAT GGGCACAAGT ACTGTTCACT	360
CCAGCCAATC GTTATGAAAC TGGACTGGGG CCATnAAATG	400

(2) INFORMATION FOR SEQ ID NO: 4075:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4075:

GGTCAGAAC GTCGTATGnA GTTCGnTCCC TATCCGTCGT GGGCGTAGGA AATTTGAGAG	60
GAGCTGTCCT TAGTACGAGA GGACCGGGAT GGACATACCT CTGGTGTACC AGTTGTCGTG	120
CCAACGCATA GCTGGGTAGC TATGTGTGGA CGGGATAAGT GCTGAAACTC TAAGCATGAA	180
GCCCCCTCA AGATGAGATT TCCCAACTTC GGTTATAAGA TCCCTCAAAG ATGATGAGGT	240
TAATAGGTTT CGAGGTGGAA GCATGGTGAC ATnTGGAGCT GACGAATACT AATCGATCGA	300
AGACTTAATC AAAATAATG TTTTGCAGCA AATCCACTTT TACTTACTAT CTAGTTGAA	360
TGATAAAATTA CATCCATATG	380

(2) INFORMATION FOR SEQ ID NO: 4076:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4076:

CAACGACTCG AAGACACAAT GTCTTCTCCC CATCACAGCT CAGCCTTAAC GAGTACCGGA	60
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TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTTCGCCTATC	120
CTACTGCGTC CCCCCATCGA TTAAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA	180
TCCATGCCT ACGCCTGTCG GCCTCAGCTT AGGACCCGAC TAACCCAGAG CGGACGAGCC	240
TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC AnCCGTCTTT CGCTACTCAC	300
AnCGGCATTC TCACTTCTAA GCGGTCCACA TGTCTT&GA TCATGCTTnA AGGCCTTAGG	360
AAGGTTCTTA CCATGGTCAA	380

(2) INFORMATION FOR SEQ ID NO: 4077:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4077:

GCAGGGTCTGA CTCTAGAGGA TnCCCACGCG CGCAAGATT AAATCGAAGA AACCAGCAAC	60
AGATTCCTCA AAATAGCGCG GCGAACAAACG AAACATCAAA TAGTGCACCT GCAGCTGTA	120
ATGGTGTAGC ATCAACGCCA CCAAGTGCAC CAAGTGGCGA TACTGCACCA ATAATAATG	180
TTACGCAAAA TACCGCACCA AATAGTAATA ATGCGCCTGT ATCGACTACA CCACAAAGTA	240
CAAGGGGGGA AnAAAGATGG TCAAAGTTTT GTAGATATAA CAACAAACACA AGTCAGCACA	300
GCTAACGAGA ACACACAAAA CATTACAGAT AAAGATGTTA AATCAATGGA AGCGGCATTA	360
ACGGGCTCTT	370

(2) INFORMATION FOR SEQ ID NO: 4078:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4078:

AAACATTTA TCAAATGGCA GAAGGACATG TGCCAAGACC ACCAGCGATG GTTGAACAT	60
TGACTTATAT TAAAGAGTTT ATGAACCAAG TTAGTCGCA TAGCTAGTAT GAAACGTGGT	120
GTGCGCATGG GAACTATCAA GCTTGAAAGA TGTGGTACTA CATGCGTTGG ATTAGGGAT	180
CGGTACTTTA TATGAAGACG TGCTGCTTCC ATTAAATGAG TGATGCGATT TTGGCATGAA	240
GGTCACCTTA AATGTACATT GTTGTAAATAA AATTGCCTAT nAAATTTTA GCACATAAA	300

(2) INFORMATION FOR SEQ ID NO: 4079:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4079:

TTGAAGTAAC TAAATTAATA TTATGTTGTT CAATTAAAAG CTTCATACAA ACCTAATCTA	60
TTTGCACTCC ACCGCTAACCA CCGAACACTT GTCCGGTTGT ATAACTTGAT TCTTCTGACG	120
CTAATAGCAC ATAAGTTCCA CATAACTCAA CAGGTTGACC TGCACGACCT AAAGGTGTTT	180
TTTGACCAAA TGTTGGGATT TTACTTTGAG GTTGTCCACC AGAAATTGT AATGGTGACC	240
AGAATGGACC AGGCGCTACA CAGTTCACTC TAATTCCCTT TGGTCCTAAT TCTTCTGAAA	300
AACTTTAGT TAATGAAATA ATTGCTGCCT TTTGAGGGG CATAATCCAT GAAGAATAnG	360
GCCAGGGAnT AAAACCTGG ACnAAAGAAG CCGTGGAAAT	400

(2) INFORMATION FOR SEQ ID NO: 4080:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4080:

TCGTTGGACA CAATCTGAAA AATAAATAGA TATAAATTG CGAGATATAT TCGTATTTAT	60
AGTAAAATTA AATAAAGAGA TTATATAACA CGAGGAGTAG TAAGTATGAA ATTTAGAAA	120
TATATAGATC ACACTTTATT GAAGCCTGAG TCAACACGTA CGCAAATCGA TCAAATCATC	180
GATGAAGCGA AACATTACAA TTTTAAATCT GTATGTGTGA ATCCAACACA TGTTAAATAT	240
GCAGCAGAGC GACTAGCTGA TTCAGAGGTG CTCGTTGTA CGGTAATAGG ATTCCCATT	300
GGTGCCTCGA CAACTGGCAA CGAAAGCATT TGAAACAGAA GATGCAATTG AAAATGGTGC	360
AGATGAATTG GACATGGTCA TCCACATCGG CGCATTAAAA	400

(2) INFORMATION FOR SEQ ID NO: 4081:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4081:

CGACTAGTGA GCTATTACGC ACTCTTTAAA TGATGGCTGC TTCTAAGCCA ACATCCTAGT	60
TGTCTGGCA ACGCACATCC TTTCCACTT AACATATATT TTGGGACCTT AGCTGGTGGT	120
CTGGGCTGTT TCCCTnCnCG AACACGGACC TTATCACCCA TGTTCTGACT CCCAAGTTAA	180
ATTAATTGGC ATTCGGAGTT TGTCTGAATT CGGTAAACCG AGAGGGACCC CTCGTACCAA	240
ACAGTGCTCT ACCTCCAATA ATCATCACTT GGAGGGCTAGC CCTAAAGCTA TTTACGAGA	300
GAACCAGCTA TCTCCAGGTT CGATTGGAAT TTCTCCGChA CCCTCAGTTC ATCCGCTCA	359

(2) INFORMATION FOR SEQ ID NO: 4082:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4082:

TTTGACATTT AGTGTAAGCG TnTTACAAAT AAAGCGTGTGTT GTTTTGAAAT TAAATGCATT	60
TCACATTAGT ATTCAATTAA TTTTTAGGAG GAATTATAT GACATTGAA AAAGAAACGG	120
TCTAAAAAAC ATTATTCCT GAAGATGTAC TTAGTATTGC TAAAGGTTA ACAGACGGTG	180
AAGTCGAATT TTTACAACAA GTAGATTCAAT TGGCTAGAAA GTAAGTACCG TGGAAAATAT	240
TAATCAACAT TGGATAGACG CTACTGTACC CGAGGACTAT TTTAAAGATC TGGGGAGAAT	300
TAAATTATTT TAACAATCCA TTACTTTACA AGGATCGTC CAAACGCCAA AnGGCCTAGT	360
CCAECTATTT nCAGTTTT	379

(2) INFORMATION FOR SEQ ID NO: 4083:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4083:

TTGAAACAGC CAGAGGTGTT TTATACCCAG GTGTTTCAGA TATGTATGAT GCGAAACAAT	60
ATGTTAACCC AGTnAATAAT TCTTGGTCGA CAAATGCGCA ACATATGAAT TTCAATTG	120
TTGGAACATA TGGCCTAAC AAAGATGTTG TAGGCATATC TACTCGTCTT ATTAGAGTGA	180

CATATGATAA TAGACAAACA GAAGATTAA CTATTTATC TAAAGTTAAA CCTGACCCAC	240
CTAGAATTGA CGCAAACCTCT GTGACATATA AAGCAGGTCT TACAAACCAA GAAATTAAAG	300
TTAATAACGT ATTAATTAAC TCGTCCGTGA AATTATTTAA GCCGATAATA CACCATTAAA	360
TGTnCnCAAT ATTACCCnGG GTAGCGGGTT TTAGTTCCGG	400

(2) INFORMATION FOR SEQ ID NO: 4084:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4084:

AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCnAGGCAT CCACCGTGCG	60
CCCTTAATAA CTTAATCTAT GTTCCATCC TACAGGAAAC GCGTTAGTAA TCTTGTGAGT	120
GTTCTTCGA ACATAGCGAT TATTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC	180
ACTCGGTTTT GCTTGGTAAA ATCTATATT TACTTACTTA TCTAGTTTC AATGTACAAT	240
TTCTTTTAG TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTATGT	300
TAAATAAACCA TTCAAAACTG AATACAATAT GTCACATTAT TCCGCCATCT nCTGAAGAAG	360
ATGTTnCCGA ATATnATCCT TAGAAAGGAG GTGGATCCCA	400

(2) INFORMATION FOR SEQ ID NO: 4085:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4085:

TTACTTATCT AGTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA	60
CCTCCTGCGT GCAAAGCAGG CGCTCTCCCA GCTGAGCTAA GCCCCCCAAAT AGGTATTAAA	120
TTAATGGTGG GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCCTCT	180
GAACCAGCTG GAGCTATAGG CCCATTAATT TGGAATGAAC AAACATTCAA AACTGGAATA	240
CAATATGTCA CGTTATTCCG CATCTTCTGG AGAAGATGT TTCCGAATAn ATCCTTAnGA	300
AAGGAGGTGA TCCnGCCGCA CCTTCCGATG ACGGCTACCT TGGTTGACGA nTTGCACCCC	360
AAGCATTGT TCCCACCTTC GACGGCTGAG CTCCTAAAG	400

(2) INFORMATION FOR SEQ ID NO: 4086:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4086:

GTCATTGGAA	ACTGGAGnAC	TTGAGTGCAG	AAGAGGAAAG	TGGAATTCCA	GTGTAGCGG	60
TGAAATGCGC	AGAGATATGG	AGGAACACCA	GTGGCGAAGC	GACTTCTGG	TCTGTAAC TG	120
ACGCTGATGT	GCGAACGTG	GGGATCAAAC	AGGATTAGAT	ACCCTGGTAG	TCCACGCCGT	180
AAACGATGAG	TGCTAAGTGT	TAGGGGTTT	CCGCCCCTTA	GTGCTGCAGC	TAACGCATTA	240
AGCACTCCGC	CTGGGGAGTA	CGACCGCAAG	TTGnAAACTC	CAAAGGAATT	GACGGGCGCA	300
CAAGCGTGGG	AGCATGTGGT	TTAATTGAA	CCAACGnATA	GAACCTTACC	AAATCTTGGA	360
C						361

(2) INFORMATION FOR SEQ ID NO: 4087:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4087:

GACCTTGCAG	GACTCGAAC C	TGCGACC A	CGGTTATGAG	CCGTTAGCTC	TAACCAACTG	60
AGCTAAAGGT	CCTAAATATA	ATTTTACAAC	TAATAAATAG	TGGCGGTGGA	GGGGATCGAA	120
CCCCCCACCT	CACGGGTATG	AACCGTACCG	TCTAGCCAGC	TGAGCTACAC	CGCCTTATAT	180
AGTTTGTAAA	TAATATGGT G	GAGACTAGCG	GGATCGAAC C	GCTGACCTCC	TGGTGCAA A	240
GCA GCGCTC	TCCCAGCTGA	GCTAAAGCCC	CCATAAATAA	TTACAGTATA	TCGGGAAGAC	300
AGGATTGAA	CCTGCGACCC	CTTTCCAAA	CCAAGTGCTT	TTACCAAGTT	GGTACTTCCn	360
GTATAATT A	ACGGGCCGA	TAGGAGTT CG	GAACCCTTAA			400

(2) INFORMATION FOR SEQ ID NO: 4088:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4088:

AGCTATTATT TTTGACAGAT TCCATATCGT TCAACATTAA AATAGAGAAC TTAATAAGTA	60
TCGTGTACAA GTTATGAATG AATACCGTAA TAAAAAAGGA CCTGATTATA CAATTTTAA	120
GAATAACTGG AAAGTCCTAT TGATGGATAC TAGTAAAACC ATATTTAGTA AATACAGATG	180
GAATAAAATCT TTTAAGGCTT ATAAACGCTC ATCTGACATT GTAGGAATTC ATGCTTCAA	240
AAGACGATAT ACTACGACAC TCCTACGAAC TTGTCCAAG GGATTACGGA AAAGGCCCTA	300
AGGGTTATGT TAATTGGCCC TAAATTTATT AAATGCGTTT GAAATTCACT TAGTTAAAAA	360
GTCTGTGAGT GA _n GGGTGTA TGGGAAAGTG GTTAAAATAT	400

(2) INFORMATION FOR SEQ ID NO: 4089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4089:

ATCGTTTAG ATAAGACGGG TACATTACAA ATGGTCGTCC AGTCGTGACA GATTATCATG	60
G TGACAATCA AACGCTACAA CTACTTGCTA CTGCTGAAA AGATTCTGAA CACCCATTGG	120
CAGAAGCCAT TGTCAATTAT GCAAAAGAAA AGCAATTAAT ATTAAC TGAG ACAACAACAT	180
TTAAAGCAGT ACCTGGCCA TGGTATTGAA GCAACGATTG GATCATCACC ATATATTGGT	240
TGGTAACCGT GAAATTAAATG GCTGACAATG GATATTAGCT TGCCTAAGCA TATT _{Tn} GG	300
TGGATTAAAC ACATTATGAA CGAGATGGTA AAAC TGCTAG CTCATTGCTG TTGAATTATT	360
nCATAACGGT ATCA	374

(2) INFORMATION FOR SEQ ID NO: 4090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4090:

AATTGAACGT CAAACTCTGT GACATATAAA G _n CAGGTCTT ACAAAACCAAG nAAATTAAAG	60
TTAATAACGT ATTAAATAAC TCGTCAGTAA AATTATTTAA AGCAGATAAT ACACCATTAA	120
ATGTCACAAA TATTACTCAT GGTAGCTGTT TTTGTTCGGT TGTGACAGTA ATGACGCGT	180
TACCAAATGG CGGAGTTAAA GCAAAATCTT CAATTCAAT GAACAATGTG ACGTATACGA	240

CGCAAGACGA ACATGGTCAA GTTGTACAG TAACAAGAAA TGAATCTGTT GATTCAAATG 300
ACAGTGCACC AGTAACAGTG ACACCACAnT TACAAGCAAC TACTGAAGGC GCTGTATTAA 360
TTAAGTT 367

(2) INFORMATION FOR SEQ ID NO: 4091:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4091:

TAATATTATA TTGCTAGTAG TTGACTGAAT GAAAATGCGC TTGCAACAAG CTTTTTCAA 60
CTCTAGTCAG GGGCCCCAAC ACAGAGAATT TCGAAAAGAA ATTCTACAGG CAATGCGAGT 120
TGGGGTGTGG GCCCCAACAC AGAGAATTTC GAAAAGAAAT TCTACAGGCA ATGCGAGTTG 180
GGGTGTGGGC CCCAACACAG AGAATTCGA AAAGAAATTC TACAGGGCAA TGCGAGTTGG 240
GGTGTGGGCC CCAACATGAG AGAAATTGGA TTCCCAATT CTGACAGACA ATGCAAGTTG 300
GCGGGGGCCC CAACACAGAA GCTGGACGAA AATCCTTGAA CGAATGAATG TGGAATTGG 360
CGGGGGGCCA ACACAGAAGn TGACGAAAAT nCTnGAACCA 400

(2) INFORMATION FOR SEQ ID NO: 4092:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4092:

GCATTTCTCA TAACACAAGG AATTCACAAGA AGTCCGGCTA CTGGATCACA AACTAAACCT 60
AATAAATTAC TTATCGCTAA TGCCATAGCG TGCCCGGATG CTTCTGGTGA TCCTCCGAAT 120
ATAGCTACTG CTGCAGCTGC GGCCATTGCA GATGCTGAAC CAACTTCAGC TTGGCAGCCA 180
CCTGTTGCAC CAGCTACACT TGCATTGTT GCTACGACAC GCCCAAACAA TGCTGAAGTG 240
AATAAGAAAT CAATCATTGC TCTTCTGTTA AATCATGTGT TTTTCTAATT AAAAAGTGCA 300
CCGGGAATGG TAnCCGAGGG AAnCAGCTGT GGGCGTTGCA CAAATAATAC CCCATCGCAG 360
CATTTGACCT TCATTTGGTT GCAATGGAA CCTTGACTG 400

(2) INFORMATION FOR SEQ ID NO: 4093:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4093:

TGACTTACGT ACTGTTAAC CAATCGATGT TGACACAATT GTAGCTTCAG TTGAAAAAAC	60
TGGTCGTGCA GTTGTAGTTC AAGAAGCACA ACGTCAAGCT GGTGTTGGTGCAGCAGTTGT	120
AGCTGAATTA AGTGAACGTG CAATCCTTTC ATTAGAAGCA CCTATTGGAA GAGTTGCAGC	180
AGCAGATACA ATTTATCCAT TCACTCAAGC TGAAAATGTT TGGTTACCAA ACAAAAATGA	240
CATCATCGAA AAAGCAAAAG AAACTTAGA ATTTAATAC ATTTTAAAAG TTAACGAATT	300
AGCGTATTTT AGTCTCATTG ATTAAAnATGA AATGnGnTAA TTTACGGAAT CCTA	354

(2) INFORMATION FOR SEQ ID NO: 4094:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4094:

CGTTAACATG AAGTTACGTT CTTTTATAAA AAGATTAAA CGCGTTATTA ATCTTGTGAG	60
TGTTCTTCG AACACTAGCG ATTATTTCTT ATGAATTCAA GCTTATTAA AACTCTTTAT	120
TCACTCGGTT TTGCTTGGTA AAATCTATAT nTTACTTACT TATCnAGTTT TCAATGTACA	180
AATAATGGTG GAGACTAGCG GGATCGAACCC GCTGACCTCC TGCCTGCAGA GCAGGCGCTC	240
TCCCAGCTGA GCTAAGCCCC CAAATAGGnA TTAAATTAAT GGTGGGCCTA AGTGGACTCG	300
AACCACCGAC CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT A	351

(2) INFORMATION FOR SEQ ID NO: 4095:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4095:

ATTGTTGCGA CTGGCACACC CGAAGATATT GCTCAGACAA AGTCATCATA TACAGGAAAG	60
TATTTAAAAG AAGTACTTGA ACGAGATAAA CAAAATCTG AAGATAAATA AGATTTAAAAG	120

AAGTGAAGGA TGTTATAATT TATCCTTCGC TTCTTTTAT TAATTTAGTA ATGAATAGTA	180
GAAAGAAAAG ATGCGTAAAA AGAATTATGT TAAGATAGGG TCAATCTAGA GTAGTTAAC	240
ATAAAATCGAA CTnGGAGTGG GACAGAAATG ATAAAGAACATC ACTAATGATT TATTATGTAG	300
TGGTTCTTG TCATTAGCCA CAGCTATTG TGTACTTAAA AnTAGGTATG CCAGTGTGCA	360
CTCCTTGAGA GGAAATACTn ATTT	384

(2) INFORMATION FOR SEQ ID NO: 4096:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4096:

CTGCATCTTC ACAGGTACTA TGATTCACC GAGTCTCTCG TTGAGACAGT GCCCAAATCG	60
TTACGCCTTT CGTGGGGTC GGAACCTTACC CGACAAGGAA TTTCGCTACC TTAGGACCGT	120
TATAGTTACG GCCGCCGTTT ACTGGGGCTT CGATTCGTAG CTTCGCAAA AGAGCCGACT	180
CCTCTTGAAC CTTCCAGCAC CGGGCAGGCG TCACCCCTGAT GACATCACCT TACGGTTAG	240
CAGAGACCTG TGTTTTGAT AAACAGTCGC TTGGGCCTAT TCACTGCGGC TCTTCTGGC	300
GTAAACCTn AAAGAGCACC CCTTCTCCCG AAATTnACGG GGTCATTTG GCCGAGTTCC	360
TTAACGAGnA TTCGCTCGGT GCAACTT	387

(2) INFORMATION FOR SEQ ID NO: 4097:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4097:

CCACTCACAT TCACACATCG ATTACACACAC CGCACTCAGC ACTCAGnATA CCGCATTAG	60
CATTCAGCAC AGCGnACTCA GACTCAGAAC AGCGATTAG ACTCGGATAG CGACTCAGAC	120
TCAGATAGCG ACTCAGATTC GGATAGCGAC TCAGACTCAG ATAGCGATTC AGATTAGAT	180
AGCGATTAGG ACTCAGACAG TGATTAGAT TCAGACTCAG ATAGCGACTC AGATTCTGAC	240
AGCGATTAG ACTCAGACAG CGACTCAGAC TCAGACAGTG ATTCAAGATTC AGACAGCGAC	300
TCAGATTAG ATnGCGACTC AGACTCAGAT AGCGACTCAG ATTCAAGATAGCGATTAGGAC	360

TCAGACAACG ACTCAGATT C AGATAGCGAT TCAGATT CAG

400

(2) INFORMATION FOR SEQ ID NO: 4098:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4098:

TCGTACCTGA ACTACTTGT ATTAAAATAG TTACAACGAT ACCTGCAATA ACACCTAATA	60
CTGGATTGAT GTAAATTTG TTTAAAATAT CTCGTAGCCT GTCTCCTGCT GATGCTTGAA	120
GCCCGTCTCC CATGATTTT AAGCCGTAAA GGAAAATACC TAAACCACCT AAAAAGGAGA	180
AAATGACTTC TGTAACCGAC ATTTCCATTA TTTCACCTCA AATAAGCTTT ATATTTAGAT	240
TATCGCTTAT AATTGTAAAT TTAATGTTAA GATTAGGTAA AATTATTTAA CAATATATGT	300
TATTTGTATA TGACTTGTAA AATATGTCA CTTATTATGT AAATTTCAAG TGGTGGnAAT	360
GGCCAGTTG CCAAGCACTG GTTTGACCAAn ATGGnGGCAn	400

(2) INFORMATION FOR SEQ ID NO: 4099:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4099:

ATCCTTTCC ACTAACATA TATTTGGGA CCTTACCTGG TGGTCTGGC TGTTTCCGG	60
CCGAACACGG nACCTTATCA CCCATGTTCT GACTCCAAG TTAAATAAT TGGCATT CGG	120
AGTTTGTCTG AATTGGTAA CCCGAGAGGG CCCCTCGTCC AAACAGGGCT CTACCTCCAA	180
TAATCATCAC TTGAGGCTAG CCCTAAAGCT ATTCGGAGA GAACCAGCTA TCTCCAGGTT	240
CGATTGGAAT TTCTCCGCTA CCCTCAGTTC ATCCGCTCAC TTTCAACGTA ATCGGTT CGG	300
TCCTCCATTC AGTGTACCT GAACTTCAAC CTGACCAAnG GTAGATCACC	350

(2) INFORMATION FOR SEQ ID NO: 4100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4100:

TAGAACTTGT TGCCAAACAG CATGCTTAAT TTCAATATCT TCTTTGACTG CTTCGATATA	60
TAAATCAGCA TCATCATTG CCAAGTCATC ATCAAAATTA CCATATGTTA AATGACTCGC	120
TAGATTTAAG TCGAATAGTA GGGCCGTTT CTTATCTGTA ATTTTATCGT AAGATTTTT	180
CGCAATGAGA TTTGGATCGT TTTTGTCAC TACAATATCT AATAGTTTA CTTTAAGTCC	240
AGCATTACACA AAAAGTGCTG CCAGTTGGAG CGCCCATTGT GCCTGCGCCA AGAACGGnTA	300
CTTTATTAAT TGGTCATAGT GAnTCCnCCC ATTTAGTTGA GGGATAAAT ACCATT	357

(2) INFORMATION FOR SEQ ID NO: 4101:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4101:

TAACTCAGGC TGGGGACATA AATCAATATT CTATGCTCTA CGAATTATAT TGGCAGTAGT	60
TGACTGGnCG AAAATGCGCT TGTAACAAGC TTTTTCAAT TCTAGTCAGG GGCCCCAACAA	120
CAGAGAATTG CGAAAAGAAA TTCTACAGGC AATGCGAGTT GGGGTGAGGG CCCAACACAA	180
GAAGCTGACG AAAAGTCAGC TTACAATAAT GTGCAAGTTG GGGATGGGCC CCAACAAAGA	240
GAAATTGGAT TCCCAATTTC TACAGACAAT GCAAGTnGGG GTGGGACGAC GnGATAAATT	300
TTGCGAAAAT ATCATTTCTG TCCCACCTCCC ATCAAAAGAA TGACAT	346

(2) INFORMATION FOR SEQ ID NO: 4102:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4102:

AATGATGAAA ATCAATTAGA CAAAGCAGGT AAATTAAGTG ATGTCGCGTC ATTAAAGGAA	60
GCGATTACACA ATCGAGAACATC ACAAAAGTACA ACTGGTATCG GCGAAGGTAT TGCCATTCCA	120
CATGCCAAAG TGGCCGCAGT TAAGTCACCA GCTATTGCGT TTGGTAAATC TAAAGCAGGC	180
GTAGATTATC AAAGTTGGG ATATGCAACC AGCACACTTA TTCTTATGA TTGCAGCGCC	240
AGAAGGTGGC CCCAACACAA TTCTAGATGC TTTACTAAAG TTGnCTGGTA TTTTAATGGG	300

ATGAAAATGT ACGTGAGGAA ATTnTTACAT GGCTTCATCA nCTGAAGAAG TACTAGCGAT	360
CAT	363

(2) INFORMATION FOR SEQ ID NO: 4103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

GAGTGCAGCG GATAACATTA AACCGACGAC AnCTTTTTA TGTCAGGTT TAGCTGTGTG	60
ATAAATTGCA AGTGGGCAC CACATAAGCC GAACATCATC GTAATAAAC GGCCTGACAT	120
AAAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGa TCACCAAGTT GAGCAAAGAA	180
GATGTTCTGC GTACCTTGAA CTAAGTGCC C TTGACTTCT AAAGTACCAC CAAGTGCCGT	240
CTGCCAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACCA ATCTTAAGAT	300
GAAGCCATAA rCAAAAGTAC CsGTTGGcAC CTGTTtTCGT TACAAATCCA CCAACATGtK	360
AaTGCCGGTT TGTATGGTTG GCCCAAnTGA nAACATCATA	400

(2) INFORMATION FOR SEQ ID NO: 4104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4104:

AATTGAGAAT TTGTCGCTAT TTGTAAATTG TATCCTGGCT TAAGTTGGCC AAAGTGTCTT	60
ATTTTTTAA AGTATTAAA AGTAAAATTA CATGTTAATA CGTATATTAA TTGGCGAGAC	120
TCCTGAGGGA GCAGTGCCAG TCGAACGAGG GGCCCCAACCA CAGAAGCTGA CATATAGTCA	180
CTTAACAAACA ATGTGCCGGT TGGGGTGGCT GAGACGGCAC CCTAGGAAGG GACCCGTCA	240
CAAAAATTCT ATTTATAGAA TTTTACAGTA ATGTGCCAGA TGGGCATAGC GACCCATTCA	300
ATACGAnTAT nTGAAnTAAAT AGAGAACAGC AGTAAGATAT TTTCTAATTG AAAATTAT	358

(2) INFORMATION FOR SEQ ID NO: 4105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4105:

GACGCGTTAC CAAATGCCGG AATTAAAGCA AAATCTTCAA TTTCAATGAA CAATGTGACG	60
TATACGACGC AAGACGAACA TGGTCAAGTT GTTACAGTAA CAAGAAATGA ATCTGTTGAT	120
TCAAATGACA GTGCAACAGT AACAGTGACA CCACAATTAC AAGCAACTAC TGAAGGCCT	180
GTATTTATTA AAGGTGGCGA CGGTTTGAT TTCGGACACG TGAAAGATT TATTCAAAAC	240
CCGCCACATG GGGCAACGGT TGCATGGCAT GATAGTCCAG ATACATGGAA GGAnTACAGT	300
CGGTAACACT TCATAAAAAC GCGGTTTGTn ACCATTACCT AATnGTCAAG GGTACGGCGT	360
TAATGTTGA AGGTTCCCGT TCCAAGGTTT TTTCCCGTTT	400

(2) INFORMATION FOR SEQ ID NO: 4106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4106:

GAAGTTAACG TCCTTAGCGT CGATGGTAGT CGAACTTACG TnCCGCTAGA GTAGAACGTn	60
TGCCAGGCAG TTTTTAATC AAATTTGGT TAAAAAATAA AATGGACAAG ATAAAAAAAG	120
TTATTGACTT AAATGTTAAT AAAATGTATA ATTAATTCTT GTCGGTAAGA AAAATGAACA	180
TTGAAAATG AATGACAATA TGTCAACGTT AATTCCAAA AACGTAACTA TAAGTTACAA	240
ACATTATTTA GTATTATGA GCTAATCAA CATCATAATT TTTCATGGGA GAGTTGGAT	300
CCTGGGCTCA GGATGGAACG CTGGGCGGCG TGCCCTAATA CATGGCAAGT CnGAGCGAAC	360
GGGACGAGAA GGCTTGCTT CTCCTGGATG TTAACCGGCn	400

(2) INFORMATION FOR SEQ ID NO: 4107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4107:

GATTGTGCCA CGCTTTAAC CGAAATACAA CATCATCATT GACAATTGT TGATTTGAAA	60
AATCTTTCTC TTCAATAAAT ACATACGTT GCATCGTATG TGCTTCATG TAACTCAATA	120

TTGGTTTAA ATGCATTCA GGAATTAAAT AATGTTACT AGAACCTGCT GTCGCTACAA 180
GTCCTATTAC CTTGTCACGA AACGCATTGA CTGGAAGTAG ATCAAACACA TTTnnCAAAG 240
CACCAAGGGAT GGAAAGCTTG AAAAATTGGA AAACCAATAA AAATCACATC AGCCTGCATT 300
AACGACGTCG TTAATTATA TACATCTCCT GTAGTATCTA GnT 343

(2) INFORMATION FOR SEQ ID NO: 4108:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4108:

ATACAAAACA CCAGGTCGTG AAGATAAACCA ATCACAAAGCG GCTACTGCTT CAGCAACTGA 60
ATTACCATAT GCAGTATTAG AAGCTATGGG TGGCAAAGCA AACATTAAAC ATTTAGACGC 120
TTGTATCACA CGTCTACGGT TGAAGTTAAC GACAAATCTA AAGTTGATGT TCCTGGTTG 180
AnAGATTTAG GCGCATCTGG TGTATTAGAA GTCGGCAATAATATGCAAGC AATTTTGTT 240
CCTAAATCTG ACCAAATCAA ACATGAAATG CAACAGATTA TGAnTGGTCA AGTAGTAGAA 300
AATCCTACTA CTATGGAAGA CGATnAAGAC GAAACTGTTG TGGGTTGGCA G 351

(2) INFORMATION FOR SEQ ID NO: 4109:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4109:

CCTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60
TTTTTAAATA CTAAAATACA TGTTGGAATA CTTGTCCCAT AGAAAATATT GGCTGGTAAC 120
CCAATCACGG CTTCTAAGTA GTTCTTTCT TCTATTAAAT AGCGACGnAT CACACCTTCT 180
GCGGCACCAC GGAATAATAC ACCATGTGGG AGTACGACTG CnATGGTACC TTCATCGTCT 240
AAGGTAATGT ACCCTGTGGT TGAATAAAGG CAAAATCTGC TTTGGGATTT TGGCGCAACT 300
TTGCCCGTAA CCACTGAATC GTTCATCATT TTCAAATTG TGAATCnGCT GGTCCATTG 360
CACTGTA 367

(2) INFORMATION FOR SEQ ID NO: 4110:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4110:

GTCGTCCGAT TGAAGGATGG AGTACTGTCG CATTGGAA AGACTGGCAA GGACCAC	60
GTTGCAGAA CGGAACAAGT TGGTTCTATT TTGCAACAGA CCAATGGAAA TATGAAGAGT	120
CAAATGTAGA TCGTTAAAAA TCTCCATTAG CTAAAACAGA GGAGTTAAAG CATAACATC	180
CAGCTGATTA TAATGTTTA GCAGCTAGAC TTGGTTGGTT ACCATCATAT CCACAATTAA	240
ATAAAAATAG TTTGTTGTTT GCAGAAGAAG CTAAAGATGA AGGTATAGAT TCAAATGAAG	300
CGATTTGCC ACGTGCAATT GATGAAGTGA ATCAAAACCA AACACCATTG GCCATAnGAA	360
AATCCTGATT TGGAAAAGGA TCCTnCCAAA ATCCAnATT	400

(2) INFORMATION FOR SEQ ID NO: 4111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4111:

TCAGATGAAG CTAAAGTAA AGGTATTACA TGTGCAAGTG CAGGTAATCA TGCTCAAGGT	60
GTTGCCTATA CAGCTAAAAA ACTTAATTAA AACGCTGTTA TCTTTATGCC AGTCACTACA	120
CCTTTACAAA AGGTAAATCA AGTAAAGTTC TTTGGAAATA GTAACGTTGA AGTTGTACTC	180
ACTGGTGATA CATTGATCA CTGTTAGCT GAAGCTTTA CTTATACAAG TGAACATCAA	240
ATGAACTTA TAGATCCATT CAATAATGTT CATAACAATT CTGGACAAGG TACGCTTGCT	300
AAAGAAATGC TAGAACAAAGC AAAGTCnGGA CAATGTTAAC TTTGATTATC TATTTGCCGC	360
AATTGGTGGT GGCGGTTAA TTTCCAGTAT TAGTACTAAC	400

(2) INFORMATION FOR SEQ ID NO: 4112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4112:

GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA GTCAAACGCT CACATACGGC	60
TTCGTTTCA TTATTTAAA TGCTCATTAA CATAAGTAAA CTCTGCTTTA AAATAATTAA	120
ACTCATTGTC TGCTAACGT TTTCTTTAT AAAAGATT AAACGCGTTA TTAATCTTGT	180
GAGTGTCTT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACCTTT	240
TATTCACTCG GnTTTGCTTG GGAAAATCTA TATTTACnT ACTTATCTAG TnTTCAATGT	300
ACAAATAATG GTGGGCCCAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGGCGTGC	360
GG	362

(2) INFORMATION FOR SEQ ID NO: 4113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4113:

CAGGTGGTT TGCGAAAAGT GAAGTATGGC GTCAAATGAT GTCAGATATA TTTGACACAG	60
AGTTAGTGGT TCCTGAAAGT TATGAAAGTT CATGCTTAGG TGCCTGCGTG CTCGGACTTA	120
AAGCTGTAGG TGACATTGAA GATTTTCAA TCGTTTCATC GATGGTCGGT GCCACAAACA	180
ATCATA CGCC GATTGAAGAA AATGTCACTG TTTACCAAGA GATCGTATCC ATTTTTATCA	240
ATTAAAGTCG TTCTTAACA GAGAATTATG ACAAAATTGCA GATTCAACG CCACATATCG	300
CTGAAATAAA ACnCCATAAA TACGnCACTC AAGCATCTTA GATAAAGTTG TnGGCCATGC	360
TAC	363

(2) INFORMATION FOR SEQ ID NO: 4114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4114:

GGTCTGGGCT TGGTTCCGGT TCTGGGTCTG GACTTGGTTC TGGATCTGGC GTTGGTTCTG	60
GTTCTGGGTC TGGACTTGGT TCTGGGTCAA CCGGCGGCC TGGAGTTGGG TCTTTCGGAT	120
TTACTGCTGA ATCACCATCA GCACTTCCAC CACCATACG TACAACATTC TCATTATTCC	180
AACCGAAAAT ACTGTAGTCT CTATTTGTTA CAGGATCAAC ATTTTCTTGA ATAACCTGAG	240
TTTTAAGTT CTTACCTGTA TTGTCGTAAT GCCCTTCTAC TAATACTACA TATGTTTTAG	300

TAATATCACC AAATTAATAC TAGCTACATT GGATGCnCAT AATAGATCTA TTTTAAATGG 360
nCTGTACTCC TTAAGGTAGA GCATTGGACT GCA 394

(2) INFORMATION FOR SEQ ID NO: 4115:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4115:

GGCGATTATA TTAAAAAGCC AATTACAGAA TGTAGTGGTA ATGAAATATG CCAAGAACATGG 60
CTGTATCACT TAGGTGTATC AACTGACAAA ATTGAAGACT TAGCAAAACA TGCATCTAAT 120
ACGATTCCCTG TTTATATGCC ATATATCACA TCTTATTTCA TGACGCGTGC TATCGGCGAC 180
AGACCTTAG TCGTCCCGCA TCAATCTCAG AACTTAGCAT TTATTGGTAA CTTTGCCAGA 240
AACAGAGCGA GACACTGTAT TTACAACAGA ATATTGGTT CGTACTGCCA GGGAAAGCTGT 300
TTATCAATTA CTAAATATAG ATCGTGGTAT TCCAGAAAGT ATCAATAAGT CCATTGGATC 360
TTnCGCGTnC TTAATGGGAT GGCCATATAC GAACTGGATG 400

(2) INFORMATION FOR SEQ ID NO: 4116:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4116:

AACATATTTT AAGTAGGTGA ATGAATGGTA AATGAACAAA TCATTGATAT TTCAGGTCCG 60
TTAAAGGGCG AAATAGAAAGT GCCGGGCGAT AAGTCAATGA CACACCGTGC AATCATGT 120
GCGTCGCTAG CTGAAGGTGT ATCTACTATA TATAAGCCAC TACTTGGCGA ATGTCGTCGT 180
ACGATGGACA TTTTCCGACT GTTAGGTGTA GAAATCAAAG AAGATGATGA AAAATTAGTT 240
GTGACTTCCC CAGGATATCA ATCCTTTAAC ACGCCACATC AAGTATTGTA TACAGGnAAA 300
TTCnGGGTAC GACAACACGA TTATAGGTG TTAAGTGGGT TAGGTATTGA AAGTGGTTG 360
GTCnGGCGA ATGTTTCCA ATTGGTAAA AGGCCATGG 400

(2) INFORMATION FOR SEQ ID NO: 4117:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4117:

AATAAAAAGG AACAAACGA TGGCTATTGA TATGGACACA AATCATAAAAT AGCTGCTTTG	60
TTCCTTTTTT AATTTATATA TTTAnAATAC ACATATCAA GAGCCTCGAG ATATAAGTCA	120
ATGTACTAGG CCACACAATT TAATATTGAC AGTAATTACC CGAACGAAAA TGCGCCCCGG	180
GGCCCCAACCA TGGGGAAATT CGAAAAGAAA TTCTACAGAC AATGCAAGTT GGCGGGGCC	240
CAACATAGAA GCTGGCCAAT AGTTAGCTTT CAATAATGTG CCAGTTGGGG TAAGGGCC	300
AACACAGAAG CTGGCCAATA GTCAGCTTC AATAATGTGC CAAGTTGGGG TAAGGGCCC	360
CCACCACAGG GAATTCGAA AGAAATnCT	389

(2) INFORMATION FOR SEQ ID NO: 4118:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4118:

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC	60
TGTGGATTAA TATTATGCCT GGCAACGTTG TACTCTAGCG GAAAnTAAGTT GACTACCATC	120
GACGCTAAGG AGCTTAACCTT CTGTGTTCGG CATGGGAACA GGTGTGACCT CCTTGCTATA	180
GTCACCAGAC ATATGAATGT AATTTATACA TTCAAAACTA GATAGTAAGT AAAAGTGATT	240
TTGCTTCGCA AAACATTAT TTTGATTAAG TCTTCGATCG ATTAGTATTC GTGCAGCTCC	300
ACATGTCACC ATGCTTCCCA CCTCGAACCT ATTAAACCTC AnCATCTTG AAGGGGATCT	360
TATnAACCGA A	371

(2) INFORMATION FOR SEQ ID NO: 4119:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4119:

GCACATTAG CCCAGTTAGA GAAAGATTGA CCTAATCTAT CCAACCAATC AGCCGACAT	60
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TGAAACAGTG	GTGCTAATTG	CGGTGAATAAC	ATTGACTAAT	CCGTCACCAA	AACCACCTGC	120
AGCACTTAAT	AGCTTGTAA	ATACCGAAAC	ACCCGTTGTA	TTCATCATAT	TAAAGAATCT	180
TGAAGCTACA	CTGCTATTTT	CAGCCCATTn	AAGCACGCTT	TGAGACGCTT	CTTCCATTCC	240
TCTTGAAATA	CCACTAAAAA	ACGGnTGTAA	GCTCTGCATT	GCAGTTTAA	CAGTATTAA	300
ACCATTTGCA	AGAGTTGTGA	AGnTAGCGGA	TTGATTTGC	T		341

(2) INFORMATION FOR SEQ ID NO: 4120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4120:

GGTGAGAAA	AGCCAACACA	GCTAGGGTAG	TATCCCACCA	GCGCCTCCAC	GTAAGCTAGC	60
GCTCACGTTT	CAAAGGCTCC	TACCTATCCT	GTAAAGCTG	TGCCGAATT	CAATATCAGG	120
CTACAGTAAA	GCTCCACGGG	GTCTTCCGT	CCTGTCGCGG	GTAACCTGCA	TCTTCACAGG	180
TACTATGATT	TCACCGAGTC	TCTCGTTGAG	ACAGTGCCA	AATCGTTACG	CCTTCGTGC	240
GGGTCGGAAC	TTACCCGACA	AGGAATTTCG	CTACCTTAGG	ACCGTTATAG	TTACGGCAG	300
CGTTTACTGG	GGCTTCGATT	CGTAGCTTCG	CAGAnAACG	CACTTCCTGT	TAAACCTTTC	360
CAGCACCGGn	CAGGCGTTCA	CCCTnATTAC	ATCAACTTTA			400

(2) INFORMATION FOR SEQ ID NO: 4121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4121:

AATAAATCTT	GCTTTATTCT	TTTTACCAGT	AATATCTAAA	TGAGTTGGAT	ATTTAACTTT	60
CGCATTAAATT	TCAATATTAA	ATTGCGTTAC	CGCGACAAGC	GCAAACACAA	CATACATAAT	120
AAGATTGGCT	AAAAAGATAT	AGTTAAAGCT	AAATTCTGCG	ACAAAGCCGC	CCATTGCAGC	180
ACCGACAGCC	ACACCAATAT	TTTGCCTAA	GTATATCGCA	TTAACGTTT	GTCTTCCGCC	240
ATTGGCCAC	ACTGCTCCAG	CCATAGCGTA	TATCAGGA	ATAATCATTC	CGCCACCAAA	300
CCCTAACATT	ACCAGGCCAT	ACCAGCATAAC	CCAGGGCCAC	CCGnGGAAGG	AAATTAAGTA	360

GCGGTGGTAC TACCAAnGAC CAGTGGAAAGG TnCCAATTAA

400

(2) INFORMATION FOR SEQ ID NO: 4122:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4122:

GATAACTAAT AAAGTTAGT TAAGTATTAA AATAACAAGT AGTATGTCAT TCTAAGCT	60
AGAACAGATA TACTACTTGT TTGTTTTGT GGAAAATTGA GTATATTCAA AAGGATAAGn	120
ACGAGAATT CGTTATTAAA CTACGAATTC TCGATTTTT TATATTTAA GATAGGTTA	180
TTCTGAAAA CTTAATAGAA AGGGGTTTGA CAAAGCTAAA GTGAAGTTG ACGgTATAAA	240
CGCAAATTAA ATATACTTT ATAGAAAATT AACTCAGGCT GGGACATAAA TCAATATTCT	300
ATGCTCTACG GAGGTATATT GGCAGTAGTT GACTGAACGA AAnGCGCTTG TnACCAGCTT	360
TT	362

(2) INFORMATION FOR SEQ ID NO: 4123:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4123:

AATTATTAAG GTTGCTACAT GATAAATATC ACATGCATT TATCCACATG GTTGGTTTT	60
CGCGAGGTGG TTTACAAGGA TTGTTGACAT TTCAAGACTT ACCAGTAACA AGTTATACAA	120
TCTGGGGTGG TGTCTCAGAT ATTGATTAA TGTATGAAGA ACGTGTGAT TTAAGAGGCA	180
TGCTACGAAG AATGATTGGT CATCCGAAAA AAGATCGAGC GGGCATATGA GGCACGCAA	240
GCGATTCAA ACATTAATGA AACAGTCCG CCAATATTAA TTGTACATnG GAGGGGAAAG	300
ACCCAGCAAG TTGGGTATTn CATCATGCGT ATTATTTAA GC GGACCAAC TA	352

(2) INFORMATION FOR SEQ ID NO: 4124:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4124:

AACCAGGTGA TCTACCCCTG GTCAGGTTGA AGTCAGGTA AACTGAATG GAGGACCGAA	60
CCGACTTACG TTGAAAAGTG GAGCGGATGA ACTGAGGGTA GCGGAGGAAA TTCCAATCGA	120
ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTAGGGC TAGCCTCAAG TGGATGATTA	180
TTGGGAGGTA GAGCACTGTT TGGACGAGGG GCCCCTCTTC GGGTTTACCA ATTCAGACA	240
AACTTCCGAA TGCCAATTAA TTTGAACCTn GG&TTTCAGA ACATGGGTGA TAAGGTCCnT	300
GTTTCGnAAn GGGAAACAGC CCAGACCACC AGTTAAGGTC CCCAAATGTA TGTTTAAGTG	360
GAAAAGGGTT TTGGCGTTGC CCCGACAACT AGGATGTTGG	400

(2) INFORMATION FOR SEQ ID NO: 4125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4125:

GGCTTATTAA TCAAAAAATT TATAAAGAAT ATGTAGAAAA CTTTTATTAA CATGAGGCT	60
ACACGCTACA ACAGAAAATT AAAATTTAA TTAGCTTATA CATTGTAATA GGTTTTCAA	120
TTTATATGGT GGATGTTCTT GCAGTCCGTG TAGGATTAAT CATAATGGTT ATCATACAAA	180
CCGCTGTACT CTTTACATTT GTAAAAACAT TACCCAAATC AAATCATAAA ATAGAGGAGT	240
GATTGCCCAT GTTTATGGCA GAAAATAGAT TACAATTACA AAAAGGCAGT GCGGAAGAAA	300
CGATTGAACG TTTTACAAT AGACAAGGTA TTGAAACTAT TGAAGGCTTC CAACAAATGT	360
TTGTCACTAA AACATTAAT ACCGGGATAC AGCCGAGTAA	400

(2) INFORMATION FOR SEQ ID NO: 4126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4126:

AATCTATATT TTACTTACTT ATCTAGTTT CAATGTACAA TTTCTTTTA GTCAAGCGCT	60
CGCATAAGCA ATATCACTTT AACCAAAAAA TATTGAAATG TTAAATAAAC ATTCAAAACT	120
GAATACAATA TGTCACATTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA TATATCCTTA	180

GAAAGGAGGT GATCCAGCCG CACCTTCCGA TACGGCTACC TTGTTACGAC TTCACCCAA	240
TCATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAAGGGTT ACTCCACCGG CTTCGGGTGT	300
TACAAACTCT CGTGGGTGTG GACGGGGCGG TGTGGTACAA nGACCCGGGG AACGTnATTc	360
AnCGGTAGCA TGGCTGGATC TAACGATTa CTAnGCAGAT	400

(2) INFORMATION FOR SEQ ID NO: 4127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4127:

CGAAATTG AGTAAAAGAT GTGCAACCAAG CGAAACCAAC TGTGACTGAA ACAGCGGCAG	60
GAGCGATTAC AATTGCACCT GGAGCAAACC AAACAGTGAA TACACATGCC GGTAACGTAA	120
CGACATACGC TGATAAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC	180
GTCGCAATAA TACGAGTCCA TGGGTGAAAG AGCATCTGC AGCAACTGTA GCAGGTATTG	240
CTGGAACTAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GGATACAATT	300
CCAAGTTGGT TGCAACGCCA AGGAAGCGGA GAGACCAGTG AAGTGATTGA GCCACCGTAA	360
TGGTTGGnTT CCCCAGTTG TCGGCAAnCCA CAACCGGAAC	400

(2) INFORMATION FOR SEQ ID NO: 4128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 4128:

GATTAGTGA AAGTTGGTTG TACTATTACC GTTAAAATTT GGAGATTATC TGTCGTCTTC	60
AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC CATGTCAAAG TACCATTGc	120
AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GCCTACGCGT TACATGAAAA ACGGAGAAC	180
AGCAGAACAA TTATTACGTC AGCTTATAGA AAAAGATGAA GCACTAGCTA AGTATGTCAT	240
GGGTTGTGAT GAAACAGCTT GGTGGTCATA TATGGGTCCA GATAATGATA TTTTCCAAGA	300
TCCATTAnGG CCATCTAACT GTTCCAGCTA AGGAAAGTAT CCCCGAAGTG GCTAAGCCCC	360
AAAATGATTA CGCCAACCAAG CTAGTGGTCC ATGCCAGC	400

(2) INFORMATION FOR SEQ ID NO: 4129:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4129:

AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA TAGATGGnGG AGGGGGGCAG	60
ATTCGAACTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC	120
CCCTCCAGCT TATTCAATATA ATTTAATAAT CAAAATGGTG GAGAATGACG GGTCGAACC	180
GCCGACCCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGG AGCTAATTCT CAAAAATAAT	240
GACTCCTGAC GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGTGTTC TTGAACCGCT	300
TGGACCAAGG GAGCCATGGC TCCAACAGGT GAGGGACTCG AACCTnACGG ACCGATTGG	360
TTnAACAGCC GGAT	374

(2) INFORMATION FOR SEQ ID NO: 4130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4130:

TTTnACATGC ATCTGAATCT CTAATTTAA AnAAATATGn ATATAAATAA GACAGTAAA	60
ATTAAATTTC AGTTGTTGCA ATTTCTTCAT CTGTAGGTAC ATCATCGTTA AGGCCAACAA	120
GTCCTTCAGA AACATTCGT GAATGATAAC CGATAACGTT AAGAACrCsA ATCATATCGA	180
TATATAGTAA TCCGCCTTT GTTGTACATT CACCACGATT AAGGCGTTA ATATGACCTT	240
TGCGTAGTTT ATGTTCAATA TTAAATGATT CTCTACTACG TTCTACAATT TCATCTTTT	300
TCGTTTGTC ATAAACATCT AACATGTCGA TGGCTTATC AAATGACTCA GCAAATGGT	360
TGGAATAAnT TATCCATACC GCGTTGTGCA TCTnCTGGTA ATGCGAATAT CTTCATCATG	420
TTGGCGGTTT T	431

(2) INFORMATION FOR SEQ ID NO: 4131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4131:

TTTAGTTGAA GGCGGTGTG TCGCATTGC TGTTGTTGC GGTGCTTCTA CTTAGTTGA	60
GGGCGGTGTG GTCGCGTTG GTTTGATTG CGGTGCTTCT ATTTAGTTG AGGGCGGTGT	120
TGATGTGGTG CTTCCACTTT AGGnAAnTGA GTGTTGTCGC GTTTGCTGCT TGCCTGTCG	180
TTGTGATTAC ACCTGTTGTT AAAAGGCCTA GTGCTAAACT TGTTTAGCA ATCGTTGTTA	240
TTTCATAGT TGTATGCTCC ATTGTAATT ATAGATTG TTGATAACAT TCATTGAATC	300
ATACAGCTTT ATTATAGAGG CGTATTGCTC CATTACATT AACCTGTnT AACCAGATTG	360
GAAGCAGCGT TGAATnAAAT GAAGAAAGCC AGAAGTTCGT	400

(2) INFORMATION FOR SEQ ID NO: 4132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4132:

CCATTCACTG TATGTCTTG GCCACCACCT TGACGTTGTT GTTGCTGTTG TGATTTGA	60
TTAGCTTGTGTT GTTGATTTG ATTATTTGT GCTTGATTGT TCGCTTGATT AGCGTTGTTT	120
TGATCATTAT CAGATTCACTC TTTAGTCGCT TTGCTTGAT CCTCTTTGA TTTATCACTG	180
TCTGTAGATT TTGATTTATC TTTAGAAGCG TCTTAGATG TGTCTTGTC TTTACTTTCA	240
TCAGCATTAT TTTTATTTGT ATTGCGATT TTATTTCTT TTGTACCATT ATTATGATTG	300
TTTAATGCCA TGCCTCCAAA TATCGCTAAA TGCACCGATA AATnAGTACA GCTGCAATGA	360
ATGGTAACAA TACTTGGGC CAGnCACCGT TTTACGGTn	400

(2) INFORMATION FOR SEQ ID NO: 4133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4133:

TTGAATACTT TTCTTCCACA CAAATGTATA TCTATTGGCA TTAGCTTCTA CTTTGTCACC	60
ATCAATAAAA ATTGAATTAT TATCAATAAG ATTTGCTTT AAACATTGAC TATGGAACGT	120
AATAAATAAA GATTCAATTA ACGCATCAGT ATTAGGATTC ACTCTAAAAC GATTAATAGT	180

TTTATAAGAA GGTGTTGAT TTTGAGCTAA CCACATCATT CGAATACTGT CAGAAGTAA	240
TTTCTCTATT CTTCGACCAG AAAATACAGA TTGAGTATAT GCATATAAGA TGATTTTAA	300
CATCATTGGGATGATAG GATGTTGCAG CACGATGATG TCTGAATTCA TCGAATTGC	360
TAnCGGGTAC CGTTCCACCA ATTCCATTAA CATATCGCGG AATATCATT TGAGGAA	417

(2) INFORMATION FOR SEQ ID NO: 4134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4134:

GGTTTAATAT GGACCTTGCG CGTnTTTATG TTCAATATTA AATGGATTCT CTACTACGTT	60
CTACAATTTC ATCTTTTTC GTTTGTCAT AAACATCTAA CATGTCGATG GCTTTATCAA	120
ATGACTCAGC AACATGGTTG nAATAATTAA TCCATACCGC GTTGTGCATC TTCTGTAATG	180
CGnAATATCT TCATCATGTT GGTCGTTTA ATTGAGCGAC ATACTCTTCT GTTAGCTCTG	240
CTACTTTAA AATAGAGCGA TTGACATCAA ACATAACTGC TAAACGCTCA ACGTCTGCCT	300
TCGTAATGGC TTTTGTAGAA ATTCTAACTA AATAATTTCG AATGCTATCA TTGT	354

(2) INFORMATION FOR SEQ ID NO: 4135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4135:

CTGGGATCGC CACCTTAAG TCTAACAAACC TTGTTATATC GACGCGCTGCTTCCACGATA	60
CAGTCATTAA TTTTTCTTG CTGAATATGT TTTGCATACG GCTTTTACCC AACATCGATA	120
ATTCAGTAG TCAAATTCCG ATATTGTAAA ATTAACGGAT TCACTAATCG ATCATATAGA	180
ATGACATCCG CTTCACGTAT TAAACGCTCA GCCTTTTCG TCAAATAATT CGGATTACCT	240
GGACCCGCAC CTATCAAGTA AACCTGCCA TATTCCCTCA CAGACATATA TATACGGTCC	300
CGTCTGTAAC TTCTACCTCA TAAACATCTA CACAACCTTC ATCAGGTCTG GACAATACCT	360
GnATTAAACA ATTTTGATC GTGGGGGGGC AAATACATAT	400

(2) INFORMATION FOR SEQ ID NO: 4136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4136:

ACCACTGAAT CGTTCATCAT TTTCA A TTT TGAATCTGCT GTCCATTTCG CACTGTATGG	60
TGGGTTCGCA ATAACCGCAT CAAATGTATT GCCTAAAAAG GCTGGATTT CCAATGTGTC	120
ATCATTACGG ATCTCGAAGT TCTCATAACG CACATCATGT AATAACATAT TCATGCGTGC	180
TAAGTTGTAT GTAGTATTGn TACGTTCTTG TCCGAAATAA CGATACACTT GGTTTCTTT	240
ACCAACACGT AACAAACAATG GAACCGGAnC CACATGTTGG GTCGTACACG TGGACGTAAT	300
TTATCnTTAC CGTGCTGTGA CAATCTTCGC CAGTATCTTA GATACTTG	348

(2) INFORMATION FOR SEQ ID NO: 4137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4137:

AGGTGGGGAT GACGTCAAAT CATCATGCC CTTATGATTG GGGCTACACA CGTGCTACAA	60
TGGACAATAC AAAGGGCAGC GAAACCGCGA GTCAAAGCAA ATCCCATAAA GTTGTCTCA	120
GTTCGGATTG TAGTCTGCAA CTCGACTACA TGnAAGCTGG nAATCGCTAG TAATCGTAGA	180
TCAGCATGCT ACGGTGAAAT ACGTTCCCGG GTCTTGTACA CACCGCCCGT CACACCACGA	240
GAGTTTGTAA CACCCGAAGC CGGTGGAGTA ACCTTTAAG GAGCTAGCCG TCGAAAGTGG	300
GGACAAATGA TTGGGGTGAA TCGTAACAAG GTAAGCCGTG ATCGGnAAGG TGC GGCTGGG	360
AT	362

(2) INFORMATION FOR SEQ ID NO: 4138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4138:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTCCCC ATT CGGAAT CTCTGGATCA	60
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AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA	120
GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC CATTTTATA	180
AGTCAAACGC TCACATACGG CTTCGTTTC ATTATTTAA ATGCTCATT ACATAAGTAA	240
ACTCTGCTTT AAAATAATTT AACTGCATTG TCTGCTAACAC GTTTCTTTT ATAAAAAGAT	300
TTAAACGCGT TATTAATCTT GTGAGTGTTC TTTCGAACAC CAGCGATTAn TTCnTGAGGA	360
ATTCAAGCCT AnTTAAAACC CTTA	384

(2) INFORMATION FOR SEQ ID NO: 439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4139:

CTCATTATGG GACGTGCACA AGATGGTTT CTTGATCAAG ACAAAATATGA CATTATTTTC	60
AAAACAGCTG AAAATTTAGA CGTACCGATT TATCTACATC CCGCGCCAGT TAACAGTGAC	120
ATTATATCAAT CATACTATAA AGGAAATTAT CCTGAAGTAA CTGCGGCAAC ATTTGCTTGT	180
TTTGGTTATG GTTGGCACAT TGATGTCGGC ATTACATACAA TACATCTnGTnTnATCTGGT	240
ATTTTGATC GTTATCCAAA GTTAAATATG ATTATTGGAC ATTGGGTGAG TTATCCCATC	300
TCCCTAGAAC GAATGGATGA AGCTTATCCG TGAACATTTG AACCACCCCG GAAGCAATAC	360
TTAAAAATAA ATTTAnTATC ACACCGGGTG GCATGGTACC	400

(2) INFORMATION FOR SEQ ID NO: 4140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4140:

CAACCACATT CGCTCGGCTC ACCTTAGAAT TCTCATCTTG AACTACCTGT GTCGGTTGC	60
GGTACGGrCA CCTATTTCT ATCTAGAGGC TTTCTCGGc AGTGTGAAAT CAACGaCTCG	120
AAGACTCAAT GTCTTCTCCC CATCACAGCT CAGCCTAAC GAGTACCGGA TTTGCCTAAT	180
ACTCAGCCTT ACTGCTTAGA CGTGCATCC AATCGCACGC TTGCGCTATC CTACTGCGTC	240
CCCCCATCGA TTAAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT	300

AAGCCTGTCG GGCTCAGCTT AAGGACCCGA CTAACCCCAG AACCGGAAGA GCCTTCCTCT 360
GGAAAAACCTT AGTCAATCCG TTGGACCAGGG ATCTCAACCG 400

(2) INFORMATION FOR SEQ ID NO: 4141:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4141:

CATATCGATA ACATGACATA ACTCATGCTG GGTTCCCCA TTCGGAAATC TCTGGATCAA 60
AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 120
TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTTATAA 180
GTCAAACGCT CACATACGGC TTCGTTTCA TTATTTAAA TGCTCATTAA CATAAGTAAA 240
CTCTGCTTTA AAATAATTAA ACTCATTGTC TGCTAACGT TTTCTTTAT AAAAAGATT 300
AACACGCGTTA TTAATCTTGT GAGTGTCTT TCGAACATAG GCGGAGTATT TCTTAAGGAA 360
TnCAAGCnTA TTTAAAACTC TTAATCAGnC GGTTTGCnT 400

(2) INFORMATION FOR SEQ ID NO: 4142:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4142:

GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTC ACTTCGCCAA GCCATTTTC 60
TTTGTGTTTA CTTTTTATTT TGACGTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA 120
CTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATGT CGCTAAAGAC 180
CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT 240
TTAGCTCTAC TAAACTCGTT GCGCTTTT CTCGGTTCGT CAGATTCAAA CGTTTCACTC 300
GCCAAGCCAT TTTCCTGGG TTACTTTAA TTTGACGTTT AAGGCATAAA AAAAAGAGAC 360
TTGCGGGCTC AAATGCGGnT CATCGCATCC ATTTTGnCn 400

(2) INFORMATION FOR SEQ ID NO: 4143:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 369 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4143:

TTTAAAATTG ACATTATTAC TGACCAAACA AGTCACATG ATCCGCTAAA TGGATATGTG	60
CCACAAGGAA GCGAAAGTAT TGCCTGAAAA AGATCCGAAA AAATATGTTG AACTGTCACA	120
AGCTTCAATG GCAAAGCATG TTGAATTAAT GCTTCCAATT CCAAAACGT GGCGCTGTAG	180
CATTTGATTA TGGTAACAAT ATTCTGTCAAG TAGCCTCAA TAACGGAnGn ATAAATGCTT	240
TTGGACTTCC CAGGTTTGT ACCAGCTTAC ATTAGACCAT TnATTCTGTG TAGGTTAAAG	300
GGCCATTCCG CTTTGCTGCG TTGGAGTGGT GGATCCAAAA GATATCGAGCGTGCCGGATG	360
GAGGAAATG	369

(2) INFORMATION FOR SEQ ID NO: 4144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4144:

GGAAAGATAA ATAGCTTCAT CAATGTCATG CGTCACTAAA ATAATAGTTG ATTGCCTTT	60
ATGTTTAGT TGCCTAGTT GATCCTGAAG TTTATAACGT GTAAATGCAT CTAATGCACC	120
TAATGGCTCA TCCATCAATA TAACGTTAGG CTTATGCACA TGCGCTCGAC ATAGTGCAC	180
ACGTTGTTTC ATACCCCCGG ACAGTTGCTC GGGAAAATGC TTTCCCCTGT CTTCTAAATC	240
AACTAATTAA AGCTGTGnT TAATCTCTTC ATCACTAATT TTCTGTTGTA ATCCAATCCT	300
AATGTTGTCA TTAATCGTT TCCAGGAGC AAATTATGGT GTTGAATAG CATAAACAAAn	360
CGGGAGnGGC	370

(2) INFORMATION FOR SEQ ID NO: 4145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4145:

CGAGGTAGCA AAGAACAAAT TGCGAAATAT GTACCTAAAT TACAGTCACA TGAACGTGCGT	60
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ACATGCTTG CTTTAAGTGA ACCAGAACAC GGTCGGACG TTGCnGAGG TCTTGAACAA	120
GTCGCTGAAC GCCAAGGCGA TACTTGGGTT ATCAATGGTG AAAAGAAATG GATTGGTGGT	180
GCACATGTAT CTGATGTCAT TCCAGTATTG GCAGTAAATA AAGAAACTGG GCAAACCCCA	240
TTGCTTGTA GTCAGACCAG AACAAAGATGG GCGTCGATAT TGAAGTCATT GGATAATAAA	300
ATCGCACTTC GGCATTGTT CTAACGCCCT AATTnAATT AAAnTAATGTT CAAAGTAGGA	360
TGAAAGCGGG	370

(2) INFORMATION FOR SEQ ID NO: 4146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4146:

TGGGGTGTGTT TTACCAATAA AGCGTTGCAA GGTGGCGGTA GTTTAATCGA TTATGGTTGC	60
CACTTGTAG CTACTAGGTA AAGATATGGT GCCGCATGAA GTCTAGGAAA AACATATAAT	120
CAATTGAGCA AACAAACCGAA TCAAATTAAT GATTGGGAA CATTGATCA TACTAAATTT	180
GATGTCGATG ATCATGTTAC TAGTTATATG ACATTGCCA ATCGAGCAAG CATGCAGTT	240
GAATGTTCGT GGTCTGAAA TATCAAAGAA GATAAGGTT ACGTTnTTT ATCAGGAGGA	300
GGATGGCGGT ATCCAATTAA TTTCCATTG GAAATATATG GnGCCCGTT TTGGGAACnC	360
ATTTTTGGA AAGCCAAGCT	380

(2) INFORMATION FOR SEQ ID NO: 4147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4147:

TACTTATCTA GTTTCAATG TACAATTCT TTTTAGTCAG GCGCTCGCAT AAGCAATATC	60
ACTTTAACCA AAAAATATTG GAATGTTAAA TAAACATTCA AAACTGAATA CAATATGTCA	120
CATTATTCCG CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC	180
AGCCGCACCT TCCGATACGG CTACCTTGGT ACGACTTCAC CCCAATCATT TGTCCCACCT	240
TCGACGGCTA GCTCCTAAAA GGTTACTCCA CCGAnTTCGG GTGTTACAAA CTCTCGTGGT	300
GTGACGGCG GTGTGTACAA GACCCGGGAC GTATTCACCT GGCAGCTTn CTGGGTTTAC	360

(2) INFORMATION FOR SEQ ID NO: 4148:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4148:

CACCATAACAT GCGAAATGGA CAGCAGATTG AAAATTTGAA AATATGAAC GATTCAAGTGG	60
TTACGGCAAG CTTGCCCAA AATCCAAAGC AGACTTTGCC TTTATTCAAC ACATGGTACA	120
TTACCTAGAC GATGAAGGTA CCATGGCAGT CGTACTCCCA CATGGTGTAT TATTCCGTGG	180
TGCCGCAGAA GGTGTGATTG GTGCGCTATT AATAGAAGAA AAGAACTACT TAGAAGCCGT	240
GATTGGGTTA CAGCCAATAT TTTCTATGGG nCAAGTATTG CAACATGTAT TTGTTATTAA	300
AAATGTCGCC ACAAGACGCC ACGTACTATT ATCGATGCAT CCAATGATTT GAAAAGGAAA	360
AATCAAACCA TTAAGCGTGC CAAGCGACGA TATnGCnCTA	400

(2) INFORMATION FOR SEQ ID NO: 4149:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4149:

CAGCTATTGA TATCGATTAC CATACTGCTG TGGATAGCGA CAGGTTCACG TTGGAGGATA	60
CACTGAGTCC TCTGAGGAAT CAAATCCAAT TGACTTTGAA GAATCTACAC ATGAAAATTC	120
AAACACATCAC GCTGATGTTG TTGAATATGA AGAAGATACA AACCCAGGTG GTGGTCAGGT	180
TACTACTGAG TCTAACTTAG TTGAATTTGA CGAAGAGTCT ACAAAAGTA TTGTAACTGG	240
CGCnTGAGCG ATCATACAAC AGTTGAAGAT ACGAAGAATA TACACTGAAG TAATCTGATT	300
GAATAGTGGG TGAATACCTG AAGAGCATGn TCAGCACAAG ACCAGTCGAG GAATnACTAA	360
AACCATCATC ATATTnCAT CTGGTTAGGA CTGAAATGGC	400

(2) INFORMATION FOR SEQ ID NO: 4150:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

AAGGACGACA TTAGACGAAT CATCTGGAAA GATAATCAA	60
GAAGGTAATA ATCCTGTAGT CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG	120
GAGCACGTGA AATTCCGTCG GAATCTGGGA GGACCATCTC CTAAGGCTAA ATACTCTCTA	180
GTGACCGATA GTGAACCAGT ACCGTGCAGG AGAAGGTGAA AAGCACCCCG GAAGGAGTTG AAATAGAAC	240
TGAAACCGTG TGCTTACAAG TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTGTA GAATGAACCG	300
GCGAGTTACG ATTTGATGCA AGTTAACAT AAATGTGGAG CCGTAGCAGA ACnnGTTnTG AATAGGC	360
371 AATAGGC GTT A	

(2) INFORMATION FOR SEQ ID NO: 4151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4151:

TCAGCTTTTGATATGTAT TTTATAATGT ACAGCTCGTT GACnnTAATT TTCCTTATAT	60
TAAGTGCCAT CAATACAAAA CCTAGCTCTC GTTTAACTTT ATTTATTCT CGAACTGACA	120
TTCGAGTGAA CCCAAAATAG CCTTCATAAA TCCAAAAGCA GGCTCTACAT CAATTTTCT	180
TTGACTATAG ATGTTTTCG TTTCTGGTTC AGAAAGCTTT TGATTAATTG GGACTTTAAA	240
GTATTCCCAA TTATAATTCT TCATGGATTT TCTTATTGGG ATTCGAATT TGGTTTCATG	300
CATTGATGTC TCAAAGAACCA TGATGGAACA GTCCAnCACA TTCCAGATAG TTTGGAAGTC	360
TCGTTT	366

(2) INFORMATION FOR SEQ ID NO: 4152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4152:

TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC	60
CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT	120

TTAGCTCTAC TAAACTCGTT GCGCTCTTT CTCGTTTGT CAGATCAAA CGTTTCACT	180
TCGCCAAGCC ATTTTCTTT GTGTTTACTT TTTATTTGA CGTTTAGAC ATAAAAAAA	240
GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTG TTGCCTGGCA ACGTTCTACT	300
CTAGCGGGAC GTAAGTGGCT ACCATCGACG CTAAGAACCT TTCCTGGACT TGGTGGACAA	360
TCGChTGCT CCTTCCTCCT CCTCGGGCTC TCGGCTTACG	400

(2) INFORMATION FOR SEQ ID NO: 4153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4153:

TGATATTCT GTACCACCTA TAATCGTTT AATCGATGGG GGGACGCATA GGnATAGGCG	60
ACGTGCGATT GGATTGCACG TCTAACAGT AAGGCTGAGT ATTAGGCAA TCCGGTACTC	120
GTAAGGCTGA GCTGTGATGG GGAGAAGACA TTGAGTCTTC GAGTCGTTGA TTTCACACTG	180
CCGAGAAAAG CCTCTAGATA GAAAATAGGT GCCCGTACCG CAAACCGACA CAGGTAGTTC	240
AAGATGAGAT TCTAACGGTGG AGCGAGCGAA CTCTCGTTA AGGACTCGGG CAAATGGACC	300
CCGTTACTTC GGGGAGAnGG GTGCTCTTA nGGGTTTACG CCCAGAGAG CCCCATTGAA	360
TAAGGCCAA GCGnTGTTT ATCCAAAACA CGGTCTCTGC	400

(2) INFORMATION FOR SEQ ID NO: 4154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4154:

TTTAGCAAT CATTAAACA GTCAGTCATA TTAAAGGCTG GCTAACGATT GTTATCTnGT	60
nCAGATTGT AAGTTAAGAT TTCTTGTAA GTGTATGCAG CACCATATGC TTCAAGTGCC	120
CATACCTCCA TCTCACCAAA ACGTTGTCCA CCGAATTGCG CTTTACCGCC AAGTGGTTGT	180
TGTGTAACAA GTGAATATGG TCCTGTTGAA CGCGCATGTA ATTTATCATC AACCATGTGC	240
GCAAGTTCA ACATGTACAT TACACCTACT GAAATACGGT TATCGAATGG TTCACCTGTA	300
CGTCCATCAT AAAGTACAGT TTTACCATCA CGAGCCATAC CAGCTTCTTC AATTGTTGGA	360

CCATACATCG TCATCGTTG CACCGTCAAA TACTGGTGGA

400

(2) INFORMATION FOR SEQ ID NO: 4155:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4155:

GATCCGAAGT TACCAACAGG AGAGAAAGAG GAAGTTCCAG GTAAACCAGG ATTAAGAAT	60
CCAGAACAG GAGATGTAGT TAGACCACCG GTCGATAGCG TACAAAATA TGGACCTGTA	120
AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTG AGAAAGAACG TAAATTTAAT	180
CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG TGAGAAGACA	240
ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA AGGTGAATCG	300
AAAGAAGAAA TCACAnAAGT CCAGTTAATG AATTAACAGA TTCGGTGGCG AGAAATACCG	360
C	361

(2) INFORMATION FOR SEQ ID NO: 4156:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4156:

CAAAGTGACA GGTGGTGCAT GGTTGTCGTC AGCTCGTGT GTGAGATGTT GGGTTAAGTC	60
CCGCAACGAG CGCAACCCCTT AAGCTTAGTT GCCATCATTA AGTTGGGCAC TCTAAGTTGA	120
CTGCCGGTGA CAAACCCnGGG GnAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA	180
TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG CGAGTGCAAG	240
CAAATCCCCTT AAAGTTGTT TCAGTTCGGA TTGTAGTCTG CAAATCGACT ACATGAAGCT	300
GGGAATCGCT AGTAATCGTT AGATCCAGCA TGGCTAACGG TGGAnTACGT TTCCCGGGGT	360
CCTTGTACCA CACCGCCCCGT	380

(2) INFORMATION FOR SEQ ID NO: 4157:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4157:

TGGAGAAGGA CCCAAAATG TTGCCGTTTC AAGGTTATGT TTTACAACAT TTCGAACCTA	60
TGGATGATGG ATTCTGCCAA GTTAAAATAA CTGAAGATGT ATTGGAGCAA TTCGGTATTCT	120
AGCCAAATGA AGCATCTCAG TTTGTTAATA CAATTGCTGA CATCAAAGGC TTGAAAATAT	180
GGGTATTTGC AGTCGATGGA AGGTAATGAA ATCAGATGTC GATTACGTTCAAAAGGGCAA	240
TTGGATTATT AATGATATTG CGCAGATTTT GGTGGCGGTG GTCATCCGAA TGCAGTCAGGA	300
GTTTCAGTGG ACCAGCTGGG GTGGAnTTGA GCCACTTGCT ACCAGCTTTA CGGCACCAAA	360
ACTTnACTTA TAGGAAGGGG CCCATTCCAT CCAGGTGGGC	400

(2) INFORMATION FOR SEQ ID NO: 4158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4158:

AAATCTCTGG GATCAAATCT TACTTACAGC TCCCCAAAGnCATATCGTCG TTGTAACGT	60
CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT	120
TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTAT AAAAAGATTT	180
AAACGCGTTA TTAATCTTGT GAGTGTCTT TCGAACACTA GCGATTATTT CTTATGAATT	240
CAAGCTTATT TAAAACCTTT TATTCACTCG GTTTGCTTG GTAAAATCTA TATTTTACTT	300
ACTTATCTAG TTTTCAATGT ACAAAATAATG GTGGAGACTA GCAGGATCGn n	351

(2) INFORMATION FOR SEQ ID NO: 4159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4159:

AGTTAAAGGA ACTTTAAAG TGGTTGGCCG CCGTnATTGC CTTCCTnACC TTTTGTCCT	60
TCTCTTGTAT CTTTTCTGT CCCTGGTGCT AAATCmGGAT TAAATTACG TTCTTTCTTG	120
AATGGAATyT CTTCTTTTC TACAATCGAG TCTCCTTTA CAGGTCCATA TTTGTTACG	180

CTATCGACCG GTGGTCTAAC TACGTCTCCT GTTTCTGGAT TCTTAATTCC TGGTTTACCT 240
GGAACCTCyT CTTTCTCTCC TGTTGGTAAC TTCGGATCAA ATCGTCTCG ATGACCTGGT 300
GTTATCGTTT CTGGTCCGTA TTCTGTTAAT TCATTAATCG GATCTTTGT GATTCTTCT 360
TTTGGTTCAC CnTTnACGAA TAATnACTCC AGTAAAGGAT TTTTAAGTG TTGGTGTGCGT 420

(2) INFORMATION FOR SEQ ID NO: 4160:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4160:

ACGATAATGG TGACGGGTTA CAAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGTCCT 60
CCACGTAATC TAGCGCTCAC GTTCAAAAGG CTCCTACCTA TCCTGTACAA GCTGTGCCGA 120
ATTCAATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCAGGGTAACC 180
TGCATCTTCA CAGGTACTAT GATTCACCG AGTCTCTCGT TGAGACAGTG CCCAAnTCGT 240
TACGCCTTTC GTGCAGGTG GAACTTACCC GACAAGGAnT TTCGCTACCT TAGGACCGTT 300
ATAGTTACGG CCGCCGTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAn TAACCACTC 359

(2) INFORMATION FOR SEQ ID NO: 4161:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4161:

ATTGACTAAG GTTCCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA 60
GGCCGGnAAC GGTAGGGCGA TGGATAACAG GTTGATATC CTGTACCACC TATAATCGTT 120
TTAATCGATG GGGGGACGCA TAGGGATAGG CGAACGTGTC GATTGGATTG CACGTCTAAG 180
CAGTAAGGCT GAGTATTAGG CAAATCCGGT ACTCGTTAAG GCTGGAGCTG TGATGGGGAG 240
AAGACATTGT GTCTTCGAGT CGTTGATTTC ACACTGCCGA GAAAAGCCTC TAGATAGAAA 300
ATAGGTGCCG GTGACCGCAA ACCGACACAG GTAGTnCAAG ATGAGAAnTC T 351

(2) INFORMATION FOR SEQ ID NO: 4162:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4162:

AnCGTCCTGC TTTGCACGCC AGAGGTCAGC GGTCGATCC CGCTAGTCTC CACCATTAT	60
TTTTTACACG ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT TCCAAAAAAC	120
GTAACATAAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT CATAATTTT	180
ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA CATGCAAGTC	240
GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG AGTAACACGT	300
GGATAACCTA CCTATAAGAC TGGGGATAAC TTCGGGAAACCGGAGCCAAT ACCGGATAAT	360
AnTTTGAACC GCATnGGTCC AnAAGTGAAA GACCGGCTTG	400

(2) INFORMATION FOR SEQ ID NO: 4163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4163:

ATTTTATATA TGAAATAATC TGGGACAACA TTCATAAATC TTATTGTCGT CCATTTTTT	60
AAAATAATAC CAATCTCATT TTTAAATTCT AAACTTGGTT TCGTATAATA CGCTCTTAAA	120
TCTTAAATT TAGGATTAT TTCTGTTGGT ACTTGTTTG TGGTTGGCGA TTGTGGTGTG	180
TCTGATTTAG TAGATTGCAT TGGTTGTGGC GTGTTGTTG ATGGAGGTGT TGTCACTTA	240
GTTGnAAGGC GGTGTTGTCG CATTGCTGT TTGTTGCGGT GCTTCTACTT TnATTGCAGG	300
CGGTGTTGTC GCGTTGGTT TTGnATGCGG TGCTTCTATT TT	342

(2) INFORMATION FOR SEQ ID NO: 4164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4164:

TCACGACACG AGCTGACGAC AACCATGCAC CACCTGTCAC TTTGTCCCCC GAGGAAGGGC	60
TCTATCTCTA GAGTTGTCAA AGGATGTCAA GATTTGGTAA GGTTCTTCGC GTTGCTTCGA	120

ATTAACCAC ATGCTCCACC GCTTGTGCGG TTCCCCCA ATTCTTTGA GTTTAACCT 180
TGCAGTCGTA CTCCCCAGGC GGAGTGCTTA ATGCCTTAnT GCCAGCACTA AAGGGCGGA 240
AACCCCCCTAA ACACCTAGCA CTCCATCGTT TACGGCGTGG AACTACCAGG GTATCTAAC 300
CTGTTGATC CCCACGCTTT CGCACATCAG GTCATTAACA GACCAGAAAT CGCTTGGCCA 360
nGGGGGTnCC nCCAAAACCT TGAGGATTAA ACGGTAAAAA 400

(2) INFORMATION FOR SEQ ID NO: 4165:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4165:

TAATTATTTG CTATTATAC GAAAGCAGAA TCTCCAGTCA AAGCGCGTCC AATTACTAAG 60
GCATTAATT CATGTGTACC TTCGTACGTG TAAATCGCTT CTGCATCAGA GAAGAAACGT 120
GCAATATCAT AATCGTCAGC TAGTATGCCA TTACCCACCTG TAATACCGCG GCCCATAGCT 180
ACTGTCTCAC GCAAACGTAAC GGCATTACATC ATCTTCGCCG TTGAAGTTGC AACCTCGTCA 240
TATTCACCAC GTGCTTGCAT ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGAGCTAAA 300
TTAnCTTGCA TCATTGCTAG CTTTCCTGTA TTAACGGAA TTACTAATnG GTTGCCTGAAT 360
GCTTACGCTC AGGGACnTAA CnAAGTGGCA CGTAAGCGGC 400

(2) INFORMATION FOR SEQ ID NO: 4166:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4166:

AAAGTTCTTT GGAAATAGTA ACGTTGAAGT TGTACTCACT GGTGATACAT TTGATCACTG 60
TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCA 120
TAATGTTCAT ACAATTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAAGCAA 180
GTCTGACAAT GTTAACCTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTC 240
AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG GAAAATTATA GGTGTTGGAA 300
CCTTCAGGTG GCAAGTAGTA TGGTATGGAA TCnGGTGGTG GGTAAATAAT CCnGGTnGTC 360
CACATTGGCC CTAATAACCG ATAAAATTG GGGGGCCGGG 400

(2) INFORMATION FOR SEQ ID NO: 4167:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4167:

CTTATAATCC ACACCCCTGAG CAAACGCTnC TTATGACAGA GTATTAAAAT AAGCCGATAA	60
AGATACACAC CTTTACCGAC TATTTAAAAT ACACTCACC AATTCACTTT AATTAAATGG	120
ATTGAAGTAA CTAAATTAAT ATTATGTTGT TCAATTAAAA GCTTCATACA AACCTAATCT	180
ATTTGCACTC CACCGGTAAC ACCGAACACT TGTCCGGTTG TATAACTTGA TTCTTCTGGA	240
CGCTTAATAG CACATAAGTT CCACATAACT CAACAGGTTG ACCTGCACGG ACCTAAAGGT	300
GTTTTTGTA CCAAATGnTT GGGGATTTA CTTnGTGGGT TGTCCACCAAG AAATTGTT	358

(2) INFORMATION FOR SEQ ID NO: 4168:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4168:

TTTCTTGACC ATATGGACGT AAAGAGATGT TAGCATCACA ACGTAAAGAT CCCTCTTCCA	60
TCTTAACGTC TGATACACCA GTGTATTGAA TAATTGAACG CAATTTTCT AAATATGCAT	120
ATGCTTCTTT AGGTGAACGA ATATCTGGTT CAGATACGAT TTCAATTAGC GGTGTACCTT	180
GACGGTTCAA GTCAACTAAT GAATACTCAC CTTTATGTGT TGACTTACCA GCATCTTCTT	240
CCATGTGGAA GACGAGTAAT ACCGATTCTGT TTTGTTTCAC CGTCGACTTC GATATCGATA	300
TATCCATTAA CACCAATTGG TTGATCAAAT TGAGAAATTG AGAGCTTnTG GnTTAGCTGG	360
ATAGAAATAG TTCTTACGGT CAACTTAGAT CCGTTGCGAT	400

(2) INFORMATION FOR SEQ ID NO: 4169:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4169:

ACCATGTTG AATGAATCCA TTGGAATCAT TATTGAAGTA AATTAAGGAA TCTATAATGT	60
TCGTTAAATA AAACTGATCC CGTTGTGCTT CACACCCGAT AGATAGGGAT TTACAGAAA	120
ATTCAGGTCT CTTCCACGTC ATATTTGGAC CCATCGAAAA TTCGGGTTCT CAAATCATCG	180
AACATAACAA AAGAAGCTAA GCAACATGTA GGCGTTGTC ACTTAACTTC TTGTTTTCC	240
GATGACAGCT TCTATTTAGA GAATGTCATG ATTATTTAT ATTCACTTCA ATGTTATCAA	300
TATTAGTGCC ATCTATGACA TCTGCCATGC GATTTCTTG TAATTTTTG TGCAATCAAC	360
GTGTACnTCC ACGGTTTCA TTTAAAnAACAA ATTACCGGA	400

(2) INFORMATION FOR SEQ ID NO: 4170:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4170:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCTAA GGTAGCGAAA	60
TTCCTTGTCTG GTAAAGTTCC GACCCGCACG AAAGCGTAA CGATTTGGGC ACTGTCTCAA	120
CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG ACAGGACGGA	180
AAGACCCCGT GGAGCTTTAC TGTAGCCTGA TATTGAAATT CGGCACAGCT TGTTACAGGA	240
TAGGTAAGGA GCCTTGGAA ACGTGAGCGC TAnTTTACGT GGnAGGCGCT GGGTGGGGA	300
ACTTACCCCTA AGCTGTGTTG GCTTTCTAAC CCGCACCAAnT TATCGTGGTG GGGAGACCAT	360
GGTCAAGCGG GGCATTTGA ATGGGGGGCG GTTCG	395

(2) INFORMATION FOR SEQ ID NO: 4171:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4171:

TACATTATAG CTTTAATCGT TTGAAGTATA GTTGAAACC AGTAGTCACA GCTGTTCAAG	60
GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG TACTTTACTC ACCTATTGTT GTCGCTGCAA	120
GTGAAACATA TATCGGTCTT GTTGAAGCAG GTGTTGGCTT ATTACCGAGT GGCGGTGGCC	180
TTGCAGAAAT GGCTGATCGC ATATTACGCA CATCGCATAA GTTTGATGAC AAACAAGCTT	240

CCATGACAAA AGTACTGACG AATATCGCAT TGC G AnGCT CTACAAATGC CTTTGAGGCA	300
CGTCGTATGG GTATTACCG TGGATACAGA TACGATnATT TCCAATACAG CACAACGnGT	360
CGAAGTGGCG C	371

(2) INFORMATION FOR SEQ ID NO: 4172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4172:

ATGGTGGAGA TAGCGGGATC GAACCGCTGA CCTCCTGCGT GCAAAGCAGG CGCT T CCCA	60
GCTGAGCTAA GCCCCCATAA TAATTACAGT ATATCGGGAA GACAGGATTC GAACCTGCGA	120
CCCCTTGGTC CCAAACCAAG TGCTCTACCA AGCTGAGCTA CTTCCCGTAT AATTAACGCG	180
CCCGATAGGA GTCGAACCCA TAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG	240
CTACGGGCGC ATATGTTTT ATTGAAAATn GTGCCGAGGA CCnGAATGAA CCGGTACGTG	300
ATCATTACCG CAGATTTAA GTCCTGTGCG TCTGCCAGTT CCGCAnCCCG GACTATAAAA	360
T	361

(2) INFORMATION FOR SEQ ID NO: 4173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4173:

GTACAGATGC ATTGTTAAC AATCAGTTGC A CAGCTGTT GAAACTGGTA GAGTATCTAA	60
TGGTGATTAA ATCATTATTA CTGCTGGTGT ACCAACTGGT GAAACTGGAA CTACTAATAT	120
GATGAAAATC CACCTAGTTG GTGACGAAAT TGCTAATGGT CAAGGTATTG GACGTGGATC	180
AGTTGTTGGT ACTACGTTAG TTGCTGAAAC TGTTAAAGAT TTAGAAGGTA AAGATTATC	240
TGACAAAGTT ATCGTTACTA ACTCCATCGA TGAAACGTT GTACCTTATG TAGAAAAAGC	300
TTTAGGCTTA ATTACAGAAG AAATGGTATT nCACACCCAG TGCCATGGTT GGTTAGGAAA	360
AGnAATCCCA CCGTTGTAnG	380

(2) INFORMATION FOR SEQ ID NO: 4174:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4174:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAG	60
CTGAGCTGTG ATGGGGAGAA GACATTGAGT CTTCGAAGTC GTTGATTCA CACTGCCGAG	120
AAAAGCCTCT AGATAGAAAA TAGGTGCCCG TACCGCAAAC CGACACAGGT AGTCAAGATG	180
AGAATTCTAA GGTGGAGCGA GCGAACTCTC GTTAAGGAA CTCGGGCAAA ATGGACCCCG	240
TTAACCTCGG GAGAnGGGTG CTCTTTAGG GTTAACGCC AGAAGAGCCG CnTTGAATAn	300
GCCCAAGCGC TGTTTATCCA AAACACAGTC TCTGCTnAAC CGTAGGGGAT TGTATAGGGG	360
CTTACGCCTG CCCGGTGCCT GGAAGGTTA AAAGGGTGGT	400

(2) INFORMATION FOR SEQ ID NO: 4175:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4175:

AGCCATGGCT CAGCGAGGTA GGACTCGAAC CTACGACCGA TCGGTTAACCA GCCGATAGCT	60
CTACCACTGA GCTACTGTGG ATTAATATTA TGCCTGGCAA CGTTCTACTC TAGCGGAACG	120
TAATTCGnAC TACCATCGAC GCTAAGGAGC TTAACTTCTG TGTTCGGCAT GGGAACAGGT	180
GTGACCTCCT TGCTATAGTC ACCAGACATA TGAnTGTAAAT TTATACATTC AAAACTAGAT	240
AGTAAGTAAA AGTGATTTG CTTCGAAAAA CATTATTTT GGATTAAGTC TTCGATCGAT	300
TAGTATTCGT CAGCTCCACA TGTGCACCAT GCTTnCCACC TCGAACCT	348

(2) INFORMATION FOR SEQ ID NO: 4176:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4176:

CATTTTTTA AAATAATACC AATCTCATT TTAAATTCTA AACTTGGTTT CGTATAATAC	60
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GCTCTTAAAT CTTTAAATTT AGGATTATT TCTGTTGGTA CTTGTTTGTT GTTGGCGAT	120
TGTGGTGTGT CTGATTTAGT AGATTGCATT GGTTGTGGCG TGTTGTTGA TGGAGGTGTT	180
GTCACCTTAG TTGAAGGCAGG TGTTGTCGCA TTTGCTGTTT GTTGCAGGTGC TTCTATTAA	240
GTTGAGGGCG GTGTTGTCGC GTTTGGTTT GATTGCGGTG CTTCTATTAA AGTTGAGGGC	300
GGTGTGAnT GTGGTGCTTC CACTTAGGG nAAGATnAGT GGTG	344

(2) INFORMATION FOR SEQ ID NO: 4177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4177:

CAGAACCTTG nAATGAATCG CGATGGAATA TCTCTATCTG nAAACAGATT TCTTTTGTC	60
CGCCAATGGC CTTGGAATTG TTTAAATAAA TCTATTTGCG CTTCTTATC AATGTCATAAA	120
CCTAATGCTT TTAACCTCTC TGAGAAGCGT GTTACCAGA TAATTTCCCT AATGGAAGTT	180
CAGTCGTGCT TACACCAACA AGTTGAGGTG TCATAATTTC ATATGTTCA CGATGTTTA	240
ATACGCCATC TTGGTGAATA CCTGATTCA ACTAAATGC ATTTGCCAA CAATTGCTTT	300
ATTCTAGGC ACTCGAATAC CTGCATATCT TGAnATTAAA TCCGAGGTGTT TAGTTCCCTCG	360
AG	362

(2) INFORMATION FOR SEQ ID NO: 4178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4178:

GGAGCTAATA CCGGATAATA TTTGAAACCG CATGGTAAAG nTGGAAAGAC GTCTTGCTG	60
TCACTTATAG ATGGATCCGC GCTGCATTAG CTAGTTGGTA AGGTAACGGC TTACCAAGGC	120
AACGATGCAT AGCCGACCTG AGAGGGTGAT CGGCCACACT GGAACTGAGA CACGGTCCAG	180
ACTCCTACGG GAGGCAGCAG TAGGGAATCT TCCGCAATGG GCGAAACTTn ACGGAGCAAC	240
GCCCGTGAG TGATGAAGGT CTTCGGATCG TAAAACCTTG TTATTAGGGG AGGACATATG	300
TGTAAGTAAC TGTGCACATT TTTGACGGTA CCTnATCAGG AAGCCACGGT TTACTAGGGG	360

CCCAGAAGCC CCGGTTAATA CGTGGGTGGG nAAGGGTTT

400

(2) INFORMATION FOR SEQ ID NO: 4179:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4179:

GTTGTTTCAG CAGCGACACA GTGTATTCA TTCTTAGAAA ATGATGACTC AAACCGTGCA	60
TTGATGGGTG CGAACATGCA ACGTCAAGCA GTGCCTTGA TGAATCCAGA AGCACCATT	120
GTTGGTACAG GTATGGAACA CGTTGCAGCA CGTGATTCTG GTGCGGCTAT TACAGCTAAG	180
CACAGAGGTC GTGTTGAACA TGTTGAATCT AATGAAATTC TTGTTCGTCG TCAGTTGGA	240
AGAGAACGGC GGTTGAACAT GAAAGGTGGA TTAAGATCGC TATCCATTAG CTAAATTTAA	300
ACGTTCAAAC TCAGGTACAT GTTACAACCA ACGTCCAATC GTGCCAGTT GGGAGATGTT	360
GTTGGnnnTA C	371

(2) INFORMATION FOR SEQ ID NO: 4180:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4180:

AAAGGGAATC GAATTTCTT TCTCTTCCTC CGGGTACTAA GATGTTTCAG TTCTCCGGGT	60
GTGCCTTCTG ATATGCTATG TATTCACATA TCGATAACAT GACATAACTC ATGCTGGGTT	120
TCCCCATTCTG GAAATCTCTG GATCAAAGCT TACTTACAAC TCCCCAAAGC ATATCGTCGT	180
TAGTAACGTC CTTCATCGGC TTCTAATGCC AAnGCATCCA CCGTGCGCCC TTAATAACTT	240
AATCTATGTT TCCACCATT TTATAAGTCA AACGCTCACA TACGGCTTCG TTTTCATTAT	300
nTnAAATGCT CATTACATA AGTAAACTCT GCTTTAAAT AATT	344

(2) INFORMATION FOR SEQ ID NO: 4181:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4181:

CCGTGATCGG AAGGTGCGGC TGGATCACCT CCTTTCTAAG GATATATTGGAACATCTTC	60
TTCAGAACAGAT CGGGAAATAAC GTGACATATT GTATTCAAGTT TTGAATGTTT GTTCATTCAA	120
ATTAATGGGC CTATAGCTCA GCTGGTTAGA GCGCACGCCT GATAAGCGTG AGGTCGGTGG	180
TTCGAGTCCA CTTAGGCCA CCATTAATT AATAACCTATT TGGGGGCTTA GCTCAGCnGG	240
GAGAGCGCCT GCTTTGCACG CnGAGGTCAG CGGTTCGATC CCGCTAGTCT CCACCATTAT	300
TTGTACATTG AAAACTAGAT AAGTGAAnGTA AAAATATAGA TTT	343

(2) INFORMATION FOR SEQ ID NO: 4182:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4182:

CAGAGCCAAC TCGTATGTGA TTTGTCTGCG CCAATGTATG CATCATCAAA AGTTCTGGAC	60
TACTACACGC AAACGCTGGT ACATTATGAT GTTCCGTAAA CCAAATTGCG TTAAAGCCAA	120
GTCGATCTGC TAATTTGCA AGTGTCACTG AATCTTGCAA TGCCTTTGT GCATCCTTAC	180
CTTCATCTAT TAAGGCATAG TCTAATACGC TTAATTAAAC CAATCCGTCA TCTCCAAACT	240
TATCCTGTCA TGTCAAACCG ACATAACATT TTAGCGTCTT AATACCATTTC CTCTTCATA	300
TACCCACGTA TATGATAACG TTTTCAATAA CTTTATATCT TTCGCCTTAT TTnCTTTCA	360
TATCATATTT CAGACTACAA ATGCATCATA GTTAATTAAA	400

(2) INFORMATION FOR SEQ ID NO: 4183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4183:

AAAGTATGAA AGATGGTAGT GACGCCGGTTG GTGATTGGGC TGTATTGAAT GCACTCATT	60
ACACAGCTGC AGGTGGTTCA TGGATTCAT TCCATCACGG TGGCGGTGTT GGCATGGGAT	120
ATTCACTTCA TGCGGGTATG GTTGTGTTAG CAGATGGATC AGAGCGTGCT GAAGGAAGAT	180
TGGAACGTGT ATTGACGACT GACCCAGGTA TGGTGTGCCCC CGACATGTTG nATGCTGGCT	240

ATGACATCGC TATTCAAACA GCTAAAGAAA AAGGTATTCA nATTCCAATG ATTGGTGAAA 300
GCAGGTGATA AGTAATGAAT GATTTAATAT TAATCAnATA GCAGAnTATT TTTACC GGTT 360
CCAACAGATA AACCTTGAA GGGTTAGGTA TTAGATGCAT 400

(2) INFORMATION FOR SEQ ID NO: 4184:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4184:

TTCCCTGTGC ATCGGCATCA CTATTATTAG CATGACTCAA TTATTGGAT CACAATATGT 60
CATTGCAGTT ATCATTGGTT TCGTCATATG TGCGATAGGT AATGGTTAG TCGAACACC 120
TGGACTTACG ATTGCAATT TCAGTATGCC TAATGAnAAA GTTGGTTAG CTACAGGATT 180
ATATAAAATG AGTGGTACAT TAGGTGGCTC CTTGGTATA GCACTAAGTA CTACAGTTT 240
CAGTATGTTA CAACTAAACT ATGCACCAAG TGTAGCTGCA ACCGTAACAT TTATAGTCAG 300
CATTGTATTG ATGnTCCTTG GGTnCATTGT CTGCATACAT GA 342

(2) INFORMATION FOR SEQ ID NO: 4185:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4185:

AAGCATACTC TGAAGCGGTG AACAAAAATA GAACAGATCA CATTAGACAT TTACTTGAAT 60
TTAAAGCATG TACACCGATT GACATCGACC AAGTTGAACC GGTAAGTGAC ATTGTCAAAC 120
GCTTTAATAC AGGGCGATG AGTTATGGAT CGATTCAGC GGAACACATG AAACGTTAGC 180
ACAAGCCATG AACCAATTAG GTGGAAAGAG TAATAGTGGT GAAGGTGGCG AnATGCAAAA 240
CGTTATGAAG TACAAGTTGA TGGAAGCAAC AAAGTAAGTG CGATTnAACAGTTGCTTCT 300
GGCGTTTG GTGTACTAGT GATTATTTAC CACCTGCCAA GGAATTCCAA TTAnACTTGC 360

(2) INFORMATION FOR SEQ ID NO: 4186:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4186:

CCCAAGCGGA ATTCTAAAAT GATCGTCGCT CCATTCTTCA TTTTAATAAAA TCCAAACGCA	60
GAATCTTCAA CTGTAAATTC ATCTGGATTG CATGAACCCC AAGCGTTGC CGCATGATGC	120
TGTTTATTTA ATTTATGGAA TGTTGAACCC ATCACTGATT CTGGTTCATA ATTATCCATC	180
ATCCATAACG TTAAATCTAA AGCGTGTGTA CCGATATCGA TTAATGGTCC TCCACCTTGG	240
AGCTTCTTCG TCTAGAAAGA CACCCCATGT TGGTACTGCT CGACGACGAA TGGGCATGTG	300
nCTTTCCGAA GTTAAATGTC TCCTA G TGCG CCACGTTGGC GCTGCCTGGA TGGAAAATTG	360
GACGATCTGC TCGGGAAACG AATTGGATA AACnGATGGG	400

(2) INFORMATION FOR SEQ ID NO: 4187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4187:

GAATCATCTG GCAACCnCCC CCAAAGAAGG TAATAATCCT GTAGTCGAAA ATGTTGTCTC	60
TCTTGAGTGG ATCCTGAGTA CGACGGAGCA CGTGAAATTC CGTCG A ATC TGGGAGGACC	120
ATCTCCTAAG GCTAAATACT CTCTAGTGAC CGATAGTGAA CCAGTACCGT GAGGGAAAGG	180
TGAAAAGCAC CCCGGAAGGG ATGTGAAATA GAACCTGAAA CCGTGTGCTT ACAAGTAGTC	240
AGAGCCCGTT AATGGGTGAT GGCGTGCCTT TTGTAGAATG AACCGGCGAG TTACGATTG	300
ATGCAAAnGTT AAGCAGTACA TGTGGAGCCG TAGCGAAAGC GAnGTCTGA	349

(2) INFORMATION FOR SEQ ID NO: 4188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4188:

TGGATCCTGA GTACGACGGA GCACGTGAAA TTCCGTCGGA ATCTGGGAGG ACCATCTCCT	60
AAGGCTAAAT ACTCTCTAGT GACCGATAGT GAACCAGTAC CGTGAGGGAA AGGTGAAAAG	120
CACCCCGGAA GGGGAGTGAn ATAGAACCTG AAACCGTGTG CTTACAAGTA GTCAGAGCCC	180

GTAAATGGGT GATGGCGTGC CTTTTGTTAGA ATGAACCGGC GAGTTACGAT TTGATGCAAG	240
GTAAAGCAGT AAATGTGGAn CCGTAGCGAA ACGAGTCTGA ATAGGGCGTT TAGTATTGG	300
TCGTAGACCC GAAACCAGGT GATCTACCCCT nGGTCA	336

(2) INFORMATION FOR SEQ ID NO: 4189:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4189:

CAAAGGATGT TAAGAAAATAC AATTATTAC CCAGCATTTA ATAATGGTGC TATAGAAGGA	60
ATTAATAATA AGATAAAATT AATCAAGTGA ATTCTTTTG GTTACAGAAA TTTCAACAAC	120
TTTAAAGCAC GTATAATGAT GATTTTCAGC TTGTACAAAG GAGAAAAAAA GAAGACAACC	180
AAGCCAATA ATGGACTGGC CGCCTAATAA TAAAAGCTCT AAAAGTTGTA TTTAAAAAT	240
AGTTCTTAA ATTATATACC CACCACATTG GGTGGAGGAC CTAAAAAAA GCACCTCCCC	300
AAAAATGGGA AAGTGCAAGT AGTGAGCCnT AGGAGGGTTC GGACCCCTCTn nCCCTCT	358

(2) INFORMATION FOR SEQ ID NO: 4190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4190:

TCACCAAGTT GAGCAAAGAA GATGTTCTGC GTACCTTGAA CTAAGTGCCTT TTTGACTTCT	60
AAAnGTACCAC CAAGTGCCGT CTGCCAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT	120
GGACCTAACCA ATCTTAAGAT GAAGCCATAA ACAAAAGTAC CGATGGCACC TGTTTCGTT	180
ACAAATCCAC CAACATGATA AATGCCGGCT TGTATGCTTG GCCAATGAA AAACATCAAT	240
ACACCTAAAA AGATTGCGGC AAATGCTGTG ACAATAGGGA CAnATGTAGA GCCACCAAAG	300
AAACCTAAAT ACGGTGGTAA TACCATTGTG GnTATTTGTT GTGAAGTATT GCGGTCTAA	360
TA	362

(2) INFORMATION FOR SEQ ID NO: 4191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

TGATCACCCA TGTTCTGGAC TCCCAATTGA AATTGAATTG GGCATTCGGA GTTGTCTGG	60
nATTCGGTAA CCCGnGCAGG GTCCCCCTCGT GCCAAACAGT GCTCTACCTC CAATAATCAT	120
CACTTGAGGC TAGCCCTAAA GCTATTCGG AGAGAACCGAG CTATCTCCAG GTTCGATTGG	180
nATTTCTCCG CTAACCTCAG TTCATCCGCT CACTTTCAA CGTAAGTCGG TTGGTCCCTC	240
CATTCAGTGT TACCTGAACT TCAACCTGAC CAAGGTAGAT CACCTGGTTT CGGGTCTACG	300
ACCAAATACT AAACGCCCTA TTCAGACTCG CTTCGCTAA GGCTCCACAT TTACTGCTTA	360
AC	362

(2) INFORMATION FOR SEQ ID NO: 4192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4192:

CGTGTATTAT GCCTTCTACA TTGGCCATTA TGAAAACCTTA TTATCAGGGT GCTGAACGTC	60
AGCGTGCCTT AAGTTATTGG TCTATCGGTT CTTGGGGTGG CAGTGGTATC TGTTCACTCT	120
TCGGTGGTGC AGTTGCGACA ACTATGGGTT GGAGATGGAT TTTCATCTTC TCAATTATCG	180
TTGCCGTACT TTCAATGTTA CTCATCAAAG GGACGCCTGA AACGAAATCA GAAATTACCA	240
ATACACATAA ATTTGACGTT GCAGGGCTAA TTGTTCTAGT AGTATGTTGC TAAGTTAAC	300
GTTGTCATTA CTAAAGGTGC AGCACTTGGn TACACATCAT TATGGGTCTT GGGTTGAATG	360
CCAATCGGAA ATTGTAGCAT CTTAATTTC CTAAAGGTG	400

(2) INFORMATION FOR SEQ ID NO: 4193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4193:

AATCCCATGG ACCCTCAAAT TCTTTATCTA AATAGTACCC TAATGAAGTT TTTCTGTGCA	60
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TGTGATTAAT	TTCATGTAAA	CCGATGACAC	CAACTAGCGT	TCCTTCATAC	CAAATGCCAC	120
ACTGAAATCC	ATTACCATCA	GCAAATTGCA	AAAGTCCTCT	TTAATAAAT	GCACGCGTAT	180
CTGATGGTTG	CTCAGTTGCA	TCTACCCAAG	GTAACCATTC	CCTAAGTGAA	TTTCTTGAAC	240
GATTGACTAA	ATTGAAAAGC	GCTTCTGTGT	CATGAGCTTC	TAAAATTTA	ATGTTATTGT	300
TCAATCACTT	TCATTCCAAA	CATACnATCA	CATCCTCATT	CATTnTCATA	TAATCCGGnA	360
ATGACCATAT	GAT					373

(2) INFORMATION FOR SEQ ID NO: 4194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4194:

ACAAAGGACG	ACATTAGACG	AATCATCTGG	AAAGAGAAC	AAAGGTAATA	ATCCTGTAGT	60
CGAAAATGTT	GTCTCGAGTG	GATCCTGAGT	ACGACGGAGC	ACGTGAAATT	CCGTCGGAAT	120
CTnGGAGGAC	CATCTCCTAA	GGCTAAATAC	TCTCTAGTGA	CCGATAGTGA	ACCAGTACCG	180
TGAGGAAAGG	TGAAAAGCAC	CCCGGAAGGG	AGGTGTAAAT	AGAACCTGAA	ACCGTGTGCT	240
TACAAGTAGT	cAGAGCCCGT	TAATGGGTGA	TGGCGTGCCT	TTTGTAGAAT	GGAACCGGGCG	300
AGTTtACGAT	TTGgATTGCA	AGGTTAAGCA	GTAAATGTGG	GAGCGTA		348

(2) INFORMATION FOR SEQ ID NO: 4195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4195:

AAGGCAGATG	CTCTCCCAGC	TGAGCTAATT	CTCCGATTAA	AAACTGCCTG	GCAACGTTCT	60
ACTCTAGCGG	AAntAAAGTnG	GACTACCATC	GACGCTAAGG	AGCTTAACCT	CTGTGTTCGG	120
CATGGGAACA	GGTGTGACCT	CCTTGCTATA	GTCACCAGAC	ATATGAATGT	AATTTATACA	180
TTCAAAACTA	GATAGTAAGT	AAAAGTGATT	TTGCTTCGCA	AAACATTTAT	TTTGATTAAG	240
TCTTCGATCG	ATTAGTATTC	GTCAGCTCCA	CATGTCACCA	TGCTTCCACC	TCGAACCTAT	300
TAACCTCATC	ATCTTGAGG	GATCTTATAA	nCGAGTTGGG			340

(2) INFORMATION FOR SEQ ID NO: 4196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4196:

TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAAATTAA TGAAAGATAC AGTAGGTGCT	60
GATGTAGAAC TAAAAGCATC AGGTGGCGTA CGTAATTTAG AAGATTCAA TAAAATGGTT	120
GAAGCAGGTG CGACACGTAT TGGTGCGAGC GCnGTGTTCA AATTATGCAA GGTTTACAAG	180
CAGATTCAAG TTACTAATAT ATATnAATnT TGGGAGTGATAGCTATGACA AGACCATTAA	240
ATCGTGTACA TTTAATCGTA ATGGATTCAAG TAGGTATTGG TGAAGCGCCA GACGCAGCTG	300
ATTTTAAAG ATGGAGGTTC ACATACTTTT A	331

(2) INFORMATION FOR SEQ ID NO: 4197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4197:

GTAGACGTCC CGATAGCCGT TACGCATGGT TACGATGTGT ATTGGTGTGCG GCATGGGTGC	60
AGCTGCTATA TTTGAATATG TGCCTTAGAA TGGTTGATTT TGGATGAAGC GGATTGTTT	120
TGTTATTGAA TGAAGTAGGC TGAAGTTGAA GCCAGTTGAA GTTGAAGCGG GTTGAAGCAA	180
TTTCGTTTA TTGAATGAAG CTGTGTGAAA TATAGTGATT GAACAAAAAA AGTGGTTAA	240
TGGGATGGTG GTTATTGCG TTTAGAATT TAACATTTAC ACGTCTAATT TTAAATCATT	300
GTTTAAATT TTATGAATCG AAGCCCTTG GATTTAATAn TATTGCTAAT GCnAGTAAC	360
nATCTGATTG T	371

(2) INFORMATION FOR SEQ ID NO: 4198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4198:

GCGACCCCAA CCTTGGCAAG GTTGTnATTC TACCGCT EAA CTACTTCTGC ATATGCGGGT	60
GAAGGGAGTC GAACCCCCAC GCCGTAAGCT nAGnATCCTA AGTCTAGTGC GTCTGCCAAT	120
TCCGCCACAC CCGCAAATGG TGAGCCATAG AGGATTGAA CCTCTGACCC TCTGATTAAA	180
AGTCAGATGC TCTACCAACT GAGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTG	240
ACCCCCAACC TACTGATTAC AAGTCAGTTG CTCTACCAAT TGAGCTAGGC CGGCAATATG	300
TAAGAATAAA TGGTGGAGAA TGACGGGTTC GnACC GTCGA CCCTGTGCTT GTTAAGGCAG	360
ATGGTTTCC CACTGGGTA AATTTCCGA TTTAAAAATG	400

(2) INFORMATION FOR SEQ ID NO: 4199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4199:

ATCAGTTGCT GTTGCGCCTT GTGGTAATGA ATTTACTAGT CGTACACCAA TAACCTCTGG	60
AATTGGGAAA TAAGAAGGTT GTCCAAGCAT TCCAGCTTCA GCTTCAATAC CACCAACACC	120
CCATCCTAGT ACGCCAATAC CATTATCAT TGTTGTATGT GAATCAGTAC CAACTAATGT	180
ATCTGGAAAT GCAGTTTTT CACCATCTAC ATCACGAA@ TGTACAACAC TTGCTAAATA	240
TTCTAAGTTA ACTTGGTGAA CTATTCCAGT TGCAGGAGGG AACTGCATTG TAATTATCAA	300
ATGCTTTCGG TTGGCCAAT TTAAAAAACT GGATAACGTT CATnGTTACG TTCCAATTCC	360
TAATTTCCnA ATTACGGTTC CA ⁿ GAGCTTC TGGGATTTG	400

(2) INFORMATION FOR SEQ ID NO: 4200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4200:

CAACCTTAT TGGTAAAAC ACCCCAGCCA GGCACTTAC GCCTACGCAT CGCTTGTACA	60
CGTGCTACTA nAGGTTTACC AACCACACCT GATTCAATTG CTTTTTAGC AGTAATTGCC	120
ACATCTGTGT GACGATAATG ATATGCGACA GTTAATAATT TGTGATTTT ATTAGCCGCT	180
TCAATCATGC GATCACACTC TTCCGTCGTC ATCGCCATTG GCTTTCACCA CAATACATGG	240
CACACCATGG TTCAATGCnT CTATAGAAAG ATCAGCAGGA ATTTATTAGG TGTACAAATG	300

ACCCATCAAC AAGTTAAC AGCTCGCTAG GTGnC

335

(2) INFORMATION FOR SEQ ID NO: 4201:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4201:

ATGATGTGGC GGTGGTGAAA TCAGACCGAT ACCTGCCTT GACCCTCTTG TCTTCGCAAT	60
CCACGGATAT ACCTTAGTAC CAGGTAATTG ACCACCTTCA CCAGGGCTTG CACCTTGC	120
AACTTTAATT TGAATTCTT TGGCATGTTG TAAATAATCA CTAGTTACAC CAAAACGCC	180
AGAAGCAACT TGTTTAATCG CACTTACTTT GTTGCTTCCA TCAACTTGTA CTTCATAAACG	240
TTTGCATCT TCGGCAACTT CACCACTATT ACTCTTCCA nCTAATTGGG TCATGGGCTG	300
TGCTAACGTT TCATGTGCTT CCGnTGnAAT CGATCCATAA CTCATCGGCC CCGTATTAAA	360
GCGGTTGGAC	370

(2) INFORMATION FOR SEQ ID NO: 4202:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4202:

CAGCTAGCGA CTTACCTTGA CGTTTGnGT ATTCAATTCCA GCTTTGTnGG AATGAGtCGG	60
gATATAAGCA TCTTAGATA ATGCACCATC AACTAATGGA TATTTATGTC CAGTTGGaGC	120
CAGAAATCAT AAACGTCTTC AGTGTAAAGCA ACAGCATCTT CaTTTAATGC CAAAATGCTT	180
GGaTTAgTGC AATAACCATC GCAACTGnGC CAnACCTGT GTTGGCTCGC CGCCTGAATT	240
CAATCCATAA CGTGCTGTAT CTGTAGCAAT AACTAATACT TTTTCATTG GTCTAGTTGC	300
TAAATAATCT TTAGCTAATT GAATTGCTGG TGTTGCAGCA TAACAAGCTT CTTTCATTTC	360
AAAGCAGCGT GCAAAAGGTT	380

(2) INFORMATION FOR SEQ ID NO: 4203:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4203:

TGCTCCATTT CTCACATTTG GTATTTCAAA GGTATACCAA GTCGTATGGG ATTATTACTT	60
GACATGTCAC CAAGAGCATT AGAAGAAGTT ATTTACTTTG CTTCTTATGT TGTTGTAGAT	120
CCAGGTCCAA CTGGTTAGA AAAGAAAACT TTATTATCTG AAGCTGAATT CAGAGATTAT	180
TATGATAAAAT ACCCAGGTCA ATTCGTTGCA AAAATGGGTG CAGAAGGTAT TAAAGATTAA	240
CTTGGAAAGAG ATTGATCTTG ACGAGGAACT TAAATTGTTA CGCGATGAGT TGGGAATCAG	300
CTACTGGGTC CAAAGACTTA CTCCGTGGCA ATTAACGGTT TAGAAGTTGT TnGAATCATC	360
CCGTAATCCA GGGTACCACC CTCCnnGGnT GGATTAGA	400

(2) INFORMATION FOR SEQ ID NO: 4204:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4204:

AAATTCTTCC GCCCTGTAAT TCCTTAACCG CTTCAACGGC ATCGTnAATn TCTTACATTT	60
AGATAAAAGAT GCATTGCAAG ATATCGTCAA CTTATTATTA GACGATGTAC AAGTTACATT	120
AGACAAAAAA GGTATTACGA TGGACGTTTC TCAAGATGCG AAAGATTGGT TAATTGAnG	180
AGGCTATGAT GAAGAATTAG GTGCACGTCC ATTAAGACGT ATTGTTGAAC AGCAAGTACG	240
TGACAAAATT ACAGATTACT ATTTAGATCA TACAGACGTT AAACATGTGG ATATAGATGT	300
TGAGGATAAC GAATTAGTCG TAAAAGGTA	329

(2) INFORMATION FOR SEQ ID NO: 4205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4205:

GGTAAACAAA AAACCTCCCT TTGGAAGCGA ATTATGGAGC GGAAGATAGG ATTTACACCT	60
ATACCTCGTT CCGGGAAGGG CTGTTCTAA AAGTTGAAC ACTCCCGCAA ATATTAAATT	120
ATGGAGCGGA AGATAGGATT TACACCTATA CCTCATTCCA GGAAGGAATG TATTCTAAGA	180

GTTGAAATAC TCCCGCATT A TTATTAAATT ATGG&CGGA AGTAGGATT GCACCTATAAC 240
CTCGTTCCGG GAAGGAGCTG TTTCTAAAAG TTGAACTACT ACCGCATAAA CCTGGTGGCG 300
GCAACCGnAT TTGAACCCGT GATnAAGGTT TTGCAGACCT nTGCCTTTAC CACTTGG 357

(2) INFORMATION FOR SEQ ID NO: 4206:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4206:

TACTTTGTGA ATCCAGAAAA CTTTGAGGAT GTCACTAATA GTGTGAATAT TACATCCC 60
AATCCAAATC AATATAAAAGT AGAGTTAACG CCGCTGATG ATCAAATTAC AACACCGTAT 120
ATAGTAGTTG TTAATGGTCA TATTGATCCG AATAGCAAAG GTGATTAGC TTTACGTTCA 180
ACTTTATATG GGTATAACTC GAATATAATT TGGCGCTCTA TGTCACTGGGA CAACGAnnAG 240
CATTTAATAA CGGATCAGGT TCTGGTGACG GTATCGATAA ACCAGTTGTT CCTGAACACC 300
TGATGAGCCT GGTGAAATTG AACCAATCCA GGGATCAGAT CTGACCCAGG TCAGATCTGG 360
CAGCGATCTA ATCAGnAGCG GTCAGATCGG GnAGGATCAC 400

(2) INFORMATION FOR SEQ ID NO: 4207:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4207:

AAAAAGTTGA GAAAATGTT TGAATCAGCA AACGTTGTGC AATCGAAATT TCCACACC 60
CAAAACCTGC TTTAATCGCG CGTAATGTAG CATCGCnGwk ACTGCTGAAT GATGCTATTG 120
ATTTTCTCAT GAGACATGGC GATAACATCG TGTTtCAATC GGTGAATGCA ATGwCATAGG 180
GCTTGGTCCA TACACCTTTC CAAAATTAA AATGGCTTGA TTTGAAAAAC GACCAG&TG 240
CGCTACTGGG ATAATAGCGA GGCTACCATG TTGTTTCATC GTAGATCCC 300
TCCAGGGATA CAACCATCAT GATCAATATT AAAnCATATC CAACCATTGA CCATAAGGTC 360
AATGTAACAC GCCGGTGACT TCATCCAGCT GAATAGACGC GT 402

(2) INFORMATION FOR SEQ ID NO: 4208:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4208:

GAAGAGTTGC AGCAGCAGAT ACAATTATC CATTCACTCA AGCTGAAAAT GTTGGTTAC	60
CAAACAAAAA TGACATCATC GAAAAAGCAA AAGAAACTTT AGAATTAA TACATTTAA	120
AAGTTAACGA ATTAGCCGTG ATTTAGTCT CATTGATTAA AATGAAATnG TTAATTACG	180
AAATCTTAGG AGGGCAAAAA CGTGGGCATT TGATTTAGA TTACCCGATA TCAGGGGAAG	240
GTATCCACGA AGGTGAAATT GTAAAATGGT TTGTTAAAGC TGGAGGATAC TATnGGAAGA	300
AGACGATGTT TTAGCTGGAG GTACAAAACC GATAAACAG TAGTAGAAAT CCCCATCCAC	360
CAGCATCTGG TACnGGTAAG	380

(2) INFORMATION FOR SEQ ID NO: 4209:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4209:

AATAAACCTC AGGCTATTCA ATGGCATACA AATTAAACGA ATGAGCGATT CACTACTATC	60
GCACATCGTG GCGCAAGTGG CTATGCACCC GAGCATACTGT TTCAAGCATA TGATAAGAGT	120
CATAATGAGT TAAAAGCATC TTATATCGAA ATTGATTAC AACGTACCAA AGATGCCAT	180
TTAGTTGCTA TGCATGATGA AACTGTTAAC CGTACAACAA ATGGACACGG TAAAGTTGAG	240
GATTATACCC nTGATGAATT AnAACAGTTA GATGCAGGAA GTTGGTTAAT AAAAAATATC	300
CnAAATACGC CAGAGCAGTA TTAAAATGCT AAAGTACACAC TTAGGTGGAA TTTAGGACGT	360
ATTGGCCCGA TGCCAAACnTT TATATTGAAC CAAGACCTG	400

(2) INFORMATION FOR SEQ ID NO: 4210:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4210:

GCCCACAAACC ACAAAAGGCTG TAGGCTACAA ATATGGAGAC GGCAGGGATTG GAACCCCGCGT 60
CCAAAGGTCC TGATACACAT CTTTCTACGT GTGTAGTTA TCGATAGGTT TCGCATCATG 120
AAAAGTGATA AACAAACCAAC ATGATGCTAG TTTGATTAAG TTTCTTCTAA ACAGATTCA 180
AACGGCATTnG TTAGCATATC CTATTAAGGT TGAATCGCGT TAACAGCACA TAGGAAATGC 240
TGTAGGCAGA TGCAGAGTGC GATTAGGCAG CTACTGCGAA ATTATTGTnT GATTGCCAG 300
TTATTATnAA CTGTGTGGTG TTGATGACGA 330

(2) INFORMATION FOR SEQ ID NO: 4211:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4211:

AAATCATCTT ATGACTGCTT TTTATTATAC TTTACATTTC TCGTTTCGTC AGATTCAAAC 60
GTTTCACTT CGCCAAGCCA TCTTTCTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT 120
AAAAAAAGAG ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACCTTTG CCTGGCAACG 180
TTCTACTCTA GCGGAACGTA AGTTGACTA CATCGACGC TAAGGAGCTT AACTTCnGTG 240
TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC CAGACATATG AATGTAAATT 300
ATACATTCAA AACTAGATAG nAAGTAAAAG TGATTTCGC 339

(2) INFORMATION FOR SEQ ID NO: 4212:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4212:

GCGATGGTTG AAACATTGAC TGATATTAAA GAGTTTATGA ACCAAGTTGA ECGCATAGC 60
TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120
CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180
CGATTTGGC ATGAAGGTCA CCTnAAATGT ACATTGTTGT AATAAAATTG CCTATAAAAT 240
TTTTAGCACA TAAAATAAGA GGGGCCAnCC ATTTTAGACT ATAACAAACGG TTGGCTCTT 300
GAATTGTAAA AAGAAAACCA TACGCTATGn TATT 334

(2) INFORMATION FOR SEQ ID NO: 4213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4213:

CTATGATTTC ACCGAGTCTC TCGTTGAGAC AGTGCCAAA TCGTTACGCC TTTCGTGCGG	60
GTCGTTACCC GACAAGGAAT TTCGCTACT TAGGACCGTT ATAGTTACGC CGCCGTTAC	120
TGGGGCTTCG ATTCTAGCT TCGCAGAGTA nACCCACTCC TCTTAACCTT CCAGCACCGG	180
GCAGGCGTCA CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT TTGATAAAACA	240
GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGGCGTTA ACCCTAAAGA GCACCCTTC	300
TnCCGAAGTT TACGGGGTCA nTTTGCCGAG TT	332

(2) INFORMATION FOR SEQ ID NO: 4214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4214:

CGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTGGCT ACCATCGTCG CTAAAGACCT	60
TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTACTCATTT	120
AGCTCTACTA AACTCGTTGC GCTCTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC	180
GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TAnTTTGACG TTTTAGACAT AAAAAAAAGA	240
GACCTTGC GG TCTCAATGCG GCTCATCGCA TCCATTTTT GCCTGGCAA CGTTCTACTC	300
TAGCGGAACG TAAGTTGGGT ACCATCGACG CTAAGAACCT TCTTGGAnTG TGGACAACGn	360
TGG	363

(2) INFORMATION FOR SEQ ID NO: 4215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4215:

ACTCATCATT ACAATTGGGA CATAACGTCT ATTAAAAnCGT GTGCCATTTG GAGTCCACTT	60
TTATTTGTAT TGTATAGAGA GAAATAAAAAA GAnACCTTGT TTTACAAGGTTCTAATACG	120
TTATGTTATG TAAATAACAG TTAATTATAC CGGTGGTCGG GGTGAAACCG ACACTCCACA	180
AGTGGAACGG GGATTTGAG TCCCAGCGGT CTGCCAATTC CGCCACACCG GCTTAATGGT	240
AAACAAAAAA CTTCCCTTG GAAGCAATT A TGGAGCGGAA GATAGGATT ACACCTATAC	300
CTCGTTCCGG GAAGGACGTG TTCTAAAAGT TGACTACC	338

(2) INFORMATION FOR SEQ ID NO: 4216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4216:

ACGGTGATCC CATAATGCTT GAACATCAAT TTCATCCATT AATGTTACAT GAGGTGCAGT	60
ATGCTTAGAG TTAACCATTG CTTTCGCAAT TGCTCTACGC ATAGCAGGGA TTTTTTCAGT	120
TGTTTCTGGG AAGTCGCCTT CTAATGTTAC TGCTGCAGGT GCTGCAGGAG TTTCAGCAAC	180
TTCTTCACCT GTAGCTGAAG CAGCTGATTC ATTTGAAGCT GTTGGTGCAC CACCATTAA	240
GTATGCATCT ACATCTTCTT TTGTAATACG ACCATTTTA CCAGATCCAG AAACGTCTT	300
AATGnTAACA CCTnTTCAC GTGCGTATTA CGACTGAAGG CATGCCTTAA AGTCnGGTT	360
CACCACTCTC AGTTGAGAGC ACAGGGCTGC nCGCTGGCGC	400

(2) INFORMATION FOR SEQ ID NO: 4217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4217:

AGGGAATCGA ATTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT	60
GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC	120
CCCATTGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA	180
GTAACGTCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA	240
TCTATGTTTC CATCCTACAG GAAACGCGTT ATTAATCTTG TGAGTGTnCT TTGAAACATA	300

GGCGGATTAT TTCTnATGAA TTCAAGCTA TGTGAAAACT CnTTA

345

(2) INFORMATION FOR SEQ ID NO: 4218:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4218:

GGCGCCCTCG TGCCAAACAG TGCTCTACCT CCAATAATCA TCACTTGAnG CTAGCCCTAA	60
AGCTATTCG GAGAGAACCA GCTATCTCCA GGTCGATTG GAATTTCTCC GCTACCCTCA	120
GTTCATCCGC TCACTTTCA ACGTAATCGG TTCGGTCCTC CAnTCAGGT TACCTGAACT	180
TCAACCTGGA CCAAGGGTAG ATCACCTGGn TTGGGTCTA CGACCAAATA CTAAACGCC	240
TATTCAGACT CGCTTCGCT GACGGCTCCA CATTACTGC TTAACCTTGC ATCAAATCGT	300
AACTCGCCGG TTGCATTCTA CAAAAGGCAC GCCATGCACC CATTA	345

(2) INFORMATION FOR SEQ ID NO: 4219:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4219:

TCTTATGACT GCTTTTATT ATACTTTACA TTTCTCGTTT CGTCAGATTc AAACGTTTC	60
ACTTCGCCAA GCCATTTTC TTTGTGTTG CTTTATTG GACGTTTAG ACATAAAAAA	120
AGAGACCTTG CGGTCTCAAT GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC	180
TCTAGCGGAA CGTAAAGTTC GnACTACCAT CGACGCTAAG GAGCTTAACt TCTGTGTTCG	240
GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGGAAT GTAAATTATA	300
CATTCAAAAC TAGATAGTAA GTAAAGTGGn TTTGCTTCGC AAACCCnTTAT TTTGGTTAGT	360
CTTCGTC	367

(2) INFORMATION FOR SEQ ID NO: 4220:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4220:

AAGAGCCTT CTTGACTTGT GACAATCGCT TGCTTCTTC CTCTCCTTCG GCTCTCACTT	60
ACTCATTAG CTCTACTAAA CTCGTTGCGT TCTTTCTCG TTTCGTCAGA TTCAAACGTT	120
TTCACTTCGC CAAGCCATT TTCTTGCTGT TTGCTTTTA TTTGACGTT TTAGACATAA	180
nAAAAAGAGA CCTTGGGTC TCAATGCGGC TCATCGCATH CATTTCGC CTGGCAACGT	240
TCACTCTAGC GGAAAnTAAGT CGAACTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGTT	300
CGGCATGGGA ACAGGTGTGA CCCCCnTGGC TATAGTCACC AG	342

(2) INFORMATION FOR SEQ ID NO: 4221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4221:

ACCGGATGAC AGCCCCAGGA TGCGATGAGC CGACATCGAG GTGCCAAACC TCCCCGTCGA	60
TGTGAACCTCT TGGGGGAGAT AAGCTGTTAT CCCCGGGTA GCTTTATCC gTTGAGCGAT	120
GGCCCTTCCA TGCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCCTG CTCGACTTGT	180
AGGTCTCGCA GTCAAGCTCC CTTATGCCCTT TACACTCTAT GAATGATTC CAACCATTCT	240
GAGGGAACCT TTTGAGCGCC TCCGTTACCT TTTAnGAGGC GACCGCCCCA GTCAAACGTG	300
CCGCCTGACA CTGTCTCnCA CCACGATAAG TGGCGnG	337

(2) INFORMATION FOR SEQ ID NO: 4222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4222:

GGCGCTTGAC TAAAAAGAAA TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT	60
TTACCAAGCA AAACCGAGTG AATAAAGAGT TTTAAATAAG CTTGAATTCA TAAGAAATAA	120
TCGCTAGTGT TCGAAAGACA TCCACCAAGn TTAATAACGC GTTTAAATCT TTTTATAAAA	180
GAAAACGTTT AGCAGACAAT GAGTTAAATT ATTTAAAGC AGAGTTTACT TATGTAAATG	240
AGCATTAAA ATAATGAAAA CGAGCCGTAT GTGAGCGTTT GACTTATAAA AATGGTGGnA	300

ACATAGATTA AGTTATTAAG GGCGCACGGT GGGTGCCnTG GCACTTAGAA GCCGCTGAAG	360
G	361

(2) INFORMATION FOR SEQ ID NO: 4223:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4223:

CGGTAGAATA CAACCTTGCC AAGGTTGGCG TCGCGGGTTC GATCCCGTC TTCTGCTCCA	60
TTATTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC TTAAAATCCT GCGGTGAGAG	120
ATCACCGTAC CGGTTCGATT CCGGTCTCG GCACCATTG AGCGCCCGTA GCTCAATTGG	180
ATAGAGCGTT TGACTACGGA TCAAGAGGTT ATGGGTTCGA CTCCTATCGG GCGCGCCATT	240
TTTAAATTAA TTGAATAACG GGAAGTTAGC TCAGCTTGGT AGAGCACTTG GTTGGGGAC	300
CAAGGGTCGC AGTCGAATC CTGTCTTCCC GATTACTCnT AAnTCCATTG AnGGGGGCTA	360
GCTCAGTGGG GAGAGCGCTG CTTGCACGCA GGAGGTACG	400

(2) INFORMATION FOR SEQ ID NO: 4224:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4224:

CATAATATAC TCTTAAGTGT AAAGGGGAAT TTCCTGGGT ATAATTGCG TGTGCACCTT	60
GAGTGACTTC TACCATTTA TAGTCAAATT GCTTAGTTC GTTGGTTA ACGCCGACAC	120
TCGCAAATGT ATAATCAAAG AACTTCACAA TATTGTTGCC TAAGAACCT TTGAATTCAA	180
TAGTGTCAATT TCCAGCAATT TGTCGGCAA CAATACTTGC TGCAGGGTG AGCGCCCCCA	240
GnCAAAAGGA CCACTAGCCG GTAGAATCGA CATGTCGATA ATGTGATGGT TGCCAATAAT	300
CGCCTATTGC ATAATGTTG GACCATTGGT TCCAAATTAA TCGTTACCGG TATGAAACCT	360
TTCGATCCAG TTGGATAATT GAACTTCGnA AATTGATTG	400

(2) INFORMATION FOR SEQ ID NO: 4225:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 328 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

GGGTTCAATT TCTGCATACC AATCGATGCC AGCTCTATT CTGACAATAT CCATATATTT	60
TGAAATTTC TCTAATTCTT TGCCACTAAC CTTTCACCA TTCAACCAAA ATTGATCCTG	120
TGTTAACTGG TCGTTAAAAG TGACTTTCGT TTCAGTGTAA AATTTTCTA ATGTAACAGA	180
TATGCTATTA TTCATTGGAA TGATTAGTGC TTCATCTTT TTACCCCAAT ATTTTATnAG	240
TGCAATATTC GTATGTGCAC GTGCTTGCC ACTnnTAATC AACGCATTAAC CCTCCTAAAT	300
TCTCAATCCA AGTATGTGCT GCACCAGC	328

(2) INFORMATION FOR SEQ ID NO: 4226:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4226:

TGACGGGTTG GAACCGCCGA CCCTCTGCTT GTAAGGCAGATGCTCTCCCA GCTGAGCTAA	60
TTCTCCGATT TAAAAGTGC TGGCAACGTT CTACTCTAGC GGAAnGTAAG TTGnACTAC	120
CATCGACGCT AAGGAGCTTA ACTnCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC	180
TATAAGTCACC AGACATATGA ATGTAATTAA TACATTCAAA ACTAGATAGT AAGTAAAAGT	240
GATTTTGCTT CGCAAAACAT TTATTTGAT TAAGTCTTCG ATCGATTAGT ATTGTCAGC	300
TCCACATGTC ACCATGCTTC CACCT	325

(2) INFORMATION FOR SEQ ID NO: 4227:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4227:

GCGCAACTCA CACAACAAGG TGGCAATCAC TCTGAACAAA GTGCGGCAAn TTnTTCAACA	60
AGCAGCACAC ACAAGGGCA ACAAGGTGGC AACGGCAATT ATTTAGAACAA AATTGGTCGT	120
AACCTTACGC AAGAAGCAG TGACGGTTA TTAGATCCAG TCATTGGTCG TGGATAAAAGA	180

AATTCAAGnA ACTGCTGAAG TTTTAAGTAG' ACGAACTAAA ACAAATCCTA TATTAGTTGG 240
AGAACGCTGGT GTTGGTAAAA CTGCGATTGT TGGAAGGTTT AGACAGGCA ATCGTTGGAA 300
GGAAATGTAC CAGCAGCAAT CAAAGACAAA G 331

(2) INFORMATION FOR SEQ ID NO: 4228:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4228:

AGAGGGTCGT TGCCTTACCG CTTGGCTATA GCCATTAATA ATAAGGGCGG CTGAAGGGGA 60
TCGAACCCTC GAATGTCGGA ACCACAATCC GATGTGTTAA CnCTTCACCA CAGCCGCCAT 120
GGCAGGGGCA GTAGGAATCG AACCCACACC AAAGTTTGG AGACCTCTAT TCTACCGTTG 180
AACTATGCCCT CTATTAAAAA TAATAAATGG AGGGGGGCAG ATTGAACTG CCGAACCCGA 240
AGAGCGGATT TACAGTCCGC CGCGTTAnC CACTTCGCTA CCCCTCCATA AATGGTGCCG 300
GCCAGAGGAC TTGnAACCC CAACCTAATG GTT 333

(2) INFORMATION FOR SEQ ID NO: 4229:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4229:

CTCTTACTTT GTAAACCAAA TCTTAAATTA AAATATTGAA AATGCAATGn ATCCTTAATA 60
TTTTTATTAAA CCTATAATTA CTTATTAAAA ATAACACACA ATATTCTAA AGTTTTAAAA 120
ATATTCTGTT TTATCACCTA CTATTAGTGG AAAAGTACA TTGCAATTGT ATATAGTTG 180
CATAACGCTT CAAAAGTAAT TTCTTTTTG TTTAGTTCAA AAAAATTAG AGGTGATGTT 240
ATATGAATAA CGGTTTTTC AATAGCGACT TTGATTCAAT TTTTCGAGGA TGATGAAAGA 300
TATGCAAGGT TCAAATCAAG TCGGAAACAA AAGTACTATA TTnATGGTAA GGAGTTTCAC 360
CTGAGGACTG GCGCAACTnC ACACACCAGG TGGCCATCAC 400

(2) INFORMATION FOR SEQ ID NO: 4230:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4230:

CATTAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTC ACTCCCCTTC	60
CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGTTCACT ATCGGTCACT AGAGAGTATT	120
TAGCCTTAGG AGATGGCCT CCCAGATTCC GACGGAATT CACGTGCTCC GTCGTACTCA	180
GGATCCACTC AAGAGAGACA ACATTTCGA CTACAGGATT ATTACCTTCT TTGATTCACTC	240
TTTcCAGATG ATTCGTCTAA TGTCGTCCCT TGTAACCTCG TATAGAGTGT CCTAsAACCC	300
CAACAAGCAA GCTTGGT TTGGGnTCTT GCCGTTTCG	339

(2) INFORMATION FOR SEQ ID NO: 4231:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4231:

GAAAGTCATAT GCATAACATT GGTTATCATT ATTACATACGT TCAATCGCAT CTGTTAAC TG	60
AATTCGTTA CCTGCCCTT CTTTTGCGT TTTAAATAA TCGAAAATT CAGGCCTTAA	120
TACATAACGT CCCATAATAG CTAGGnTTGA TGGTGCCGTA CCTTGTGCTG GCTTTCAAC	180
AAACTTTTTC ACTTCAGACT GACGTCCGn TTTAGTTAAT GGGTCAATAA TTCCATAACG	240
ATGAGTATCT GCTTCCGGAA CTTCTGGAC ACCTATAACT GAGTGCCCTG TnTCTTCATA	300
AACGTCAATC AACTGTTCA CTGCTGGCAC TTCAGAGTCA ACAATATCG	349

(2) INFORMATION FOR SEQ ID NO: 4232:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4232:

CCCAGCTCGC GTACCGCTTT AATGGGCGAA CAGCAAGCGC CTGTGGGAnC GACTACAGCC	60
CCAGGATGCG ATGACCGACA TCGAkGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG	120
GAGATAAGCC TGTTATCCCC GGGGTAGCTT TTATCCGTTG aGCGATGGCC CTTCCATGCG	180

GAACCACCGG ATCACTAAGT CCGTCTTCG ACCCTGTG ACTTGTAGGT CTCGCAKTCA 240
AGCTCCCTTA TGcCTTTACA CTCTATGAAT GATTCCAAC CATTCTGAGG GAACTTTGaG 300
CGCCTCCGTT ACCTTTAGG AGGCGACCGC CCAGTCAAAC TGCCCGCCTG ACACTGTCTC 360
CCACCAACGAT AAGGTGCG 377

(2) INFORMATION FOR SEQ ID NO: 4233:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4233:

GGCTAGCCTC AAGTGATGAT TATTGGAGGT AGAGCACTGT TTGGACGAAG GGCCCCTCTC 60
GGGTTACCGA AGTTCAGACA AACTCCGAAT GCCAATTAAG TTTAACCTGG GAGTCAGAAC 120
ATGGGTGATA AGGTCCGTGT TCGAAAGGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA 180
AATATATGTT AAGTGGAAA GGATGTGGCG TGGCCCAGAC AACTAGGATG TTGGCTTAGG 240
AAGCAGCCGT CATTAnAGA GTGCGTAATA GCGCACTAGT CGAGTGACAC TGGGGGGAAA 300
GGGTACCGGG GCTGAACATA TTACCGAAGC TGGTGGGTTG TCCTTGGAC AnTTn 355

(2) INFORMATION FOR SEQ ID NO: 4234:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4234:

ATCCGCCTCC CGCAATATTT TATAGGTCTC GT~~A~~TGTAGC G~~n~~TTAACACG CCTGCCTGTC 60
ACGCAGAGAT CGCGGGTTCG ATTCCCGTCG AGACCGCCAT CATTACATTT TTATTATGGT 120
TCAGTAGCTC AGTTGGTAGA GCAATGGATT GAAGCTCCAT GTGTCGGCAG TTCGACTCTG 180
TCCTGAACCA TTTCTTAGCC GGCCTAGCTC AATTGGTAGA GCAACTGACT TGTAATCA~~G~~ 240
AGGTTGGGGG TTCAAGTCCT CTGGCCGGCA CCATTTATGG AGGGGTAACG AnTGGGCTAA 300
ACGCAGGGCGGA CTGTAAATCC GCTCCTTCGG GGTCGGCAG TTCGAATCTG CCCCTCCAA 360
TTAATAATTT TAATAAGGGG CATAnTTCAA CGGTAnAATA 400

(2) INFORMATION FOR SEQ ID NO: 4235:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4235:

ATGCCATGTT CACCTTGT	TT AAAATCAAGG TTTGTAATGT TTCCCTTG	TGT CACGATAATA	60
GGCGTAATAT CACTCTTGC ATGATTGCGG ATGTAGTCTA AATCAAAGTT GATTAATAAA			120
TCACCTTCTT TAACTnnTTG ACCTTCCTCA ACATGTAAAG TAAAGCCTTC TCCGTTAAT			180
TTAACAGTGT CTAAACCGAT GTGGATTAAT AGTTAAAC CACTATCTGA TACAAGACCA			240
ATTGCATGnT TTGTTGGAA AATCATTG ACTTTACCGT TGAATGGTGC ACGAACTTCA			300
CCTTGTGAGG TTTGATAGCG ATACCGTCAC CCATGCATT T			341

(2) INFORMATION FOR SEQ ID NO: 4236:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4236:

GTGATGCAG CCCGTTGAGC TCTAAACCAA CTGAGCTAAA GGTCTAAAT ATAATTAC	60
AACTAATAAA TAGTGGCGGT GGAGGGGATC GAACCCCCGA CCTCACGGGT ATGAACCGTA	120
CGCTCTAGCC AGCTGAGCTA CACCGCCTTA TATAGTTGT AAATAATATG GTGGAGACTA	180
GCGGGATCGA ACCGCTGGAC CTCCTGCGTG CAAAGCAGGC GCTCTCCCAG CTGAGCTAAG	240
CCCCCATAAT AATTACAGTA TATCGGGAAAG ACAGGATTAG AACCTGCGAC CCCTTGGTCC	300
CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAAACGnGC CCGTAGGAGT	360
TGAACCCATG AACCTnTTGA TCCnTAGTnC AAACGGTCTA	400

(2) INFORMATION FOR SEQ ID NO: 4237:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4237:

nAnTTCTTGA CCTGACATCA CCTGAAATTG ATGGACATG GTCCACCAGG TCATATACTC	60
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TAATCCATGG GTCGCCGATA CCTTCAACGn ACAACATCTA CACCACTATT TCTAATACAG	120
AATCTTCTC CTGCACTACC GTTAATAAAT GCCTTACCAAC TTGTCGCACC ATAGAATGAG	180
ACGTTACCAG CAATAATTTC ATTTTGTGCGT TCTTCAAAGA GTGCTTGAC AATGACGTA	240
CCACCAAGATA ATCCTTACCA AACATAGTCA TTGCGATCTC CAGTATGATG AATCATTAAG	300
CCTTCGGTG CATATGCTGC AAGACTTGA CCAGCATGAC CATTGATA AACATTAATT	360
GTATTTCAAG GAAGTC	376

(2) INFORMATION FOR SEQ ID NO: 4238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4238:

CGATTAAAG CTAAGCCAT TTTCGCTCTT TCTCCATAGC CTAACCAAGC AATACGTGAT	60
GGTAGTCCTT GATATGAAAT TTTTCTTCA GCTAAATCAA GCCATCTTAA TAACTTTCA	120
TTTCTGGGA AAAGTTGCG CATTCTTCA TCCGCACGCT CGATATCTT TGGATCACCA	180
CTCAACGCAG CAAAGCGGAA TGGCCCTTA CCTCACAGA ATAATGGTCT AATGTAAGCT	240
GGTACAAAAG CTGGGAAGTC AnAAAGCATT TTTCACTCCG TATTGAAGGC TACTTGACGA	300
TATGnTACCA TAATCAATGC TACAGCGCCA CGTTG	335

(2) INFORMATION FOR SEQ ID NO: 4239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4239:

CCACAnTTAC AAGCAACTAC TGAAGGCGCT GTATTATTA AAGGTGGCGA CGETTTGAT	60
TTGGACACG TAGAAAGATT TATTCAAAAC CCGCCACATG GGGCAACGGT TGCATGGCAT	120
GATAGTCCAG ATACATGGAA GAATACAGTC GGTAACACTC ATAAAACCTGC GGTTGTAACA	180
TTACCTAATG GTCAAGGTAC GCGTAATGTT GAAGTTCCAG TCAAAGTTA TCCAGTTGCT	240
AATGCAAAGG CGCCATCACG TGATGTGAAA GGTCAAAATT TGCTGTTGGA CGGATGCGAT	300
GAACtACATT ACATTTGTCC AnTACAACAC AGATnGTATC ACTGCAGC	348

(2) INFORMATION FOR SEQ ID NO: 4240:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4240:

TTGATGTTAA AGATTAGCA AGGGGCGAGA GAACTGGAGA AGAGGTTGCC AACGAATGG	60
AACGTGCTTC TGTATTGGCC CAAGTAGATA TTCATCGTGC AGCAACACAT AATAAAGGTG	120
TTATGAATGG CATACATGCT GTTGTAGAA CAACAGGAAA TGATACGCGT GGTGCAGAAG	180
CAAGTGCAGCA TGCATTACGC GAGTCGTGA CGGACAGTAT CGTGGTATTG CTACATGGCG	240
TTACGATCAA GATCGTTCAA CGATTTGATT GGTACATTGG AAGTGCCTAT GACATGGCA	300
ATCGTTGGCG GTGGGTACAA AAGTATTACC AATTGCTAAG CCTTCATTAG GAGnTACTAA	360
ATGGTAGAGT CCGCCCCAAG AATTAnGnCC CTGTA	395

(2) INFORMATION FOR SEQ ID NO: 4241:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4241:

ACTAATGATT TATTATGTAG TGGTTCTTG TCATTAGCCA CAGCTATTGT GTACTTAAAA	60
ATAGGAATGC ATGAGTGCAA CTCTAnAnGn AGCATACTAA TTTCTAAAGA AAAAGTATT	120
CTTTATGTTG GGGCCCCGCC AACTTGCATT GTTGTAGAA TTTCTTTG AAATTCTTA	180
TGTTGGGCC CCGCCAACTT GCATTGTTG TAGAATTCT TTTCGAAATT CTTTATGTTG	240
GGGCCCGCC AACTAATTCC AATATATCAT TAGAGCTT AGGTCAATTGA TTTTGCGTC	300
GGACTTTAT GGCGATATGA ACCATGTAAA T	331

(2) INFORMATION FOR SEQ ID NO: 4242:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4242:

TGCATTGCAT TATTGTACTG CGTAATTGTA CCTGGCTTT TACCTTCAGT GCTTACTGGA	60
TCATCTAAAT GATTTTAGC TGTGATTAAC TCACGTTAT CCGCTTTGT AAAATGGAC	120
TCTTGTACTT CTTCAGTACT ACCATCATTG TAAGTTACTG TCACAGGAAT CGTCGTTGTG	180
CTACCACCAG CTAAATTAGT AGGCATTGCT GTGCCATTT TAATCGTTGC AGTACGTTA	240
TTAGCAACTT GAACTGCATT GTTAATTCA GCTGCTGTTA CATTGAACC ATAATCTTC	300
ACAATTnCAG TTGTGTTGAC AGATGAGnGG CGGTGCAGTA AGGACTGGAT ACACTACGAG	360
TGACCGGACT GCTTCGGGnA ATGTGATGA	389

(2) INFORMATION FOR SEQ ID NO: 4243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4243:

ATACGCATGT TAACGATCGA ATGCTTAATG TCCCAGGAAA TAAATCTATC ATAAGTTACT	60
TTAATGAAGT TGTCTCACGA CAAGGTAATC ATGTTGCGCT ATCATGAATG ATTTGACAAT	120
GACGTATGAA CATTACGCAA CTATGTGGAT GCCATTGCGC ACATGCTCCT ATCAAATGGT	180
GTGGGCAATG GTCAACGGGT TGCCTTGTTT ACAGAACGTn TTTTGGAAAT GATTGCGGCG	240
ATGTTGGCGA CAGTTAAAGT AGGTGCATCT TATATACCTA TCGATATTGA TTTCCGAAT	300
AAACGACAAG GTGCAATTGG	322

(2) INFORMATION FOR SEQ ID NO: 4244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4244:

GCCGACTACT GAAGGGnAAT CGnAATTTC TTTCTCTTCC TCCGGGGGAC TAAGATGTTT	60
CAGTTCTCCG GGTGTGCCTT CTGTATATGC TATGTATTCA CATATCGATA ACATGACATA	120
ACTCATGCTG GGTTCCCCA TTCGGAAATC TCTGGATCAA AGCTTACTTA CAGCTCCCCA	180
AAGCATATCG TCGTTAGTAA CGTCCTTCAT TGGCTTCTAG TGCCAAGGCA TCCACCGTGC	240
GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA GTCAAACGTT AACATGAAGT	300
TACGTTCTTT TATAAAAAGA TTTAAACGCG TTATTAATC	339

(2) INFORMATION FOR SEQ ID NO: 4245:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4245:

CCATTAACGG GCTCTGACTA CTTGTAAGCA CACGGTTCA GGTTCTATT CACTCCCC	60
CCGGGGTGCT TTTCACCTT CCCTCACGGT ACTGGTCAC TATCGGTAC TAGAGAGTAT	120
TTAGCCTTAC GAGATGGTCC TCCCAGATT CGACGGAATT TCACGTGCTCCGTCGTACTC	180
AGGATCCACT CAAGACAGAC AACATTTCG ACTACAGGGA TTATTACCTT CTTTGGATT	240
ATCTTCCAG ATGATTGTC TAATGTCGTC CTTGTAACT CCGTATAAGAG TGTCCTACAA	300
CCCCAACAAAG CAAGCTTGTG GGTnTTGGGC nACTTCCGG TTTCGGTTCG GCCGChAA	358

(2) INFORMATION FOR SEQ ID NO: 4246:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4246:

AAAGAGACCT TGCCTTAGA TGCCTCAT CGCATCCATT TTTGCCTGG CAACGTTCTA	60
CTCTAGCGGA ACGTAAGTnG AnCTACCATC GACGCTAAGG AGCTTAACCTT CTGTGTTGG	120
CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAAGAC ATATGAATGT AATTTATACA	180
TTCAAAACTA GATAGTAAGT AAAAGTATT TTGCTTCGCA AAACATTAT TTTGATTAAG	240
TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGGAACCTA	300
TTAACCTCAT GCATCTTGA GGGGnGCTTG ATAACCGA	338

(2) INFORMATION FOR SEQ ID NO: 4247:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4247:

CCCCGGGTAG CTTTATCCG TTGAGCGATG GCCCTCCAT GCGGA A CAC CGGATCACTA	60
AGTCCTGCTT TCGACCCTGC TCGACTTGTA GGTCTGCAG TCAAGCTCCC TTATGCCTTT	120
ACACTCTATG AATGATTCC ACCATTCTG AGGAACTTT GAGCGCCTCC GTTACCTTT	180
AGGAGGCGAC CGCCCAGTCA AACTGCCGC CTGACACTGT CTCCCACCAC GATAAnGGCG	240
GGGGTTAGAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCTCCACG TAACTAnCGC	300
TCACGTTCA AAGnTCTACC TATCCTGTAC A	331

(2) INFORMATION FOR SEQ ID NO: 4248:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4248:

ATAATCATAAC AGATGGCAAT ACAACAGCAA CTGAGACAGT GTCAAACGCT AATAATAATG	60
ATGTAATGTC GAATAATACC GGATTAAATG TACCAACTAA AACAAATGAA AATGGTTCAG	120
GAGGACATCT AACTTAAAG GAAATTCAAG AAGATGTTCG TCATTCTTCA AATAAACAG	180
AGCTAGTTGC AATTGCTGAA CCAGCATGCT AATAGACCGA AAAAGAGAAG TAGACGTGCG	240
GCACCGGCAG ATnCCTAAAT GCAACTTCCA GCCAGATCCA GCGGCTG A G CGGTAnGGAA	300
ACGGTGGTGC CACCAGTTG CCAATTACA GCGCCCATAT TACGCCAACAA ACTGGTnCCC	360
TAATGCCAA T	371

(2) INFORMATION FOR SEQ ID NO: 4249:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4249:

AATTGCATGG CATAACATCG GCGATTAAAA GATGGACGTT TTGATGATGT ACAACAAGAC	60
ATTGAAGCAG TGGTGAAGC TGCGAAGGTC ACACAGTAAA AGTGATTATT GAGACGGTAT	120
TGTTGGACCA TGACGAAATT GTAAAAGCGA GTGAATTAAC AAAAGCGGCT GGTGCGGACT	180
TCGTTAAAAC TTCAACAGGT TTTGCAGGTG GCGGTGCGAC TGCAGAACAC GTTAATTAAT	240
GAAAGATACA GTAGGTGCTG ATATAGAAGT AAAAGCTCAG GTGGCGTACG TATTnTAGAA	300
GTTCAATGA AnGGTTGAAG CAGGTGCGAC ACGTAnTGGT GCGAGCGCAG CGTTCAA	357

(2) INFORMATION FOR SEQ ID NO: 4250:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4250:

GAGCCCCAAC CAACAAGCTT GCTTGTTGGG nGTTGTAGGA CACTCTATAAC GGAGTTACAA	60
AGGACGACAT TAGACGAATC ATCTGGAAAG ATGAATCAAA GAAGTAATA ATCCTGTAGT	120
CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAACACGTGA AATTCCGTG	180
GAATCTGGGA GGACCACATCTC CTAAGGCTGA ATACTCTCTA GTGACCGATA GTGAAGnAGT	240
ACCGTGAGGG AAAGGTGAAA AGCACCCCGG GAAGGGGAAG TGAAATAGAA GCTGGAAACC	300
GGTGTGCTTA CAAGGTAGTC AnAGCCCGTT AATGGGTGAT GGCGTGCCTT TT	352

(2) INFORMATION FOR SEQ ID NO: 4251:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4251:

CATTTACTGC TTAACCTTGC ATCAnATCGT AACTCGCCGG TTCATTCTAC AAAAGGCACG	60
CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTCAC	120
TCCCCTTCCG GGGTGCTTT CACCTTCGG TCACGGTACT GGTTCACTAT CGGTCACTAG	180
AGAGTATTAA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTCA CGTGCTCCGT	240
CGTACTCAGG ATCCACTCAA GAGAGACAAAC ATnTTCGACT ACAGGATTAT TACCTTCTTT	300
GATTCAnCTT TCCAGAATGA TTCGTCTAAT G	331

(2) INFORMATION FOR SEQ ID NO: 4252:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4252:

TATTTGATAT TTTGTGCATT GCAGTCAAAC CATGGCGGAA ATTGAACCAA TACCATTGCT	60
AATTTTTCT GTGTATGTAA GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTnGC	120
CTTGTATCTG CAAATGTTT GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTGACC	80
ACAAATTCAA ATGTATCAGG CGTTTCTTT ATCCATTTCA ATATATTCT TTCCGGTTGT	240
ATCGCATAGT ATGTCGCATC TAATTCGCAA CCGGAAAATG TCCAGCATAT GTTTAAGGT	300
TATCGGTTG GCGTTCTAAA TCTGCATATA ATGAATAGTG ATCACCCCAA CCTGTTAAAT	360
CCGATGGTTA TCCAnATGAT GATCACCATG TCATCAAnACC	400

(2) INFORMATION FOR SEQ ID NO: 4253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4253:

AAAGGTATCA AAGATGTTAA AGTTACTTTA TTAAATGAAA AAGGCGAAGT AATTGGnACA	60
ACTAAAACAG ATGAAAATGG TAAATACTGC TTTGATAATT TAGATAGCGG TAAATACAAA	120
GTTATTTTG AnAAGCCTGC TGGCTTAAAC ACAAACAGTT A A AATACAA CTGAAGATGA	180
TAAAGATGCA GATGGTGGCG AGTTGACGTA ACAATTACGG ATCATGATGA TTTCACACTT	240
GATAACGGAT ACTTCGAGGG GATGACATCA GACAGCGATT CAGACTCCAG ATAGTGACTC	300
AGnCAGCGAC TCAGACTTCA GACAGCG	327

(2) INFORMATION FOR SEQ ID NO: 4254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4254:

AGATGACATT AAATAGCATC TCCTCGTGTGTT GATTATTTG GTTGGCTGAC CAATATTTAT	60
TCTAGCACGT AGAGATGCAT TTTTGTCGAC AATGGTAGAA CCTTTCTGA ACCATACGCA	120
TAGGATTGTn CTnTTTACA ATTAAAGAGC CAACCGTTGT TATAGTCTAA CAATGGTTGC	180
CCTCTTATTT TATGTGGCTA AAAATTATA GGCAATTAA TTACAACAAT GTACATTTAA	240
GGTGACCTTC ATGCCAAAT CGCATCACTC ATTTAATGGA AGCAGCACGT CTTCATATAA	300
AGTACCGATC CCTAATTCCA ACGCATGTnG	330

(2) INFORMATION FOR SEQ ID NO: 4255:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4255:

ATTAGTGATT GTAAAAAAAGT AAAACTATT C TTGGGAGTC GACATAAATC AATGTCTAGA	60
CTCTATAGTG TTGTATTTGG CAGTAGTTGA CGGGGCCCA ACATAAAGAA ATACTTTTC	120
TTTAGAAATT AGTATTTCTT ATACATGAGT TTTACTCAGG ATATCCTATT TTTAAATACA	180
CATTAGCTGT GTTTAATGAT AAAGAACAC TACATCATAA ATCTTTAATG GTTCTTTATC	240
AATTCCTTCC CCCCTCTCAT GTTTGTATC TTTAAATCAA TATAATTCAA AAAAGGGTCG	300
AAGATATGAn ATCACATCTT CGACCCTTnn TTGTACTAAT TTAA	344

(2) INFORMATION FOR SEQ ID NO: 4256:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4256:

CCAGTAATAT CTAAATGAGT TGGATATT TA ACTTCGCAT TAATTCAT ATTAAATTGC	60
GTTACCGCGA CAAGrCATnA CACAACATAC ATAATAAGAT TGGCTAAAAA GATATAGTTA	120
AAGCTAAATT CTGCGACAAA GCCGCCATT GCAGCACCGA CAGCCACACC AATATTTGC	180
GCTAAGTATA TCGCATTAAA CGTTGTCTT CCGCCATTG GCCACACTGC TCCAGCCATA	240
GCGTATATCG CAGGAATAAT CATTCCGCCA CCAAACCTAACATTACAAG CCATACAGCA	300
TACCAAGGCC ACCCGTGGAn AGA	323

(2) INFORMATION FOR SEQ ID NO: 4257:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 369 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4257:

GCTGACTTTC CACCAGCCTC TGTGTTGGGG CCCCGACTAT TTTTGAAAAG AGCGTGTAC	60
ACGGTCATTG TTTTACAGTC AACTACTGCT AAAATAAAAT TAACGAGCTT AGGGCTTTGT	120
TTTCTGTCCC AAGCTCGTTA AATCACATAT GATAATTAAT TATGCCAAC CACGATATCT	180
AGCTGCTTCT GCTGTACGTT TAATACCTAT GGATATATGC TGCAAnTCTGC ATATCTATT	240
TTCGGTTTG AGACAATTG TAAATCGTAT CAAATGCCGC TTCTAATTT TnCACGTGGC	300
TTTGCAATTG AACTTCTTCT nGCAGGACCA ATAATAACCT TGGATTATTT TGTGACCCAT	360
CGGGAGTGA	369

(2) INFORMATION FOR SEQ ID NO: 4258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4258:

CCTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT	60
TTTTAAATA CTAAAATACA TGTTGGAATA CTTGTC C AT AGAAAATATT GGCTGGTAAC	120
CCAATCACGG CTTCTAAGTA GTTCTTTCT TCTATTAAAT AGCGACGAAT CACACCTTCT	180
GC G GCACCAC GAATAATACA CCATGnGGAG TACGACGCCA nGTACCTTCA TCGTCTAGTA	240
ATGTACCAAGT GTTGAATAAA GCAAAGTCTG CTTTGATT TT GGCGCAACTT GCCGTAACCA	300
CTGAATCGTT CATCATTTCA AATTGAACT GCTGT	335

(2) INFORMATION FOR SEQ ID NO: 4259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4259:

ATTCGCTAC CTTACGACCG TTATAGTTAC GGCGCCGTT TACTGGGGCT TCGATTCGTA	60
GCTTCGCAGC nACAACCAC CCTCTTAACC TTCCAGCACC GGGCAGGC G T CACCTATAAC	120
ATCACCTTAC GGTTTAGCAG AGACCTGTGT TTTTGATAAA CAGTCGCTTG GGCCTATTCA	180
CTGCGGnTCT TCTGGCGTT AACCTAAAG AGCACCCCTT CTCCCGAAGT TACGGGGTCA	240
TTTGCCGAG TTCCTTAACG AGAGTTCGCT CGCTCACCTT AGAnTTCTCA TCTTGACTAC	300
CTGTGTCGGT TTGCGGTACG GGCA	324

(2) INFORMATION FOR SEQ ID NO: 4260:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4260:

AAGCGGTTGT TAGACAATGC ATTAAGAAAA ATTAAAGCGG AGTTTACTTT TGTAAATGAG	60
CATTTGATTT TTTGAAAATA AAGCAGTATC GGGCGCTTGA CTAAAAAGAA ATTGTACATT	120
GAAAACCTAGA TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGA	180
TTTTAAATAA GCTTGAAATTc ATAAGAAAATA ATCGCTAGTG TTCGAAAGAC ACGAGCAAGA	240
TTAATAACGC GTTTAAATCT TTTTATAAAA GAAAACGTTT AGCAGACAAT GAGTTAAAnTT	300
ATTTTAAAGC AGAGTTTACT TATGTnAATG GAGCATTGAA AATnATGAAA ACGAGCCCGT	360
ATGTGGAGCG TTTGGACTTA TAAAAATGGT GGGAAACATA	400

(2) INFORMATION FOR SEQ ID NO: 4261:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4261:

AATTAATGTG CGAGTTGGGG TGGGACGACG ATAAAGAAAT ACTTTTCTA TAGAAATTAG	60
TATTTCTTAT GCATGAGTTT TACTCAGTAA TTCCTATTAA TAAGnACACA TTAGCTGTGG	120
CTAAnTAGAG GAnACCACTA CATAATAAAAT CATT&TGGC TCTTTATCAT TTCTGTCCCA	180
CTCCCCCTGAG AAGTTAAAAA TTTTATATGT TGGCTTGTAA TGTTAAGGGA ATTAACATGG	240
TTGTCTTGTT TATATTATGT GATTCAAACA TTACTAGTCT TGGTAAATCT AATTCTGAAA	300
ATGCTAAATC TAACCCTCTA TTAAATTAA AAC	334

(2) INFORMATION FOR SEQ ID NO: 4262:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4262:

TTTCGGTCAT ATTCAAACGT TTTCACTTCG CCAAGCCATT TTTCTTG TG	60
ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGGCGG TCTCAATGCG GCTCATCGCA	120
TCCATTTTT GCCTGGCAAC GTTCTACTCT AGCGGnAGTA ATTGGGCTAC CATCGTCGCT	180
AAAGACCTTT CTTGACTTGT GACAATCGCT TGChTCTTC CTCTCCTTCG GCTCTCGCTT	240
ACTCATTnAG CTCTACTAAA CTCGTTGCAC TCTTTCTCG TTTCGTCAGA TTCAAACGTT	300
TTCACTTCGC CAAGCCATT TTCTTTGTGT	330

(2) INFORMATION FOR SEQ ID NO: 4263:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4263:

GAGGTATAACC CCGGGACGGC TGAAGGGGAT GAACCCTAC GnAATGTCGG AACACAAATC	60
CGATGTGTTA CCACCTCAC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC GAACCCACAC	120
CAAAGGTTTT GGAGACCTCT ATTCTACCGT TGAACATATGC CCCTATTAAA ATAATAAAAT	180
GGAGGGGGGC AGATTCGAAC TGCCGAACCC GAAGAGTCGG ATTTACAGTC CGCCGCETT	240
AGCCACTTCG CTACCCCTCC ATAAATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC	300
TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG	339

(2) INFORMATION FOR SEQ ID NO: 4264:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4264:

GTATTTCAAA GTAAAATTAC ATGTTAATAC GTGnTTAATG GGCGAGACTC CTGAGGGAGC	60
AGTGCCAGTC GAAGCCGAGG CTGAGACGGC ACCCTAGGAA AGCGAGCATT CAATACGAGA	120
TnTnATGAAA TAGAGAACAG CAGTAAGATA TTTCTAATT GAAAATTATC TTACTGCTGT	180
TTTTTAGGGA TTTATGTCCC AGCCTCTTAC TCTAATTATA TTCACTATCA ATTAGACAAA	240
ATGGCCATTT TCAAATATCA CGCGTTGTTT CTACCTTGA ATATATTAT TATAATTCTC	300
TTTTGGAAA ATCAGTTAAC ATTAATTAG ATGTACCGTA TTTTAACAC T	351

(2) INFORMATION FOR SEQ ID NO: 4265:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4265:

ATTTCACTT TAAAACCTGC TTCTTTGGCT TTTGCATAT AATGTTGCGA TTGTTCTATT	60
GTAAATACAC CTGTTTCACA GAAAATATCC GCAAAGTCTG CATATTGTTT TA T CCGGA	120
AGTAACGCAA TCATTCTTC TAAAAATGCC TCATTGAAC TTGCCTCTTT AGGTACAGCA	180
TGAGGCCCTA GGAAAGTATG TTTCATGTCT AAATCATATT TCTCAGCTAA ACGnTTAGAC	240
ACTTTCAATT GCTTCAGTTC ATTTTCTCTA TCTAATCCAT AAACCACCTCT TGACTTTCAA	300
CTGCAGTCAC GCCGTGTTn AATCCATAGT AAGACAAAnC ATGACT	346

(2) INFORMATION FOR SEQ ID NO: 4266:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4266:

TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT TTATTGAAAAA TGGTGCCGAG	60
GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGGAT TTTAAGTCCT GTGCGTCTGC	120
CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA CGGGATTCGA ACCCGCGACC	180
CCAACCTTGG CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA	240
GTCGAACCCC CACGCCGTAA GGnTGAGATC CTAAGTCTAG TGCCTCTGCC AATTCCGCCA	300
CACCCGCCAA TGGTGAGnCA TAGAGGnTTC GAACCTCTGA CCCTCTG	347

(2) INFORMATION FOR SEQ ID NO: 4267:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4267:

GACTTGTCT CTTGGACCTA TATCATGTT C TTTATTTCT AATGCAGGAT CTTAATTGC	60
ATCTTAAGT GATTCACTCG CTGCAGGATA GTTTTCGCA GTGTTGCTG GTTGCCTGAG	120
GTnTGTGTT GATTGTATC CTTAGGTGGC TGAGTTGTAG TTGCATTATT ATTTGATT	180
TCCGAGATT TATCTGAAGT ATTTGTATT TCTGCTGCTT GTGCTTGATG TTGAGAAAGTA	240
ATTAAAAATA GTGTACTGAC AATGACCGAT GCAACGCCTA GAGTTGATT TCTAATAGAA	300
TAGGAAAGAC CnTnAATTTT GGGTGGATGT TTGTTCA	337

(2) INFORMATION FOR SEQ ID NO: 426:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

ATACATGTTG GAATACTTGT CCCATAGAnA ATATTGGCTG GTAACCCAAT CACGGCTTCT	60
AAGTAGTTCT TTTCTTCTAT TAAATAGCGA CGAACACAC CTTCTGCCGC ACCACGGAAT	120
AATACACCAT GTGGGAGTAC GACTGCCATG GTACCTTCAT CGTCTAGGTA ATGTACCATG	180
TGTTGAATAA AGGGCAAAGT CTGCTTTGGG ATTTTGGCGC AACCTGGCCG TAACCACTG	240
GAATCGTTCA TCATTTTCA nATTTGGAA TCTGGCTGGT TCCATTTCG GCACCTGGTAT	300
GGTGGGGGTT TCGGCAATAA ACGGCATTCA AATGGTATT T GGCTAAACA AGGCCGGGAT	360
TTTCCAATG GGGTCATCA TTAAnGGGAT CnTCGAAGTT	400

(2) INFORMATION FOR SEQ ID NO: 4269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4269:

GGCTCATCGC ATCCTGGGC TGTAGTCGGT CCCAAGGGTT GGGCTGTTCG CCCATTAAG	60
CGGTACGGAG CTGGGTTCAAG AACGTCGTGA GACAGTTCGG TCCCTATCCG TCGTGGCGT	120
AGGAAATTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG	180
TACCAGTTGT CGTGCCAACG GCATAGCTGG GTAGCTATGT GTGGACGnGA TAAGTGCTGA	240
nAGCATCTAA GCATGAnGCC CCCTCAAGAT GAGATTCCA ACTTCGGTTA TAAGATCCCT	300
CAAAGATGAT GAGGATATAG GTCGAGGTTG GAGCATGGTA CATGT	345

(2) INFORMATION FOR SEQ ID NO: 4270:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4270:

AAGAATTAAT TATACTTTT ATTAAACATT AAGTCATAA CTTTTTTAT CTTGTCCATT	60
TTATTTTTA ACCAAAATT GATTAAAAAA CTGCCTGGCA ACGTTCTACT CTAGCGGAAn	120
TAAGTCGaCT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG	180
TGACCTCCtT GCTATAGTCA CCAGACATAT GaATGTAATT TATACATTCA AAACTAGATA	240
GTAAGTAAAA GTGGATTTG CTTCGCAAAC ATTTATTTG ATTAAGTCTT CGATCGATT	300
GTATTCGTCA GCTCCaCATG GTCACCAGCT TCCACCTCGA ACCTATTGGn CGCATCATCT	360
CGCAGGGAnC	370

(2) INFORMATION FOR SEQ ID NO: 4271:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4271:

TGAGGTACGT CCAGAATnGG GATGGCTAA AAATGCATCA TTTATAATTG GACGACGCCA	60
ATTAACAAAA GGCATTGATT TAGAAGGGCG GACATTTTA CACAATTATG ATTGGCGTAA	120
AGATAAAAGAT GGCACATTAT TAAATACCAT CATTCTGGT CCGGCACTTG TGGCACAAATG	180
GaTTAATTAA CAATATTATG CGTCGACAGT TGCGCCGCAT TTTTaCGGtAATGGGAATAA	240
AGCGACACAA ACCGTCACGT CAGTGTTGGT GTCATGCAAG GTAATGCGAG TGCATCTGAT	300
GTAGGGCTTA TCATGCCAA TCTGTTA	327

(2) INFORMATION FOR SEQ ID NO: 4272:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4272:

CATTCTTAA ACTCTGTAAG TACTTCTTCA ATCTCAGGGG CATCTACTAA CATATCATCA	60
GTAATATGCG TCAAATTGAT AATCGTTTCC GATAATCGTT CATGCGGATT ACTAACACCTT	120
TCAAACATTAT CGATGATTTC ACCGTTATGA ACTTTCACAG CTGCAAnTCG ATGATTTAT	180
CATACTGATT TGATAAACCA GTTGTCTCAA CGTCGAACAC AACATAAGTA GCATCTTTA	240
ATACGACATC TTGTGGTTG TATGC A TCG GGAACACCAT CATCAACTAA CATACTTCC	300
ATACCGGnAT ATCATTAA nGCCA	325

(2) INFORMATION FOR SEQ ID NO: 4273:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4273:

TCCGGCCTTG ACCTGAAGAA CACTTGTCTT GTCGTTAAGA TGACTCTAGA CTCTTATGTT	60
TATTATCAAC CGTTAATAAA CTTACCATCA AGAGTGCACC TACCC A ACT GACAGTGCAG	120
TATAGAATGG TGTACATACCT GAACCATAAT CCTTAACGG GAAAACATCA ACAGTCTTCT	180
TATTAATAGG ATTTGCAATA ATACCCGCTT GCTTTTCAA ATCATTCTTA AGTGTGTCGA	240
TnAATTGTC GACTGCATCA TCTnTGTCTA ATTTCTGAA AATTTGATT CGCTTTTTC	300
CAAATCCTTn TCCAACATCA GGCAATTAA TTTGAGAAA AATCAGCCAA ATCCGGA	357

(2) INFORMATION FOR SEQ ID NO: 4274:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4274:

ACGTTAGCAC AAGCCATGAA CCAATTAGGT GGAAAGAGTA ATAGTGGTGA AGGTGGCGAA	60
GATGCAAAAC GTTATGAAGT ACAAGTTGAT GGAAGCAACA AAGTAAGTGC GATTAAACAA	120
GTTGCTTCTG GGCCTTTGG TGTAACTAGT GATTATTTAC AACATGCCAA AGAAATTCAA	180
ATTAAGTTG CGCAAGGTGC AAAGCCTGGT GAAGGTGGTC AATTACCTGG TACTAAGGTA	240
TATCCGTGGA TTGCGAnGAC AAGAGGGTCA ACGCCAGGTA TCGGTCTGAT TTCACCACCG	300
CCACATCATG ATATTTnATT CCATAnGAGG ATTTAGCCGC CACCTGA A CTGGATTTG	360

GAAAAATGGC GAATTAAGGT TGCnGATTT CCCCGGGTAA

400

(2) INFORMATION FOR SEQ ID NO: 4275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4275:

AACGTCGTTA ATTGAATAAC GCTTATGTTA TAAGAGCACT CATAACAAAC CATAATCATC	60
TATAGATATA ACAATTACAG ATATAAGGGC TGTGTTGGC ATAGCCTTTA GATATACACT	120
TAATTCCAT TAAAATAGTA GGGATTAAAA GGGGGCTTGT CATGGATTAA AATTCAACAA	180
TTACAACATC ACTTTGGATC ACATAAAAGTA ATTCAAACT TTAATTGGA CATTAGCAAG	240
GGAGAAATAG TCACTTCAT AGGGGAAAAG TGTTGCGGA AAGTCTACTT TACTCAATAT	300
TATCGGTGGA TTTnTTCCAT CCATGnCTG GTCGTGTCCA n	341

(2) INFORMATION FOR SEQ ID NO: 4276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4276:

TAGTGATATA CGACATCACA GCATAATATT GCTTAGAAA GTCGTGCCGA ACTGGAACCT	60
ACAAGTCTAG TTGAAACACA CACTGATGTG AGTGGTTTC TTTATTAA ACATGAACAA	120
TCAGATAAGT TACTAGCATT AGCAAATATT ATTAAATCAA AGGGTTCGA TTCATAAAAT	180
TTAAAACAAT GATTAAAATT AGACGTGTAA ATTGTTAAAT TCTAAAACGG AAATAACCAC	240
CATTCCATTA AACCACTTT TTGTTCATCA CTATATTCA CACnGCTTCA TTAATAAACG	300
GAATGCTTCA nCCGCTTCAA CTTCAACTGG CTTCAACTTC nGCCTACTTC ATCATAACAA	360
ACGGTCCG	368

(2) INFORMATION FOR SEQ ID NO: 4277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4277:

ATGGAAGTAC GTGACGTTCA CTACTCTCAC TATGGCCGTA TGTGTCCAAT TGAAACACCT	60
GAGGGACCAA ACATTGGATT GATTAACCTCA TTATCAAGTT ATGCACGTGT AAATGAATTG	120
GGCTTTATTG AAACACCATA TCGTAAAGTT GATTTAGATA CACATGCTAT CACTGATCAA	180
ATTGACTATT TAACAGCTGA CGAAGAAGAT AGCTATGTTG TAGCACAAGC AAACTCTAAA	240
TTAGATGAnA ATGGTCGTTT CATGGGATGA TGAAGTTGTA TGTCGTTCC GTGGTAACAA	300
TACAGTnATG GCTAAAGn	318

(2) INFORMATION FOR SEQ ID NO: 4278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4278:

CACTTGTACT TTCTGATGTT GAGCCAGACT CTGATGTACT TACCGATGTA GATAAACTTG	60
CAATGGTCGA CATGCCGTTT GAAGTTGATG TACCTAGCGA ATCACTTAAT GATGCTGATG	120
TGCTTTGTGA ATCGGATTG CTCGTGCTTG TACCTGTTGA GTTTGAGGCA CTTTGGCTTG	180
CTGAGTTGGA GTCTACTCCG CTTTGATTCA TTGAGGCACT TAGTGACAAT GATGTACTCG	240
TTGAGTCAGA CAAACTTGTA CTCGTTGACG TACCTGACT TCCTGATGTT GATTGAGACA	300
TACTTATGCT CATTGGATGT TGAATCGGAT TTACTTCAC TTGAATGATG TTGAGTCGGA	360
TTCACTTCA CTTGTAGAAC CACTTAATGA TGTGGATGT	400

(2) INFORMATION FOR SEQ ID NO: 4279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4279:

TTTGTACTTC GATTAAAAG ATATTAGACA TAAAATCTAA AAnCAGCAGT AAGATGATT	60
ATGATTAAAA ACTATCTTAC TGCTGTTCAC TTTTTATAAT ACTTCTGAAT GTCTTCACCT	120
ATACTTCTAG TCACAGATT AAATAATCAA AAGTGCACAT TATAAAATA TCAATTCAC	180
ACTCAATGCG GCTCATCGCA TTCATTCTT GTCTAGCAAC GTTCTACTCT AGCGGAAGTA	240

AGTTAGCTAC CATCCTCGCT AAGAACCTTT CTTGACTTGT GACAATCGCT TGCTTCCTTC	300
CTCTCCTTCG GCTCTCGCTT ACTC	324

(2) INFORMATION FOR SEQ ID NO: 4280:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4280:

CTCACTAGTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT	60
GTGGATTGTC CTTTGGCATG TGnTTAGGAG AGCGTTCTAA GGGCGTTGAA GCATGATCGT	120
AAGGACATGT GGAGCGCTTA GAAGTGAGAA TGCCGGTGTG AGTAGCGAAA GACGGGTGAG	180
AATCCCGTCC ACCGATTGAC TAAGGTTTCC TGnGGAAGGC TCGTCCGCTC TGGGTTAGTC	240
GnGTCCTAAG CTGAGGCCGA CAGTAGGGCG ATGGGATAAC AGGTTGATAT TCCTGTACCA	300
CCTATAATCG TTTAATCGAT GGGGGG	326

(2) INFORMATION FOR SEQ ID NO: 4281:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4281:

TCGAACATGA GCGATTATTT CTTATGAATT CAAGCTTAT TAAAACCTTT TATTCACTCG	60
GTTTGCTTG GTAAAATCTA TATTTTACTT ACTTATCTAG TTTCAATGT ACAAAATAATG	120
GTGGGCCTAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGCGTGCCTCTAACCAAG	180
CTGAGCTATA GGCCCATT TTGAATGTT AAATAAACAT TCAAAACTGG AATACAATAT	240
GTCACGTTAT TCCGCATCTT CTGAAGAAGA TGTTCCGAAT ATATCCTTAG AAAGGnAGGT	300
GATCCAGCCG CACCTTCCGA TACGGGCTGA CCTTGTGAC GACTTGCACC CCAAGCATT	360
GTCGCCAnCn	370

(2) INFORMATION FOR SEQ ID NO: 4282:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4282:

GAGAGATGAC ACGGrACTGA ATTGGTTGA CACCACGTGA TGAATGTGAT CGTCGGCCTT	60
CTTCACGATT GnAATACTTT TACATCAAGA ACGATAACGC CAGCGCCGTG AGGTACACGT	120
AATGAAGTAT CTCTAACTTC ACGTGCTTT TCACCAAAGA TTGCATGTAA CAATCTTCT	180
TCGGCAGTTA ACTCAGTTAC ACCTTAGGC GTTACTTTACCAACTAAAAT ATCTCCATCT	240
TTTACTTCTG CACCAATATA AACGATAACCA CGATCGTCTA AGTTCTTAAG TGCACTTCA	300
GAAACATTAG GnATATCTCT TGTGATTTCC TCAGGGCCTA ACTTAGTATC ACGTGCCTCT	360
GAATCCATAC TCCTTCAATA TGAATAGAAG TATACACGGn	400

(2) INFORMATION FOR SEQ ID NO: 4283:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4283:

AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCCAAC AAGAGAAATT GGATTCCCAA	60
TTTCTACAGA CAATGTAAGT TGGGGTGGGA CGACGAAATA AATTTGAGA AAATATCATT	120
TCTGTCCCAC TCCCGATTAT CTCGTCGCAA TATTTTTTC AAAGCGATTT AAATCATTAT	180
CATGTCCAAT CATGATTAAA ATATCACCTA TTTCTAAATT AATATTGGA TTTGGTGAAA	240
TGATGGACTC TTTGCCCTCGT TTAATTGCCA TAATGTTAAT nCCATATTGT GCTCTTATAT	300
CTnAATCCAT GATAGACTGn CCCG	324

(2) INFORMATION FOR SEQ ID NO: 4284:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4284:

AAATCGTAAC GAGTGAAC TTCTTATTTAG GTGGCGAGT AACTTACTAG CACCTGACGA	60
AACGGTTTTA GATCGTATTC AATTGAAAAG GCCGGTATTG AATGAATCAC ACTTAGCAGC	120
GATTGATCAG GAACATTTA AATTAACCTA TTTATCAACG GTATATGAAG GGGATTTGGC	180

AAGATGCGTT ATAAGCATT A GCCCGTAGAA GCAGTGAAAT GCTGTnAAC AAGGGCGCTC	240
AAATTCTAGT GTTAGATGAT AGTGGATTAG TTGGATAGCA ATGGCTTG C AATGCCGATG	300
TTTACTCGCA ATGAAGTGCA TGTGCCATGC AATTGACTTC TTTAAAGCCA GATTTACGTG	360
ATGTCTAAC A AGTTTnTnC GCTAAAATCn GGGTGGAGAC	400

(2) INFORMATION FOR SEQ ID NO: 4285:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 560 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4285:

CATTTTCTT TGTGTTACT TTTTATTTG ACGTTTAGA CATAAAAAAA GAGACTCACG	60
GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC	120
TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCATCTTT CCTCAnCATC GGnTnTAGCT	180
TACTCATT A GCTCTACTAA ACTCGTTGCG CTCTTTCT GTTTCGTCAG ATTCAAACGT	240
TTTCACCTCG CCAAGCCATT TTTCTTTGTG TTTACTTTT ATTTTGACGT TTTAGGCATA	300
AAAAAAAGAG ACCTTGnCGG TCTCAATGCG GGCTCATCGC ATCCATTTT TGCCTGGCAA	360
CGTTCTACTC TAGCGGAAGT AATTGnGCTA CCATCGTCGC TAAAGACCTT TCTTGACTTG	420
TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATT A GCTCTACTAA	480
ACTCGTTGCG CTCTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATT	540
TTTCTTTGTG TTTACTTTT	560

(2) INFORMATION FOR SEQ ID NO: 4286:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4286:

GTAACACTCG GnATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GTAGCTAATA	60
CCGGATAATA TTTTGAACCG CATGGTTAAA AGTGGAAAGA CGGTCTTGCT GTCACTTATA	120
GATGGATCCG CGCTGCATTA GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA	180
TAGCCGACCT GAGAnGGTGA TCGGCCACAC TGGAACTGAGACACGGTCCA GACTCCTACG	240

GGAGGCAGCA GTAGGGAATC TTCCGCAATG GGCGAAACTG GACGGAGCAA CGCCGCGTGA	300
TGnATGGAAG GTCTTCGGAT CGTAAAACTC TGTTATT	337

(2) INFORMATION FOR SEQ ID NO: 4287:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4287:

CAATCGTGCT CAnTGCGCAT CGTnACTCAT CTGTATGTGT TCCAGCATAT ACAATTTGC	60
CATCTTTAAT GACAACGTGA CCATTTTC CAACATTAA TTCATCTAAT TCCTTACCC	120
TCAAAGGTTT ATCTGTTGAT CTCGGTAAAA TTAATTCTGG CTATATGATT AATTATTAAA	180
TCATCATTAC TTATCACCTG CTTTATCAAT CATGGAATAT GAATACCTT TTCTTAGCT	240
GTTTGAATAG CGATGTCATA GCCAGCATCA ACATGTCGGG CAACACCCAT ACCTGGGTCA	300
GTCGTCAATA CACGTTCCAA TCTTCTTC GCACGCTCTG AATCCATCTG G	351

(2) INFORMATION FOR SEQ ID NO: 4288:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4288:

CTATTCACTG CGGCTCTTCT GGGCGTTAAC CCTAAAGAGC ACCCCTTCTC CCGAAGTTAC	60
GGGGTCATTT TGCCGAGTTC CTTAACGAGA GTTCGCTGC TCACCTTAGA ATTCTCATCT	120
TGACTACCTG TGTCGGTTG CGGTACGGGC ACCTATTTTC TATCTAGAGG CTTTCTCGG	180
CAGTGTGAAA TCAACGACTC GAAGACACAA TGTCTTCTCC CCATCACAGC TCAGCCTTAA	240
CGAGTACCGG ATTTGCCTAA TACTCAGCCT TACTGCTTAG GACGTGCAAT CCAATCGCAC	300
GGTTTnGCCT ATCCTA	316

(2) INFORMATION FOR SEQ ID NO: 4289:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4289:

TTnTTTATGT CTAAAACGTC AAAATAAAAG CAAACACAAA GAAAGATGGC TTGGCGAAGT	60
GAAAACGnTT GAATCTGACG AAACGAGAAA TGTAAAGTAT AATAAAAAGC AGTCATAAGA	120
TGATTTCAAT TAGAAATCAA TTTATGACTG TTTTCTTAC TATGTGTTAA ATTAACAATG	180
AATATAACAT CTTATTTCA TTAATATAAA TATTGGAAGG ATCGAnATGA TTTACACGTT	240
GTGGAGTTG TATTAAATCA TCATGATCTT TAAGTTGAAT ACCAATAATG ACAGTACCTG	300
TATTTGAGA GATTTTTAA GT	322

(2) INFORMATION FOR SEQ ID NO: 4290:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4290:

TCATTTAGCT CTACTAAACT CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTT	60
CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTATT TTGACGTTTT AGGCATAAAA	120
AAAAAGACCT TGCGGTCCAA TGCGGCTCAT CGCATCCATT TTTGCCTGG CAACGTTCA	180
CTCTAGCGGA AnTAATTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC	240
GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTChACT AAACTCGTTG	300
CGCTCTTnTC TCGTTTCGTC AGATTTCAAA CGTTTCA	338

(2) INFORMATION FOR SEQ ID NO: 4291:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4291:

AATTGGTTA CACCAGGTGA TAATGTATCG TCGCCTTCTT CACGATTGAA TACTTTACA	60
TCAAGAACGA TACCGCCAGC GCCGTGAGGT ACACGTAATG AAGTATCTCT AACTTCACGT	120
GCTTTTCAC CAAAGATTGC ATGTAACAAT CTTTCTTCGG CAGTTAACTC AGTTACACCT	180
TTAAGGCAGT ACTTTACCAA CTAAAATATC TCCACTTTT ACTTCTGCAC CAATATAAAC	240
GATACCACGA TCGTCTAAAG TTCTTGAAGT GCACCTTnCA GAAACATTGA GGAAATGATC	300

TCTTGTGATT TCTTCCAGGT CCTAACTTGA GTGATCACGT GGCTTCTGGA TTGCAGACGC 360
TTGCAAGATG GAATGAGAAG TGAnACACGT GCATCCTTGC 400

(2) INFORMATION FOR SEQ ID NO: 4292:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4292:

AAACGTTTTC ACTTCGCCAA GCCATTTTC TTTGTGTTA CTTTTTATTT TGACGTTTA 60
GGCATAAAAA AAAGAGACCT TGCAGGCTCA AATGCGGCTC ATCGCATCCA TTTTTGCCT 120
GGCAACGTTTC TACTCTAGCG GAACGTAATT GGGCTACCAT CGTCGCTAAA GACCTTCCTT 180
GACTTGTGAC AATCGCTTGC TTCTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 240
TACTAAACTC GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA 300
GCCATTTTC TTTGTGTTnA CTTTnT 326

(2) INFORMATION FOR SEQ ID NO: 4293:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4293:

GGGGACAATT CCCTGGGGGT TCAAGTCCTC TGGGCCGGC ATCAAAATTC TTAATTAAA 60
TAAGCAGGGTG TAGTTAACG GCAAAACCTC AGCCTTCCAA GCTGATGTTG TGGGTTCGAT 120
TCCCATCACC CGCTCCATAG ATAATTAA TGAACATTGA AAACTGAATG ACAATATGTC 180
AACGTTAATT CCAAAACGT AACTATAAGT TACAAACATT ATTTAGTATT TATGAGGAA 240
TCAAACATCA TAATTTTAT GGAGAGTTG ATCCTGGCTC AGGATGAACG CTGGCGGCGT 300
GCCTAATACA TGCCAGTCGA GCGAACGGAC GAGAAGCCTG CCTCnCnGAT GTTAGC 356

(2) INFORMATION FOR SEQ ID NO: 4294:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4294:

TTATCACCCA TGTCTGACT CCCAAGTTAA ATTAATTGGC ATTGGAGTT TGTCTGAATT	60
CGGTAACCCG AGAGGnCCCC TCGTCAAAC AGTGCTCTAC CTCCAATAAT CATCACTTGA	120
GGCAGCCCTA AAGCTATTTC GGAGAGAAC AGCTATTCC AGGTTCGATT GGAATTCTC	180
CGCTACCCTC AGTCATCCG CTCACTTTAC AACGTAATCG GTTCGGTCCT CCATTCAGTG	240
TTACCTGAAC TTCAACCTGA CCAAGGTAGA TCCTGGTT TCGGGTCTAC GACAAATACT	300
AAACGCCCTA TTCA	314

(2) INFORMATION FOR SEQ ID NO: 4295:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4295:

AAGTGAAAGA ACTCGCGTG ACACCTATTG CACGATTGCGT TGGTTTAAG GCAGTAGGCG	60
TTGACCCGAA AATTATGGGT ATTGGGCCTG CATATGCGAT TCCTGAAGTA TTECACTCA	120
GCAATCTATC TGTTGAAGAC ATTGATTGAA TCGAATTGAA CGAACGATTT GCTTCTCAA	180
CGATTGCATC TATTAAAGAA GTAGGTCTAG ATATATCACG TACGAATGTG AATGGTGGCG	240
CTATTGCTTT AGGTCACTCCA TTAGGTGCTA CAGGCGCCAA TGTAAACCCG CGCGTTTACC	300
TAATGAAATG GGGTAAACCG nCCCGATAAGn CCGTAnCGCA AGGGT	345

(2) INFORMATION FOR SEQ ID NO: 4296:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4296:

TAAATTGATT TCTAATTGAA ATCATCTTAT GACTGCTTT TATTATACTT TACATTCTC	60
TTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATC TTTCTTGTG TTTGCTTTA	120
TTTGACGTT TTAGACATAA AAAAGAGAC CTTGCGGTCT CAATGCGGCT CATGCATCC	180
ACTTTTGCC TGGCAACGTT CTACTCTAGC GGAAAnTAATT CGnACTACCA TCGACGCTAA	240
GGAGCTTAAC TTCTGTGTTG GGCATGGAA CAGGTGTGAC CTCCTTGGCT ATAGTCACCA	300

GACATATGAA TGTnAATTGA TACATTGCAA AACTAGGATA GTGAAGTAAA AGTGATTTG	360
C	361

(2) INFORMATION FOR SEQ ID NO: 4297:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4297:

AACTCGTTGC GCTCTTTCT CGTTTCGTCA GATTCAAACG GTTTCACTT CGCCAAGCCA	60
TTTTCTTG TGTTTACTTT TTATTTGAC GTTTAGACA TAAAAAAAGA GACCTCACGG	120
TCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT	180
AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTC CTCTCCTTCG GCTCTCGCTT	240
ACTCATTAG CTCTACTAAA CTCGTTGCGC TCTTTCTCG TTTCGTCAGA TTCAAACGTT	300
TTCACTTCGC CAAGCCATT TnCTTTGTGT nTACTnT	337

(2) INFORMATION FOR SEQ ID NO: 4298:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4298:

GTATTCCCTCC ATTATTATAG GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA	60
CGGGAATCCT GCGTGACAGn CAGGCGTGTT ACCGCTACAC TACGAGACCA TTAGTAAAAC	120
GGAGGAAGAG GGATTGAAAC CCCCGCGAGC CGTTAAGCCC CTGTCGGTTT CAAGACCGA	180
TCCCTTCAGC CGGACTTGGG TATTCCnCA AAATTATATG GACCTnGCAG GACTCGAACCC	240
TGCGACCGAA CGTTATGAGC CTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT	300
TTTTACAAC TATAAAATAG TGG	323

(2) INFORMATION FOR SEQ ID NO: 4299:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4299:

CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT CCATTAAATG	60
AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT AAAATTGCCT	120
ATAAATTTT AGCACATAAA ATAAGAGGnG CCAACCATTG TTAGACTATA ACAACGGTTG	180
GCTCTTTAAT TGTAaaaAGA AAACCATAG CTATGnTGTT ACAAnGAAAA AGGTTCTACC	240
ATTGTCACAA AAAATGCATC TCTACGTGCT AGAATAAATA TTGGTCAGCC AACCAAAATA	300
ATCAACACGA GGAGATGCTA TTT	323

(2) INFORMATION FOR SEQ ID NO: 4300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4300:

CTAACATACC ACCTACAAGA CCTGAAGCGA AACCAAGGTTT ATCCGCAAA CTACGTGCAA	60
TGAATCCAGA TAAAATTGGA ATGATTAACG CGAATCACTT TTACTACCAA TGTTCCAAAG	120
CTGCTCTGCA AACGCATTGT ACTCTGAGCT TTTGGATTA AATGAATTG CTCCAAATAA	180
AAATACAATT GCCATTAaaa TACCACCAGA TATTACAAGT GGCAACATGT TAGAACACCC	240
GTnCATTGA AGTGTGAT AGAATGCTTT ACCTGGGGCT TGAATTTC TTGGACTGTG	300
CATTTGAGTT ACCTTTCTT TGGACCATCA CGGGGCAACA AAAGGTTGA CGACTTGTGA	360
GCTGAATGGC TTnGnTGAAT GAATT	385

(2) INFORMATION FOR SEQ ID NO: 4301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4301:

TCCTGTACCA CCTATAATCG TTTAATCGA TGGGGGGACG CATAGGAATA GGCACGTGA	60
CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA	120
GGCTGAGCTG TGATGGGAG AAGACATTGT GTCTCGAGT CGTTGATTTC ACACGCCGA	180
GAAAAGCCTC TAGATAGAAA ATAGGTGCC C GTACCGAAA CCGACACAGGTAGTCAAGAT	240

GAGAATTCTA AAGTGAACGA ACGAACTCTC GTTAAGGGAC TCGGCAAAAT GAnCCCGTAA 300
CTTCGGGGAA AAGGGTnCTC TTTAnGGTTA ACGCCCCAAA AAACCGCT 348

(2) INFORMATION FOR SEQ ID NO: 4302:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4302:

AATGGAACGT GCTTCTGTAT TGGCCAAGT AGATATTCAT CGTGCAGCAA CACATAATAA 60
AGGTGTTATG AATGGCATAc ATGCTGTTGT TTTAGCAACA GGGAAATGAT ACGCGTGGTG 120
CAGAAGCAAG TGCGCATGCA TnACGCGAGT CGTGACGGGA CAGTATCGTG GTATTGCTAC 180
ATGGCGTTAC GATCAAGATC GTTCAACGAT TGATTGGTAC AATTGCAAGT GCCTATGGAC 240
ATTGGGCAAT CGTTGGCGGT GGTACAAAG TATTACCAAT TGCTAAAGCT TCCATTAGGn 300
GCTGACTAAA TGTAGAGTCA GCACAAGAAT TGAGGTCCAT GTTAGTTGGC TGCCGTTGGG 360
TTTGAGCGG CAAAAACTTT GnCAG 385

(2) INFORMATION FOR SEQ ID NO: 4303:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4303:

AGTGCACGA TTGGTATTAA ACAAGAATTAA TATCACAAG ATTAAATAG CTTAACGCA 60
GCAATCCCTG TGTTACTAGG CGATAACATT GGTACCACGA TTACAGCTAT CTTAGCTAGT 120
TTAGCCGGCT CAATCGCTGC AAAACGTGCG GCGCTTGTAC ACGTCATCTT TAACTTAATC 180
GGGGTAATTA TCTTCACAAT TTTCTTGCCA GTTGTGATTC ATTTGATTAG TTTGTTACAA 240
GATTTATGGG CACTTAAAC CAGCGATGAC GATTGCAGTA TCACATGGnA TCCTTCAACA 300
TAACCAATAC CTTGGATTCC ATTACCAAT TTGTAGCCnG GTTACGATn GGATTGGTTA 360
CCAAGCCTTG TCCC 374

(2) INFORMATION FOR SEQ ID NO: 4304:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4304:

AAAACAGGAT ACTTCGATAA GTAAATGATT TCTGTTGTGA ATCGCGCACC ACGTTCTTA	60
ATTTTACCGA CTATTATATT AATTGGTATT TTAGGTAGTA CAGCCGGCGA TGCTGCGACA	120
ATTCTTGCC GCCGCTTGCA GCAATGCTT TTATTAAAAT TGGCTATCAC CCTATCGCTG	180
GACTAACGAT GGCATATGCT TCCGCTGTTG GAGGATTGC AGCAAAT AA GTTGTGGTA	240
TGCAAGATGC TTTGGTCTAT TCATTTACAG AACCGGCAAC ACGTATCGTT TCAGATTCTA	300
TTAAAACAAA CGTT	314

(2) INFORMATION FOR SEQ ID NO: 4305:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4305:

CGTTGCAGAA TGTGTTGAAA TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG	60
CCATTAATT ACAGGTTACCA ACCAATATAT GGTGATGATC AATCGTTGCT TCAATACCAT	120
GGCCAGGTAC TGCTTAAAT GTTGTGCT CAGTTAATAT TAATTGCTTT TCTTTGCAT	180
AATTGACAAT GGCTCTGCC AATGGGTGTT CAGAATCTTT TTCAGCAGTA GCAAGTAGTT	240
GTAGCGTTG ATTGTCACCA TGATAATCTG TCACGACTGG GACGACCATT TGTAATGGnA	300
nCCGTCCTTA TCTAAAACGA TGGGTATCAA TTTGATGnGG GCGG	344

(2) INFORMATION FOR SEQ ID NO: 4306:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4306:

AGTTTCCCTG AAAATTAATC AAGGACTTAA CATTGCGAGT CAAGGTATTG ATCAAGCTAA	60
TGGACAGTTA AATGATGCCA AAGCTTCGTC ACACAAGTTA GAA G AGAGT CGGTGATTAT	120
CAAGATGCAA TTGACGCGC GCAAGATTAA AATCGAAGAA ACCAGCAACA GATTCCCAA	180

AATAGCGCGG CGAACACGA AACATCAAAT AGTGCACCTG CAGCTGGTAA TGGTAGCA	240
TCAACGCCAC CAAGTGCACC AAGTGGCGAT ACTGCACCAA ATAATAATGT TACGAAAAT	300
ACCGCACCAG ATGAGTGAAT AATGCGCTG TATCGACTAC ACCACAAATG ACAnCCGGG	360
GAAAGATGG TCAAATT	378

(2) INFORMATION FOR SEQ ID NO: 4307:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4307:

GGACTTGGGT ATTCTCCAA AATTATATGG ACCTTGAGG ACTCGAACCT GCGACCGAAC	60
GGTTATGAGC CGTTAGCTCT AACCAACTGA GCTAAAGGTC CTAnATATAA TTTTACAAC	120
AATAAAATAGT GGCGGTGGAG GGGATCGAAC CCCCGACCTC ACGGGTATGA ACCGTACGCT	180
CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGAAAT AATATGGTGG AGACTAGCGG	240
GATCGAACCG CTGGACCTCC TGCGTGGCAA AGCAGnCGCT CTCCC A CTG nGCTAAGCCC	300
CCATAATAAT TACAGTAT	318

(2) INFORMATION FOR SEQ ID NO: 4308:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4308:

TGTACGTTTA ATACCTATGA TATATGCTGC AAGTCTCAT A TCTATTTC GGTTTGAGA	60
CAATTCTGAA ATCGTATCAA ATGCCGCTTC TAATTTCA CGTAGCTTT CATTAACCTC	120
TTCTTCAGAC CAATAATAAC CTTGATTATT TTGTACCCAT TCGAAGTAAG AAACCGTTAC	180
ACCACCAAGCA CTTGCTAATA CGTCTGGAAC TAATAATATA CCACGTTCAAG TTAAAATACG	240
TGTTGCTTCT GGTGTTGTAG GTCCATTAGC AGCTTCAACA ACGATACTAG CTTTAATATC	300
ATGTGCATTG TCCTCnGTAA TGGGTTGAA TAGCGnGGGA CTAAATGCAC ATCnAATCAA	360
CAATCCTATT GGATGTCCC AnAATTGTAC GACCAACACC	400

(2) INFORMATION FOR SEQ ID NO: 4309:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4309:

CAAATAAAACC AGAGCTAGTT GCAATTGCTG AACCACATCC TAATAGACCG AAAAAGAGAA	60
GTAGACGTGC GGCACCGGCA GATCCTAATG CAACTCCAGC AATCCAGCG GCTGCAGCGG	120
GTAGGAAACG GTGGTGCACC AGTTGCAATT ACAGGCCAT ATACGCCAAC AACTGATCCT	180
AATGCCAATA ATGCAGGACA AAATGCACCT AACGAATnGT TGTCATTTG ATGACAATGG	240
TATTAGACCA AGTACCAACC GTTCTGTGCC ACnTnAACG TTGTTAATAA CTTGCCGGGC	300
TTCACACTAA TCAATGGTGG CAAAGT	326

(2) INFORMATION FOR SEQ ID NO: 4310:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4310:

TCAAAGCGCC AATAACATCT TCTACTGAAG TTTCTTTAGA TTTAGCATTC AGTGATAATG	60
TTATTGTTGC TTTTCTTCC ATTGGAATAC TTTGATGAAT CGTTAATACA GATAGTTCTA	120
ACTTGATAT AACATCTAGT ACACGTGCCA ACATACCAAC AATATCAGTT ACATATAAAA	180
TTAATGTAAA TTCTCGATGG TCAAGCATT TATCGGCTAC TGGAAATATC GTTCTCTAT	240
ATnTATAAnA AGCACTTCTA GATAGATCAA ACTGTTAAC GGCATCATAA ATGGnCAATG	300
TCGGATCACT TTT	313

(2) INFORMATION FOR SEQ ID NO: 4311:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4311:

GGTCGAATC CAGCTAGCCC AGCCATTAGA GCCATTAGCT CAGTTGGTAG AGCATCTGAC	60
TTTTAATCAG AGGGTCAGAG GTTCGAATCC TCTATGGCTC ACTACTTGCA CTTTCCATT	120

TTGGGAAGTG CTTTTTTTA GGTTCTCCAC CAAATGTGGT GGGTATATAA TTTAAAGAAC	180
TATTTTAAA ATACAACCTT TAGAGCTTT ATTATTAGGC GGCCAGTCCA TTATTGGGGC	240
TGGTTGTCTT CnTTTTTCT CCTTTGTACA AGCTGAAAAT CATCATTATA CGTGCTTAAA	300
GTGGTGAATT CTGAACCAAA GAATCACTTG ATAATTTATC TATATAATCC TCnATAGACC	360
ATATAATGCT GGAATAATGG ATCTACAnCC TGAGTTCCAn	400

(2) INFORMATION FOR SEQ ID NO: 4312:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4312:

CGATAACATG ACATAACTCA TGCTGGTTT CCCCATTGG AAATCTCTGG ATCAAAGCTT	60
ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA	120
AGGCATCCAC CGTGCGCCCT TAATAACTTA ATCTATGTTCCACCATTAA TATAAGTCAA	180
ACGCTCACAT ACGGCTTCGT TTTCATTATT TTAAATGCTC ATTTACATAA GTAAACTCTG	240
CTTTAAAATA ATTAACATCAT TGTCTGCnAA ACGTTTCCnT TTATAAAAAG ATTAAACGCG	300
TTATTAAnCT GTGGAGTG	38

(2) INFORMATION FOR SEQ ID NO: 4313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4313:

ACGGTGATCA CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GCCAGTTCCG CCACCCCCGGC	60
ACTATAAAAA TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCAACCTT GGCAAGGTTG	120
TATTCTACCG CTGAACTAATC TCTGCATATG CGGGTGAAAnG GAGTCGAACC CCCACGCCGT	180
AAGGCATAGA TCCTAAGTCT AGTGCCTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC	240
CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCn	300
AATGGnTCTT CCATGG	316

(2) INFORMATION FOR SEQ ID NO: 4314:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4314:

AGGAAAAGTC GTTGTGATAC ATCAACCAGC TGAAGA&TA CCACCAGGTG GTGCTAAAAC	60
AATGATTGAA AATGGTGTAT TAGACGGTGT TGATCATGTA TTAGGTGTAC ACGTCATGAG	120
CACAATGAAA ACAGGTAAAA GTGTATTACC AGACCTGGTT ATGTTCAAAC AGGACGCGCA	180
TnCTTCAAAT TGAAAGTCAA GGTAAAGTGG TCATGGTTCA TCACCACATA TGGCCAATGA	240
TGCCATTGTT GCAGGTAGCT ACTTCGTAC AGCGTTACAA ACAGTGTATC TAGACGACTA	300
GGCCATTGGA ACCGGTGGTT TCACATCGGT CATTnCCGT AAAAGnCCAT TCCATG	356

(2) INFORMATION FOR SEQ ID NO: 4315:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4315:

TATCAGCATT TGTAACGTGTT ATTGTTATA ACTTCTGTGT GAAGCGCAAT ATTACAATTA	60
AAATGCCGAA AGAAGTACCG CCGAATATTT CACAAGTATT TAAGGACTTA ATTCCATTT	120
CAGCGGTAAT CATCATTCTT TATGCATTAG ATTTAGTCAT CGAACACAGCT TTAAATCAA	180
TGTAGCGGAA GGnATTAA AATTATTCGA ACCATTATTT ACAGCAGCAG ATGGGATGGA	240
TTGGTGTAC AATTATCCTT GGnGGCCTT GCATATTG GGTTGTAGGG AATCAGGTCC	300
GTCAATGTAG AGCCAGCAAT TGCAGCCATT ACATATGCGA TATCGGAGCG GACTTCAAGT	360
TGCCTCAGCG GAGGACACGC	380

(2) INFORMATION FOR SEQ ID NO: 4316:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4316:

GCTCTAGGAT GACTGATTGA ATGTCCATGA ATGAACAAACC CCTTTGTTA ATATCGAGT	60
--	----

TGGCAAATT	ACGTTTATCA	GCGTTCTAT	GATCAGTACT	TCTACGGGT	A	GCGTTCTAT	120
GTAATTTACA	TCATCTAAC	ATATAAATAC	TTCGCTATT	AATTGAAAAC	ATATCCTATT		180
ATTCTTGTC	CGTTCTGACG	TTTAATATCT	AGCCTTAGGC	ATTCACTTG	TTAATGAATT		240
TAACTTCTT	CCACTAACCG	TCCCTAAACC	CAATCCCGCA	ACAGTTTTA	ACTTTTCGT		300
TGTTGTCCTG	ACATCTCATT	AAGAAAGTTT	ATTCTGCTTA	AAACTTATAA	TCCACACCT		360
GAGCAAACGn	TnCTTATGAC	AGAGTATTAA	AATAAGCCGn				400

(2) INFORMATION FOR SEQ ID NO: 4317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4317:

CCTTATTGAT	AATGGTATGA	GAATATTGT	TCGA@TGG	A	TGAAGGTAAT	GAGTGAGAAA	60
CTGGATTTT	AAAGTATGAG	ACAATATT	TTT	AAAAAGTTCA	ATTATTAAC	TATAAGCAAA	120
TAATTGCTAT	AAAAAAGTTT	GGACGTGTAC	AATTGCAATA	TGAAGATT	TT	AAATTAATTG	180
TAAAGTATCG	TGGAGTGGGT	AACGTGTCA	AG AACATGTATA	TAATCTTGTG	AAAAAGCATC		240
ATTCTGTTAG	AAAATTAAAG	AATAAACCTT	TAAGTGAAGA	CGTTGTTAGG	AAATTGGTAG		300
GAGCTGGGCA	AAGCGCTTCG	ACGTCAAGTT	TCCTGCCAGC	ATACTCCATT	ATTGGTTCGG		360
CGGTGGGAGG	TTAAnGGAAT	TTACGGGGAG	GTTCTGGGCA				400

(2) INFORMATION FOR SEQ ID NO: 4318:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4318:

TAACTACGTC	TCCTGTTCT	GGATTCTAA	TTCCCTGGTT	ACCTGGA	ACT	TCCTCTTCT	60
CTCCTGTTGG	TAACTTCGGA	TCAAATT	CGT CTCGATGACC	TGGTGT	TATC	GTTCTGGTC	120
CGTATTCTGT	TAATTCA	TTA ATCGGATCTn	TTGTGATT	TC	TTCTCGAT	TCACCTGTAC	180
TAATAATTTC	TCCAGTTAAT	GGATTTTTA	GTGTTGGGT	CGTTATTGTC	TTCTCACCTn		240
TTTGTCCCTC	TCTTGTA	ACT TTTCTGTCC	CGGTGCTAAA	TnCGGATTAA	ATTACGGTCT		300
TTCTTGAAAGG	AATCTCTTC						319

(2) INFORMATION FOR SEQ ID NO: 4319:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4319:

AGGTGCATTG AGAGAATTG TAAATGACGT ATTAGGACCT CAAGACGATA TTACTA ATT	60
TGAATACTTA AAAAAATCTT CTCAAAATAC AGGTACTGTC AATTATTGGT ATTCAACTTA	120
AAGATCATGA TGATTTAATA CAACTCAAAC AACGTGTnAA ATCATTTCGA TCCTTCCAAT	180
ATTATATATTA ATGAAAATAA GATGTTATAT TCATTGTTAA TTTAACACAT AGTAAGAAAA	240
ACAGTCATAA ATTGATTCT AATTGAAATC ATCTTATGAC TGCTTTTAT TATACTTTAC	300
ATTGCTCGT TTCGTCAGAT TGCAAACGTT TTCACTTCGC CAAGCCCATC TTTCnTTGGn	360
GTTTGCCT	368

(2) INFORMATION FOR SEQ ID NO: 4320:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4320:

TAAGTTAGCT ACCATCCTCG CTAAGAACCT TTGTGACTT GTGACAATCG CTTGCTTCTT	60
TCCTCTCCTT CGGCTCTCGC TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTCT	120
CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTGT GTTTACTTT	180
TATTTTGACG TTTTAGACAT AAAAAGAG ACCTCACGGT CTCAACTTGC CTGGCAACE	240
TCTACTCTAG CGGAA n TAAA GTTGGnCTAC CATCGTCGCT AAAGACCTT CTTGACTTGT	300
GACAATCGCT TGCTTCTTT CCTCTCCTnC GGCTCTCGGT TAACTCA	347

(2) INFORMATION FOR SEQ ID NO: 4321:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4321:

GGGCAAGTTA CAGTGGTGCA TGGTTGTCGT CACTCGTGTC GTGAGATGTT GGGTTAACGTC	60
CCnCAACGAG CGGCAACCCT TAAGCTTAGT TGCCATCATT AAGTTGGGCA CTCTAAGTTG	120
ACTGCCGGTG ACAAAACCGTA GGAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA	180
TTTGGcTACA CACGTGCTAC AATGGACAAT ACAAAAGGGCA GCGAAACCGC GAGTCaAGCA	240
AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTTGCA ACTCGaCTaC ATGaAGCTGG	300
aATCGCTaGT aATCgTGGTC CAGCATGCTA CGGT	334

(2) INFORMATION FOR SEQ ID NO: 4322:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4322:

CTGTTAAACG ACTACAGGAA GTATTTACAA TCAAACTAAG CAAAAGTATT CAGATGCCTC	60
AGATAAAAGCT TGGGCGCATT CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTAGCAA	120
CGATATAAAA GTGCAAAGGG TTGGCTAATA GATATGGCTA ATAAATCGCG CTCGAAATGG	180
GATAATATTT CTAGTACAGC ATGGTCGAAT GCAAAATCCG TTTGGAnGG AGCATCGAAA	240
TGGTTTAGTA nCTCATTACA AnTCTTTAAA GGTTGGACT GGGGATATGT ATTCAAGAGCC	300
CACGATCGTT TTGATGCATT TCAGTTCGGC	330

(2) INFORMATION FOR SEQ ID NO: 4323:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4323:

CAATGATGCC ATGAGCAGTG CCTCCTTAA TAGCATTAA GCACTGTTT GTCGTATTT	60
TAAATATAAA TTTGGAATGA ATAATAAAAGT AGTGATTAAA TTAAGTTGTG TGATAGGAAA	120
CTTGGACATC AATCAAAGTA ATAGGCACTA AACGCTTAT TGGCGGGGCC CCAACAAAGA	180
AGCTGACGAA AAGTCACTTG CAATAATGTG CAAGTCnGGG ATGGGCCCA ACATAGAGAA	240
ATTGGGTCCG nAATTTCTAC AGACAATGCC AGTTGGCGGG GCCCCCCACAT AGAGAATTC	300
GAAAAGGAAT TCTACCAGCA ATGCCAGTTG GGGGAnG	337

(2) INFORMATION FOR SEQ ID NO: 4324:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4324:

TTACTTACTA TCTAGTTTG AATGTATAAA TTACATTCA	ATGTCTGGTG ACTATAGCAA	60
GGAGGTCACA CCTGTTCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG TCGATGGTAG		120
TCGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCCAGGCA AAAAATGGAT GCGATGAGCC		180
GCATTGAGAC CGCAAGnTCT TTTTTTATG TCTAAAACGT CAAAATAAAA AGCAAACACA		240
AAGAAAAATG GCTTGGCGAA GTGAAAACGT TTGAATCTGC CGAACGAGAA AGAGCGnACC		300
GAGTTTAGTA GA ⁿ TAAATGA GTAAGCGAGA		330

(2) INFORMATION FOR SEQ ID NO: 4325:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4325:

TTCATCCGCT CACTTTCAA CGTAATC ⁿ GT TCGGTCTCC ATTCACTGTT ACCTGAAC	60
CAACCTGACC AAGGGTAGAT CACCTGGTTT C ⁿ GGTCTACG ACAAAATACTA AACGCCCTAT	120
TCAGACTCGC TTTCGCTACG GCTCCACATT TACTGCTTAA CCTTGACATC AAATCGTAAC	180
TCGCCGGTTC ATTCTACAAA AGGCACGCCA TCACCCATTA ACAGGCTCTG AC ⁿ CTTGTA	240
AGCACACGGT TTCAGGTTCG ATTTCACTCC CCTTCCGGGG TGGCTTTCA nCTTCCCTC	300
ACGG ⁿ ACTGG TTCAC	315

(2) INFORMATION FOR SEQ ID NO: 4326:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4326:

TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGC_nGT TA_nATGCGGC TCATCGC_nTC
CACTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGAACGTAC CATCGACGCT
AAGGAGCTTA ACTTCGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC TATAGTCACC
AGACATATGA ATGTAAATTAA TACATTCAA ACTAGATAGT AAGTAAAAGT GTTTGCTTC
GCAAAACCAT TTATTTGAT TAAGTCTTCG ATCGnTTAGT ATTGTCAAC TCCACATGTC
ACCATGCTT
309

(2) INFORMATION FOR SEQ ID NO: 4327:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4327:

AAAGCTTATA AACGCTCATC TGACATTGTA GAATT_nCATGC TTTCAAAGA CGATATACTA
CGACACTCCT ACGAAC_nTGT CCAAGGATTA CGAAAAGACC TAAGGTTATGTAATTnGCCT
AAATTTATTA ATCGTTAAA TTCAGTTAGT AAAAGTCTG TGAGTAAGGG TGTATGGAAA
GTGGTTAAAT ATTATAGAAA ACATCAAAGG ATGTTAAGAA ATACAATTAA TTACCCAGCA
TTTAATAATG GTGCTATAGA AGGAATTAAT AATAAGATnA AATTAATCAA GTGAATTCT
TTTGGTTnCA G
311

(2) INFORMATION FOR SEQ ID NO: 4328:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4328:

TAGCTTCTGC GAGCTAGCGG AATCGAAGCC CCAGTAAACG GC_nGGCCGTAA CTATAACGGT
CCTAAGGTAG CGAAATTCC_n TGTCGGTAA GTTCCGACCC GCACGAAAGG CGTAACGATT
TGGGC_nGT CTCAACGAGA GACTCGTGA AATCATAGTA CCTGTGAAGA TGCAGGTTAC
CCGCGACAGG ACGGAAAGAC CCCGTGGAGC TTTACTGTAG CCTGATATTG AAATTCGGCA
CAGCTTGTAC AGGATAGTAG GAGCTTGAA ACGTGAGCGC TACTTACGTG GAGGCGCTGG
TGGGATACTA CCCTAGCTGT TTTGGTnTCT nACCCGACCA
340

(2) INFORMATION FOR SEQ ID NO: 4329:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4329:

AATCCATAGC GAAATGTATA CCATCACCCA TGCGTCCTTC TAAAGGTAAA TCTCTACCTT	60
TTTGTGCACC AGTACATAAT ATAATGGCAT CATACTCAGA TTCTAACGTT GCTTTATCAA	120
TATCAACACC GACTTCAACA CCATTAATGA AAGTAATGCC CGATTCTTCC ATTAACCTAA	180
TACGACGTCG AACCCACATCT TTATCAAGTT TCATATTCTGG AATACCATAC ATTAATAAAC	240
CGCCTGATTC TCTAGCACGT TCATAAATAG TTACTTGnTA TCCTnGTAGA TTAAGTTCTT	300
CAGCAGCAGT AATCCTGnTG GACCG	325

(2) INFORMATION FOR SEQ ID NO: 4330:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4330:

CACTTCACCA CAGCCGCCAT GCAGGnGCA GTAGGAATCG AACCCACACC AAAGGTTTG	60
GAGACCTCTA TTCTACCGTT GAACTATGCC CCTATTAAAA ATAATAATG GAGGGGGGCA	120
GATTCGAACT GCCGAACCCG AAGAGCGGAT TTACAGTCCG CCGCGTTAA CCACCTCGCT	180
ACCCCTCCAT AAATGGTGCG GGCGnGnAGG ACTTGAAACC CCCAACCAAC TGATTACAAG	240
TCAGTTGCTC TGACCAATTG AGCTAAGGCC GGCTAAGAAA TGGTTCCAGG ACAGAGTCGA	300
AACTGCCGAC ACATGGGAGC TTTCAAT	327

(2) INFORMATION FOR SEQ ID NO: 4331:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4331:

GCATCATTTC CAGCTTCCCCTTCCACATT TGAAAATTT CTCCAGTAAC AATGAAAGAC	60
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CATATACTTT	TTCCTACAAG	AGCAGGACCC	GGTAACAATA	CAGGTTGGTA	ATGCCAATA	120
ATAATGACCA	TTTCCCAAAT	GCCTAAGAAA	ATAATAAATG	TGATAATAGG	TAATATAAAAT	180
TTGTTATTTG	TGGGACGTGT	CATGAACGCG	ATGCCTCCTT	ATACAATGAC	GGTTCAACAA	240
AGTCATCATA	TGCAGGTGGA	TTAACCAAAT	GATGTTGTTT	TACCAATGTC	GTAATTCTT	300
GGATAGCCGG	ATGGnTTAAA	TTGTTAAAAT	CACCATAGGG	TGTCCCnGCC	GTGGACTGTG	360
GTAAAAACG	TCACGGACTT	TGTTAAAAn	GGTGCGTCAT			400

(2) INFORMATION FOR SEQ ID NO: 4332:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4332:

CTGGTATGCA	GATTACAC	CTGCCTCTCC	ACAAAnTnnGG	GGAGCAAA	CAGATGTGCC	60
TGAATCAAGT	GACTGGTATA	ACGCATCATA	CATTATTATG	TGGGGCTCTA	ATGTACCTTT	120
AACACGTACT	CCGGATGCAC	ATTTTATGAC	TGAAGTCCGC	TATAAAGGTA	CAAAAGTCAT	180
TTCAGTAGCA	CCAGATTACG	CAGAAAATGT	GAAATTTGCA	GATAACTGGC	TAGCACCGAA	240
TCCTGGTTCA	GATGCTGCAA	TTGCACAAGC	AATGACGGCA	TGTTATTTA	CAAGGAACAT	300
TATGTTAAAT	CCAACCTGAA	TGAACGGTTT	TTATTAAATT	ACGGTTAAAA	CCATTATTAC	360
CAGGAT						366

(2) INFORMATION FOR SEQ ID NO: 4333:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4333:

TATTATTTCA	TTGAGCAGAA	AGAAAATTAT	GGCACCAAAAC	TTTAATATTT	TTTCAATGT	60
CATTCTTTG	AnGGGAGTGG	GACAGAAATG	ATATTTCGC	AAAATTATT	TCGTCGTCCC	120
ACCCCAACTT	GCATTGTCTG	TAGAAATTGG	GAATCCAATT	TCTCTTGTT	GGGGCCCATC	180
CCCAACTTGG	CACATTATTG	TGAAGCTGAC	TTTCGTCAC	TTGCTGGTT	GGGGCCCTCA	240
CCCCAACTCG	CATTGCCTGT	AGAATTCTT	TTCGAAATTC	TCTGTGTTGG	GGCCCCTGGA	300
CTGAGAATTG	AAAAAAAGCT	TGTTGACAAG	CGCnATTTC	GTTCCATGCA	ACTGACTGCC	360

AAGAGAACnT CGTGAGAGCn ATGAAGAAGA TTGGATTTGA

400

(2) INFORMATION FOR SEQ ID NO: 4334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

CGCCCTTAAT AACTTAATCT ATGTTCCAT CCTACAGGAA ACGCGTTATT AATCTTGTGA	60
GTGTTCTTTC GAACnTATGC GATTATTCT TATGAATTCA AGCTTATTAA AAACCTTTA	120
TTCACTCGGT TTTGCTTGGT AAAATCTATA TnTTACTTAC TTATCTAGTT TTCATGTAC	180
AATTCCTTT TAGTCAAGCG CTCGCATAAG CAATATCACT TTAACCAAAA AATATTTGAA	240
TGTTAAATAA ACATTCAAAA CTGAATACAA TATGTCACAT TATTCCGCCA TCTTCTGnAA	300
GAAGATGTT	309

(2) INFORMATION FOR SEQ ID NO: 4335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4335:

nAGGACTTTT CTCGGTCAGT GTGAAAATCA ACGCACTCGT AACACAATG TCTTCTCCCC	60
ATCACAGCTC AGCCTTAACG AGTACCGGTA TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA	120
CGTGCAATCC AATCGCACGC TTGCGCTATC CTACTGCGTC CCCCCATCGA TTAAAACGAT	180
TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTCG GnCTCAGCTT	240
AGGACCCGAC TAACCCAGAG CGGACGAGGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA	300
CGGGATTCTC ACCCGTCTTT CGCTACTCA	329

(2) INFORMATION FOR SEQ ID NO: 4336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4336:

CAAAGTGACA GGTGGTCAT GGTTGTCGTC AGCTCGTGT GTGAGATGTT GGGTTAAGTC	60
CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATTA AGTTGGCAC TCTAAGTTGA	120
CTGCCGGTGA CAAACCGnnn GAAGGTGGGG ATGACGTCAA ATCATCATGC CCCTTATGCA	180
TTTGGGCTAC ACACGTGCTA CAATGGGACA ATACAAAGGG CAGCGAAACC GTGAGTGCAA	240
GCAAATCCA TTAAAGTTGT TCTCAGTCG GATTGTAGTC TGCACTCGG ACTACATGAA	300
GCTGGAATCG	310

(2) INFORMATION FOR SEQ ID NO: 4337:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4337:

CCAGCACCGG GGCAGGCGTC ACCCTCATAC ATCACCTTAC GGTTAGCAG AGACCTGTGT	60
TTTGATAAA CAGTCGCTTG GGCCTATTCA CTGCGGCTCT TCTGGCGTT AACCTAAAG	120
AGCACCCCTT CTCCCGAAGT TACGGGGTCA TTTGCCGAG TTCCTTAACG AGAGTTCGCT	180
CGCTCACCTT AGAATTCTCA TCTTGACTAC CTGTGTCGGT TTGCGGTACG GGCACTATTT	240
TCTATCTAGA nGGCTTCCTC GGCAGTGTGA AATCAACGAC TCGAAGACAC AnTGGCTnCT	300
CCCATCAGAG CTCAGCCTTA ACGA	324

(2) INFORMATION FOR SEQ ID NO: 4338:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4338:

CGGACATCAA ACGGATGCTG CTCGATTGGC AAATGCATAT AACTAGTAAC ATGATCATCG	60
ACATCAAATT TAGATGATCA AATGTcCCCC ATcATTAATT TGATTGGTT GTTGCTCAA	120
TTGATTATAT GTTTTCCTA GCACCTCATG CGGCACCATATCTTACCTA GTAGCCACAA	180
AGATAAGTCT AACAAAGTGGC AACCATAATC GATTAAACTA CCGCCACCTT GCAACGCTTT	240
ATTGGTAAAA ACACCCCAGC CAGGCACCTT ACGCCTACGC ATCGCTTGTA CACGTGCTAC	300
TAAAGGTTTA CCAACCACAC CTGATTCAAT TGCTTTTTA GCAGTAATTG CCACATCTGT	60

G TGACGATAA TGATATGCGC CAGTAATAnT TTGTGnTTT

399

(2) INFORMATION FOR SEQ ID NO: 4339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4339:

TGAGGCGATT ATTTCTTATG AATTCAAGCT TATTAAAAC TCTTTATTCA CTCGGTTTG	60
CTTGGTAAAA TCTATATTT ACTTACTTAT CTAGTTTCA ATGTACAAAT AATGGTGGGC	120
CTAAGTGGAC TCGAACCAACC GACCTCACGC nTATCAGGCG TGCGCTCTAA CCAGCTGAGC	180
TATAGGCCA TTTnTTGAA TGTTAAATAA ACATTCAAAA CTGGAATACA ATATGTGCAC	240
GTTATTCCGC ATCTTCTGAA GAAGATGTTn CCGAATATAT CCTTAGAAAG GAGGTGATCC	300
AGCCGCACCT TCCGGATAACG GCT	323

(2) INFORMATION FOR SEQ ID NO: 4340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4340:

GGCTAGCCCT AAAGCTATTT CGGAGAGAAC CAGCTATTTC CAGGTTCGAT TGGAATTCT	60
CCGCTACCCCT CAGTCATCC GCTCACTTT CAACGTAAGT CGGTTGGTC CTCCATTCA	120
TGTTACCTGA ACTTCAACCT GACCAAGGGT AGATCACCTG GTTTCGGTC TACGACCAA	180
TACTAAACGC CCTATTCAAGA CTCGCTTCG CTACGGCTCC ACATTTACTG CTTAACCTG	240
CATCAAATCG TAACTCGCCG GTTCATTCTT ACAAAAGGCA CGCCATCACC CATTAACGGG	300
CTCTGAACTA ACTTGGTAAA GCnCCGGTTT nCnGGTCAA TTTT	344

(2) INFORMATION FOR SEQ ID NO: 4341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4341:

TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGnGATAGGC GAACGTGCGA	60
TTGGATTGCA CGTCTAAGCA GTAAGGCTGA GTATTAGGCA AATCCGGTAC TCGTTAAGGC	120
TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTCACA CTGCCGAGAA	180
AAGCCTCTAG ATAGAAAATA GGTGCCCGTA CCGCAAACG ACACAGGTAG TCAAGATGAG	240
AATTCTAAGG TGAGCGAGCG AACTCTCGTT AAGGAACCTCG GCaaaATGAC CCCCGTAACC	300
TTCnGGGAAA AAGGGnTCCC CTTTAAGGGT TAACCGCCCC AAAAAACCCC C	351

(2) INFORMATION FOR SEQ ID NO: 4342:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4342:

AATAATGACT CCTACGGGAC TCGAACCCn GTTACCGCCG TGAAAGGGCG TGTACTTAA	60
CGTATGACCA AGGAGCCATG GCTCACCAAGG TAGGACTCGA ACCTACGACC GATCGGTTAA	120
CAGCCGATAG CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC	180
TCTAGCGGAA nTAAATTGCA ACTACCATCG ACGCTAAnGA GCTTAACCTTC TGTGTTCGGC	240
ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAAGACA TATGAATGTA ATTTATACAT	300
TCAAAACTAG ATAGTAAGTA AAAGTGA	327

(2) INFORMATION FOR SEQ ID NO: 4343:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4343:

ACCGCTTGGG CTGACATTTT TGGCTTGTAA AGCAGCTTGC CTACTTTTT GGCAATAGCA	60
CCATACGTTG TTAGAGTCCC ATAAGGAACC TGTCTAATT CATTCCAAAC ACACTGTTGA	120
AAATGACTAC CTGTTGGCTT TAAAGGTATT GTGATTCAG GATTGTCACC TTTAAAATAC	180
GCGTCTAACCC ACTGTGTCGC CTCTCTAAAT ATCGCTAAAG ACGTATTTTC TTCCCTAGTA	240
CCATCACCTT GTTGATTTTC AAACAAAACA GCGGTCAGAC TTACCCCATC ACTCAAAAGT	300
TCCCAAnCGTC CTGACAGGCG AAnCAGAGTG AACGCTGAGA CTCCAGAAAA ATCCCCCTnT	360

(2) INFORMATION FOR SEQ ID NO: 4344:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4344:

ATTCCGACAT CTTCTGAAGA AGATGTTnCC GAATATATCC TTAGAAAGGA GGTGATCCAG	60
CCGCACCTTC CGATACGnCT ACCTTGTAC GACTTCACCC CAATCATTG TCCCACCTTC	120
GACGGCTAGC TCCTAAAAGG TTACTCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT	180
GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCAACGT AGCATGCTGA TCTACGATTA	240
CTAGCGATTC CAGCTTCATG TAGTCGAGTT GCAGACTACA ATCCGAAC TG AGAACAACTT	300
TATGGGATTT GCT	313

(2) INFORMATION FOR SEQ ID NO: 4345:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4345:

ATTTTATCGT AAGATTTTT CGCAATGAGA TTTGGATCGT TTTTGTCAC TACAATATCT	60
AATAGTTTA CTTTAAGTCC AGCATTACACA AAAAGTGCTG CCAGTTGAGC GCCCATTGTG	120
CCTGCGCAA GAACGGTTAC TTTATTAATT GTCATAGTGA TTCCTCCAAT TTAGTTAGG	180
ATAAGATAAC CATTAAGATA ATTGGAATAA CGTTGCTATT TTATAAAATT AATTAAGTAT	240
CTTGACAGT CATCTTAGCC TCTTATTTAA GGnAAAAGCn TTATGCTTAA nATAAGTCTT	300
TTTTA	305

(2) INFORMATION FOR SEQ ID NO: 4346:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4346:

GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGCA AGTCTTACGG CATCTTCTAT	60
TTTTAAGCTT GAATTAAACA AATCATAAGC CGTATGAATA TTTAAATATG CCACCATGAT	120
TGAATGGnCC CTTTCTATTa GTTAAGTTG TGCGTAAAGC TGTAGCAAGT TGCTCAAATT	180
CATCCCCAGC TGTCCACTGA AACTCCTGGA CG@TTCGGA TGAnAACGC CAACCAAAAT	240
CTTGCgCAAT ATCCATTAAT AAACCAATTG CCCTTAGAA CGTAATCGAC ATCCGGATTc	300
AnTACCTTCA TCGACTGCAA ATACCCATAA TTTCCAGCCT TGATGTCAGC AATGTAATAA	360
CCAActGAGA TGCTCATTGG CTGATACGAT GnTCCATACA	400

(2) INFORMATION FOR SEQ ID NO: 4347:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4347:

TCTGGGTTGA GTCGGGTcCT AAGCTGAGGC CGACACGTAG GCGATGGATA ACAGGTTGAT	60
ATTCCCTGTAC CACCTATAAT CGTTTAATC GATGGGGGA CGCATAGGGA TAGGCGAnGT	120
GGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT	180
AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA GTCGTTGATT TCACACTGGC	240
CGAGAAAAGC CTCTAGATAG AAATAAnGTGC CCGTACCGCA ACCGACACAG GTAGTCCAAG	300
ATGAGATTcN TAAGGTGGAG CGACGAATCT CCGTTAA	337

(2) INFORMATION FOR SEQ ID NO: 4348:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4348:

GTAAAGACAC CGCCCTTCA CGCGTAACA CGGGTTCGAG TCCCGTAGAG GTCACCATT	60
TTTAGGTCTC GTAGTGTAGC GATTAACACG CCTGCCTGTC ACGCAGAGAT CGsGGGTTCG	120
ATTCCCGTCG AGACCGTACA AATGCCTATC CAAGAGGATA GnATTTTTTGCGTTAAAT	180
ATTATATTAA TAAAAGATAT ATGGACGAAT GATAATCATA TTGATTATC TGTTGTCCA	240
TTTCTTTAA AATGTATGAA CCTCAAGTAA CTTAGTGGTT GGATATGAAA GATAAACGTn	300
GACAATAAAA TCTTTATT	318

(2) INFORMATION FOR SEQ ID NO: 4349:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4349:

CTTTAAAGCA CGTATAATGA TGATTTCAAG CTTGTACAAA GGAGAAAAAA AGAAGACAAC	60
CAAGCCCAAT AATGGACTGG CCGCCTAATA ATAAAAGCTC TAAAAGTTGT ATTTTAAAAA	120
TAGTTCTTTA AATTATATAC CCACCACATT TGGTGnAGnA ACCTAAAAAA AnGCACTTCC	180
CAAAAATGGA AAGTGCAAGT AGTGAGCCAT AGAGGATTG AACCTCTGAC CCTCTGATTA	240
AAAGTCAGAT GCTCTACCAA CTGAGCTAAA TGGCTCTAAA TGGCTGGGCT AGCTGGGATT	300
CGAACCAACG AGTGACGGA	319

(2) INFORMATION FOR SEQ ID NO: 4350:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4350:

ACTTCGCTAC CCCTCCAGCT TATTCTATATA ATTAAATAAT CAAAATGGTG GAGAATGACG	60
GGTTCGAACCC GCCGACCCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GTAATTCTC	120
CAAAATAATG ACTCCTACGG GACTCGAACCC CGTGTACCG CCGTGAAAGG GCGGTGTCTT	180
AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACCGATCGGT	240
TAACAGCCGA TAGCTCTACC ACTGnAGCTA CTGTGGATTG AATCATTATG CCTGGCAACG	300
TTCTTACTAT AGCGGAAAnGT CAAGTTCCGC ATnACCATAC GAAGCT	346

(2) INFORMATION FOR SEQ ID NO: 4351:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4351:

ACGTCCCTCA	TCGGCTTCTA	GTGCCAAGGC	ATCCACCGTG	CGCCCTTAAT	AACTTAATCT	60
ATGTTTCCAC	CATTTTATA	AGTnAACGT	TAACATGAAG	TTACGTTCTT	TTATAAAAAG	120
ATTAAACGC	GTTATTAATC	TTGTGAGGT	TCTTCGAAC	ACTAGCGATT	ATTCTTATG	180
AATTCAAGCT	TATTTAAAAC	TCTTTATTCA	CnCGGTTTG	CTTGGnAAAA	TCTATATT	240
ACTTACTTAT	CTAGTTTCA	ATGTACAAAT	AATGGTGGGA	GAETAGCGGG	ATCGAACCGC	300
TGACC						305

(2) INFORMATION FOR SEQ ID NO: 4352:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 302 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4352:

GTTCATCAAT	TGCTAATTCC	AGTCCGCCTA	ACGGATCAAT	TTCATCCGCA	TGTATTTCA	60
CTTTAAAACC	TGGCTTCTTT	GGCTTTTGC	ATATAATGTT	GCGATTGTT	TATTGTAAT	120
ACACCTGTTT	CACAGAAAAT	ATCCGCAAAG	TCTGCATATT	GTTTACTTC	CGGAAGTAAC	180
GCAATCATT	CTTCTAAAAA	TGCCTCATTT	GAACTTGCCT	CTTTAGGTAC	AGCATGAGGC	240
CCTAGGAAAG	TATGTTTCAT	GTCTAAATCA	TATTTCTCAG	CTAAACGATT	AGnCACTTTC	300
AA						302

(2) INFORMATION FOR SEQ ID NO: 4353:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4353:

TCTACCGCTG	AACTACTTCT	GCGGTGAAG	GGAGTCGAAC	CCCCACGCCG	TAnnTGAGGA	60
TCCTAAAGTCT	AGTGCCTCTG	CCAATTCCGC	CACACCCGCA	AATGGTGAGC	CATAGAGGAT	120
TCGAACCTCT	GACCCTCTGA	TTAAAAGTCA	GATGCTCTAC	CAACTGAGCT	AAtGGCTCTT	180
CCATGGTGCC	GGCCAGAGGA	CTTGAACCCC	CAACCTACTG	ATTACAAGTCAGTTGCTCTA		240
CCAATTGAGC	TAGGCCGGCA	ATATGTAAGA	ATAAATGGTG	GAGAATGACG	GGTTCGAAC	300
GCCGACCCCTC	TGCTTGTAAG	GCAGATGCTC	TCCCAGCTGA	GCTAATTCTC	CGnTTAAA	360
CTGCTGGCnA	CGGTCTAnTC	TAAGGGGACG	TAAGGTCGAC	TACCATCGAC	G	411

(2) INFORMATION FOR SEQ ID NO: 4354:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4354:

TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTGGa	60
CGACAACTGG TACACCAGAG GTATGTCCAT CCCGGTCCTC TCGTACTAAG GACAGCTCCT	120
CTCAAATTTC CTACGACCAC GACGGATAGG GACCGAACTG TCTCACGACG TTCTGAACCC	180
AGCTCGCGTa CCGCTTAAT GGGCGAACAG ACAAGCCCTT GGGGACCGAC TACAGCCCCA	240
GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTnCCCGT CGATGTGAAc TCTTGGGGGA	300
GATAAGnCTG TTATCCCCGG GGTAACTTT ATCCGTTGAG CGATGGGCC TTACCATGCG	360
GAAACCA	367

(2) INFORMATION FOR SEQ ID NO: 4355:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4355:

GTATTTAAA TCATAGTGGT TTATGCGTCT TTTTCAAATT CTATAAAAAA TCGGATGACG	60
TGTAATCTGC CATAGATTAA CACATTCACT CGATTTATAA TAATAAGATA GACTAACATT	120
TATTGAGAGC GGGACGGAAA TGATAAAGAA CGACTAATGA TTGATTATGT AGCGATTCTT	180
TATCATTAGT CACAGCTAAT GTGTACTTAA AAATATGAAT GCATGAGTTA CACTCA _n ATT	240
AGAGGAAATA CTAATTCTA AAGAAAAAGT ATTTCTTTAT GTTGGG _n CC ACCCAACTT	300
G _n CATTGTCT GTT	313

(2) INFORMATION FOR SEQ ID NO: 4356:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4356:

GGGCTGGTTCAGAACGTCG A G CAGTTCG	yTCCCTATCC GTCGTGGCG TAGGAAATT	60
GAGAGGAGCT GTCCTTAGTA CGAGAGGACC GGGATGGACA TACCTCTGGT GTACCATTG		120
TCGTGCCAnG CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AGATCCTGAA		180
GCATGAAGCC CCCCTCAAGA TGAGATTCC CAACTTCGGT TATAAGA T C CTCAAAGATG		240
ATGAGGTTAA TAGGTTGAG GTGnGAAGCA TGGTGACAGT GGnAGCTGAC GAATACTAAT		300
CGATCGAGGA CTTAATCAAA ATAAAATGTTT TGCGA		335

(2) INFORMATION FOR SEQ ID NO: 4357:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4357:

GCTCTAAAAG TTGTATTTA AAAATAGTTC TTTAAATTAT ATACCCACCA CATTGGTGn	60
nGAACCTAAA AAAAACGACT TCCCAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT	120
TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA	180
ATGGCTGGGC TAGCTGGATT CGAACCAACG AGTGACGGAT nAAAGTCCGT TGCCTTACCG	240
CTTGGCTATA GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTGAACTG CCGAACCCGA	300
AGAG	304

(2) INFORMATION FOR SEQ ID NO: 4358:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 302 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4358:

ATAATGGTGA CGTTGATGAT GCATTAACAC AAGGTAAAGC AGCAATTGAT GCTATTCAAG	60
TAGATGCTAC TGTTAACCT AAAGCGAACC AAGCTATTGA AGT A AAGCA GAAGATACGA	120
AAGAATCTAT TGATCAAAGT GACCAGTTAA CTGCTGAAGA AAAAAGTGAA GCATTAGCAA	180
TGATTAAACA AATTACAGAT CAAGCTAAC AAGGTATTAC TGATGCAACA ACAACTGCTG	240
AAGTTGAAAA AGCGAAACTC AAGGACTTGA AGCATTGAT AACATTCAAn TCGACTCAnC	300
AG	302

(2) INFORMATION FOR SEQ ID NO: 4359:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4359:

GGTTGGGAAA TCATTCATG AGAGTGTGAA AGGGCATAAG GGGAGCTTGG ACTGCGAGAC	60
CTACAAGTCG AGCAGGGTCG AAAGAGGACT TAGTGATCCG GTGGTTCCGC ATGGAAGGGC	120
CATCGCTCAA CGGATAAAAG CTACCCCGGG GATAACAGGC TTATCTCCCC CAAGAGTTCA	180
CATCGACGGG GAAGTTGGC ACCTCGATGT CGGCTCATCG CATCCTGGGG CTGTAGTCGG	240
TCCAAGGGT TGGGCTGTTC GCCCATTAAA GCGGTACAnG GCTGGGTTCA GAACGTCGTn	300
AGAAAGTTCG GTCCCTATCC GTCCTGGGGC GTAGGAAATT TnGAGAGAG	350

(2) INFORMATION FOR SEQ ID NO: 4360:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4360:

AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC	60
GGTGTGTACA AGACCCGGGA ACGTATTACAC CGTAGCATGC TGATCTACGA TTACTAGCGA	120
TTCCAGCTTC ATGTAGTCGA GTTGCAGACT CACAATCCGA ACTGAGAACCA ACTTTATGGG	180
ATTGCTTGC ACCTCGnGGT TTCGCTGTCC CTTTGTATTG TCCATTGTCA GCACGTGTGT	240
AGCCCAAATC ATAAGGGGCA TGATGATTG GACGTTCATC CCCAnCTTCC TCCGGnTTGT	300
ACACCGGCAG TTCAACTTAG AGTGCCAA	329

(2) INFORMATION FOR SEQ ID NO: 4361:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 424 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4361:

AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTTCTA CTCTAGCGGA	60
ACGTAAGTTG GCTACCACATCG TCGCTAAAGA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT	120
CTnTCCTCTC CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGCGCTCTT	180
TCTCGTTTCG TCAGATTCAA ACGTTTCAC TnCGnCAAGC C A TTTTCTT TGTGTTACT	240
TTTTATTTG ACGTTTAGG CATAAAAAAA wGAGAcCTTG CGGTCTCAAT GCGGCTCATC	300
GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG GCTAACAAACG	360
TCGCCAAAGA CCTTTCTTGA CTTGTGACAA TCGGCTTGCT TCTTCCTCT CCTTCGGCTC	420
TCGC	424

(2) INFORMATION FOR SEQ ID NO: 4362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4362:

CACAACAAAGT ATCTAAGATA CTGGCCGAAG ATTGTCACAG ACGGTAGGGG AAGGGGGTCA	60
CGTGTACGAC CCAACATGTG GTTCCGGTTC ATnGTTGTTA CGTGTGGTA AAGAAACGCA	120
ATTnAnTCGT TATTCGGAC AAGAACGTAA CAATACTACA TACAACCTAG CACCATGAAT	180
ATGTTATTAC ATGATGTGCG TTATGAGAAC TTGAGATCC GTAATGATGA CACATTGGAA	240
AATCCAGCCT TTTAGGCAA TACATTTGAT GCGGTTATTG CGAACCCATAC AGTGCAGAAAT	300
TGGACAGCAG ATTCCA	316

(2) INFORMATION FOR SEQ ID NO: 4363:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4363:

GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTACACATAT	60
CGATAACATG ACATAACTCA TGCTGGTTT CCCCATTGCG AAATCTCTGG ATCAAAGCTT	120
ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA	180
AGGCATCCAC CGTGCGCCCT TGAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG	240
TTGATTAATC TTGTGGAGTG TTCTTCGAA CATAGCGATT ATnTCTTATG GAATTCAAGC	300

(2) INFORMATION FOR SEQ ID NO: 4364:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4364:

nTGCACTTAA GAACTAGAC GATCGTGGTA TCGTTTATAT TGGTGCAGAA GTAAAAGATG	60
GAGATATTTT AGTTGGTAAA GTAACGCCA AAGGTGTACT GCAGTTAACT GCCGAAGAnA	120
GATTGTCACA TGCAATCTTT GGGTGAAAAA GCACGTGAAG TTAGAGnATA CTTCATTACG	180
TGTACCTCAC GGCGCTGGCG GGTATCGTTC TTGCATGTTAAAGTATTCC AATCGTGCAA	240
GAAGGGCGAC GATACATTAT CCACCTGGTG TTAAACCAAT TTTAGTACGT GGTATATATC	300
GTTCCAAAAA CGT	313

(2) INFORMATION FOR SEQ ID NO: 4365:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4365:

AACCATTCGA TGCAATAGCG TCATTCTTGG ATATTAATCC CTAAATTGCC GTGATATCCC	60
GCGTCTATCT TGGCCTGTTT CAATCACTAA ATGCCTTTA CTACTTACAC CACTACGGGC	120
TAGTTAACAG TCCGACATAG CCCTCTGGTA TGCTTACAGC TACATCTGTn TTAATCACTG	180
CCTTTCTTG TGGCTCAAGT ACGACAGTTC AGCTGAGAAT ATGTCATAAAC CTGCATCCGn	240
CTTATGATT CGTCGGGCA TTCTAGCATT TTCTGATAAT AGCCTTACTT GTAATGTGTn	300
AGTCATTTC	310

(2) INFORMATION FOR SEQ ID NO: 4366:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4366:

AGTGGTACTT CTGTTAATTG GTGAATTGG ATACTGGTTA TATTCAGCTG CACCGCAAGC	60
AACTTCTATT GATGCCCTAA CTGCCTTTT ACCTCA&CA ATGGGTATGG TAATTGTTGC	120
AGTCATTTAT GGCTTATGA ATATGAAAGC AGAGAATCCA TTCCGTAATA AAATTACGTG	180
GTTACAAATT ATTCAGGTT TCTTCTTGC ATTTGGTGCT TTAACATATC TTATTCAGC	240
ACAACCTAAT ATGAATGGTT TAGCACTGGA TTTATCCTTC TCAACATCCG TGGTGCTGCT	300
ACATTAAnGG TATTAATTCT TAAACCACAT AAACGTAAA GAATGGTAAT ACAATCACGG	360
CTAGTACCAT TTAGTAGCCG CTCCGTACCG nAATTATAAA	400

(2) INFORMATION FOR SEQ ID NO: 4367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4367:

CACCTGGACG AAACGGTTT AGATCGTATT CAATTGAAAA GGCGGTATT GAATGAATCA	60
CACTTAGCAG CGATTGATCA GGAACATTAA ATTAAACTT ATTTATCAAC GGTATATGAA	120
GGGGATTTGG AAGATGCGTT AGAACATTA TGCCGAGAAG CAGTGAATGC TGTAAACAAG	180
GCGCTCAAAT TCTAGTGTG GATGATAGTG GATTAGTTGA TAGCAATGGC TTTGCAATGC	240
CGATGTTACT CGCnATAAGT CATGTGCATC AATTACTTA TAAAGCAGAT TACGnATGnC	300
TACAAATTAAATCGCTAAAT CTGGTG	326

(2) INFORMATION FOR SEQ ID NO: 4368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4368:

ATTATAGCCG AAATGCCAA AATAGATTG GACGAATATT ACGAATGGTT GCTTTACTTG	60
CATAAAATGGC TTTAGGAATA AGCATCAAGT CGCCACCAAG AATAGTAATA TCAGCTGCF	120
CAATGGCAAC TTCTGTACCT GTAnCAATGG CGATACCGAT ATCAGCTTTA ACTAATGCAG	180
GTGCATCATT TACACCGTCA CCAnCCATCG CAACCTTCTT ACCTTGTGCT TGTAGTTCG	240
CAATTGTGC AGCTTTTCT nCTGGTAGAA TATCTGCAAT AACAGTATCT ATGCCTACTT	300

GTTTGCG

307

(2) INFORMATION FOR SEQ ID NO: 4369:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4369:

TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTCAC CGGGTGTGCC TTCTGATATG	60
CTATGTATTAC ACATATCGAT AACATGACAT AACTCATGCT GGGTTCCCC ATTGGAAAT	120
CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGATATC GTCGTTAGTA ACGTCCTTCA	180
TCGGCTTCTA GTGCCAAGgC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTCCAT	240
CCTACAGGAA ACGCGTTATT AATCTTGTGA GTGTTCTTC GAACAYTAGC GATTATTTCT	300
TATGAATTCA AGCTTATTAA AAACTCCTTA TTCAATCGGT TTTGCTTGGG TAAAATCCTA	360
TATTTTACnT ACCnTATCGA GTTTCAATG TAACAA	396

(2) INFORMATION FOR SEQ ID NO: 4370:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4370:

CAGTAAGATA ATTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTAA TACAATACTT	60
CGTATTGAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT	120
GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACA TGTAATTAA CTTTACATA	180
CTTTTAAAAA ATAAGACACT TTGCCAAACT TGCACATAAA TGTTAATTC AATAATTGA	240
ATTTTCTGTG TTGGGTCCCT TCGTATAATT TAATAAATAC CACTAAACTA AaTTArTGAA	300
GTCCTTATG TATAA	315

(2) INFORMATION FOR SEQ ID NO: 4371:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4371:

GTCGTCAAAT GTACCTTCAC CAAGTAGTGA TGTACATATT TACCGCCTTG TTCAACAGCA	60
CGTGTGGCG CACCTGTAAT CGCAATGACA GGTATGCGTT CAnATATGAA CCTGCGATAAC	120
CGTTGACGGC ACTTAATTG CCAACACCAA ATGTAGAAC TAATGCAGCG AGTCCATAA	180
GACGGGCATA ACCGTCCGCT GCGTAACCTG CGTTAATTC ATTTGTATTT CCTACCCAAT	240
CTACAATGGG GTTGCTGATA ATATCGTCTA GAAAAGCGAG ATTAAAATCA CCAGGGnCAC	300
CAAAATTTT ATCGACGGCn TG	322

(2) INFORMATION FOR SEQ ID NO: 4372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4372:

CCTAAGTCTA GTGCGTCTGC CAATTCCGCC ACACCCGCAA ATGGTGAGCC ATAGAGGATT	60
CGAACCTCTG ACCCTCTGAT TAAAnAGTCAG ATGCTCTACC AACTGAGCnA ATGGCTCTTC	120
CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA GTTGCTCTA	180
CCAATTGAGC TAGGCCGGCA ATATGAAAG AATAAATGGT GGGAGAATGA CGGGTTCGnA	240
ACGGCGGAAC CCTCTGCTTG TAAAGCAGAT GCTCTCCAGC TTGAGCTAAA TCTCCGATTT	300
AAAACGTGCTG GGCAAGTTCT ACTCTAG	327

(2) INFORMATION FOR SEQ ID NO: 4373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4373:

CATTTAATT TATTGTACAG AACGAAATGT GATGTTAGTA GATCATAGGG TTATGATAA	60
TATTAAGCT GAAAACGTTA TATTTATTGG CCTTTGTGT AAACATGGAC ATTGGCATGC	120
AGTCATTTAT GACATTGCTC AAGACAAAAC TGCCGAACTC GAAATTGAAA ATATTATAGA	180
TATTCGTAT TCATTCGGTA AGACGATTCA AACCAAGAGAC ATATCCATTG ATAACATATCA	240
TCAATTTTA AACCCCATCG ATTCTAAAA AACAGCAGTA AGATGATTT CAATTAGAAA	300

ATATCTTGCT GCTGTTCTCT ATTATACAA TACTTCGTAT TGAATGGCTC GCTTTCCCAG 360
GGnGCCGCTC AGCCTGGGCC TCGACTGGCA ATGCTCCCTC 400

(2) INFORMATION FOR SEQ ID NO: 4374:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4374:

TAATGGATT TTTAGTGTG GTGTCGTTAT TGTCTTCTCA CCTTTTGTC CTTCTCTTGT 60
TACTTTTCT GTCCCTGGTG CTAAATCAGG ATTAAATTAA CGTTCTTCT CGAATGGAAT 120
CTCTTCTTT TCTACAATCG AGTCTCCTT TACAGGTCCA TATTTGTTA CGCTATCGAC 180
CGGTGGTCTA ACTACATCTC CTGTTCTGG ATTCTTAATT CCTGGTTAC CTGG~~A~~ACTT 240
CCTCTTCTC TCCTGTTGGT AACTTCGGGA TCAAATTCTG CTCGATGGAC CTGGTGTGGA 300
nCGTTTCTGG GTCCGnAAGT CTGTnGAATT GCAG 334

(2) INFORMATION FOR SEQ ID NO: 4375:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4375:

ATACATGCAA GTCGAGCGAA CGGACGAGAA GCTTGCTTnG TGAATGTTAG CGGCGGACGG 60
GTGAGTAACA CTGGATAACC TACCTATAAG ACTGGGATAA CTTCGGGAAA CCGnAGCTAA 120
TACCGGATAA TATTTGAAC CGCATGGTnA AAGCTTGCAA AGACGGTCTT GCTGTCACCT 180
ATAGATGGAT CCGCGCTGCA TTAGCTAGTT GGTAAGGTAA CGGCTTACCA AGGCAACGAT 240
GCATAGCCGA CCTGAGAGGG TGATCGGCCA ACTGGAACG GAGACACGGT CCAGACTCCT 300
ACGGG 305

(2) INFORMATION FOR SEQ ID NO: 4376:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4376:

GATAAAAGTGA AAGAACTCGG ACGTGACACC TATTGCACGA TTCGTTGGTT TTAAGGCAGT	60
AGGC GTTGAC CCGAAAATTA TGGGTATTGG GCCTGGCATA TGCGATTCCCT A AGTATTGT	120
CACTCAGCAA TCTATCTGTT GAAGACATTG ATTGATCGA ATTGAACGAn CATTGCTCT	180
CAAACGATTG CATCTATTAA AGAAGTAGGT CTAGATATAT CACGTACGAA TGTGAATGnT	240
GGCGCTATTG CTTTAGGTCA TCCATTAGGT GCTACAGGCG CAATGTTAAC CGCGCGTTA	300
CTTAA	305

(2) INFORMATION FOR SEQ ID NO: 4377:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4377:

AATGTCTTCT ACCCCATCAC AGCTCAGCCT TGAACGAGTA CCGGGTTTGn CCTAATACTC	60
AGACCTTGAC TGCTTAGACG TGACAATCCA ATACGACACG CTTCGCCTAT CCTACTGCGT	120
CCCCCCCACG ATTAAAACGA TTATAGGTTG TACAGGAAAT ATCAACCTGT TATCCATCGC	180
CTACGCCTGT CGGCCTCAGC TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG	240
GAAACCTTAG TCAATCGGTG GACGGGATTC TCACCCGTCT TTTCGCTACTC ACACCGGCAT	300
TCTCACTTCT AAGCGCTCCA CATG	324

(2) INFORMATION FOR SEQ ID NO: 4378:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4378:

CATCATGCTT AGAAAACGCT TAATTTAGGT TTTGACTTTT TAATCAGAGT ATATAAGCAA	60
AACTTATCAT ACAGGTAAGG TGTAATAAGT ATTTTTTATT AATTGAGAAT AATTATCAAT	120
TTCGCGAATG ATTCAATTCA ATTTTTAAC GTATTATTTC ATTGAGCAGA AAGAAAATTA	180
TGGCACCAAA CTTAAATATT TTTTCAATG TCATTCTTT GATGGGAGTG GGACAGAAAT	240
GATATTTTCG CAAAATTAT TTCGTCGTCC CACCCCAACT TGCATTGTCT GTAGAAATTG	300

GGGAATCCCA ATTCCCTCCTT GGTGGGGGCC CATCCCCACC TTGCACATAA TGGnAGCnGG 360
ACCTTTCCGC CGCTCCGGGG TGGGGGCCTC nACCCCAAnTC 400

(2) INFORMATION FOR SEQ ID NO: 4379:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4379:

ATAAAATATA TCACTTGAAA AATTTCATGT AGAAAAGATG ATGGATAGGC TATAAAGTAA 60
TTGTGACTGA GATGAACCTT TATGTCTTAG ACACTACAAC ACTATATTGG CAGTAGTTGA 120
CTGCGGGGCC CCAACATAGA GCAAATTGGA TTCCCAATT CTACAGACAATGCAAGTTGG 180
GGTGGGCCCC AACATGAAAG AAATACTTT TCTTAGAAA TTAGTATTTC TTATGCATGA 240
GTGTACTCAT GTTGCAGATT TTTTnAGTA CACATTAGCT GTGGACTAAT GATAAAGGnn 300
TCGCTACATA ATCCATCCAT TAGGTCGTTTC CTTGATTCA TCCCT 345

(2) INFORMATION FOR SEQ ID NO: 4380:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4380:

CTAAAGCTGn CATATGCGGC TTGCCGATGA AGCCAACCCCT GCTGCTGTTG GTACAAAATT 60
GTCGCTTCA ATTTCTGCAT ACCAATCGAT GCCAGCTCTA TTTCTGACAA TATCCATATA 120
TTTGAAATT TTCTCTAATT CTTTGCCACT AACCTTTCA CCATTCAACC AAAATTGATC 180
CTGTGTTAAC TGGTCGTTAA AAGTGACTT CGTTTCAGTG TAAAATTTT CTAATGTAAC 240
AGATATGCTA TTATTCACTGG AAGATTAGTG CTTCATCTT TTTACCCCAA TATTTTATAA 300
GTGCAATATC GTAGTGCAGG CTTGCCACTT TAACACGCAT AACTCCTAAA TCTCAACCAG 360
ATn 363

(2) INFORMATION FOR SEQ ID NO: 4381:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4381:

ACCTGAATGA CTCAAACTTG ACTTTnCGAC AATTGACTGT nCATTGGCA TAGTTGTATG	60
nCTCCATTnC GTAATTATTA GATTTGTTCG CTTACGTCTA TTGAATCATA CAGCTTTATT	120
ATAGTTAGCG TATTTGCACC TTTGCACATT AAACCATGTT TAATAATCAT TGAATCATT	180
TTAAGTAAAT TAAGGAATCT ATAATGTTCG TTAAATAAAA CTGATCCCCT TGTGGCTTCA	240
CACCCGATAG ATAGGGATT ACAGATAAAT TCAGGTCTCT TCCACGTCCA TATTTGGGAC	300
CCATCGAAAA TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACAGTAGG	360
GCCGTTGTCA CTTAACCTCT GTTTTCGA TGACAGCTTC	400

(2) INFORMATION FOR SEQ ID NO: 4382:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4382:

GnACTACAAA GCAATGGGGT TTGCCAGTTT CTTTATTAC TGACGAATAC TGGCAATGAC	60
ATCAGATACA TGTGGCAnCA CCAATCCATT TCTTTTCACC ATTGATAACC CAAGTATCGC	120
CTTGGGTTGC AGGGACTGTT TCAAGACCTC CCGCAACGTC CGAACCGGT TCTGGTTCA	180
TTAAAGCAAA GCATGTTACG CnTTCATGTG AACTGTAATT TAGGTACATA TTTCGCAATT	240
TGTTCTTGC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTGGTG AACACCGAGT	300
AGGG	304

(2) INFORMATION FOR SEQ ID NO: 4383:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4383:

GTGCATTATT TTGGAGAATT AGCTCAGCTG GGAGAGCATC TGCCTTACAA GCAGAGGGTC	60
GGCGGTTCGA ACCCGTCATT CTCCACCATT TTGATTATTA AATTATATGA ATAAGCTGGA	120
GGGGTAGCGA ATGGCTAACAC GCGGCGGACT GTAAATCCGC TCCTTCGGGT TCGGCAGTTC	180

GAATCTGCC	CCCTCCACCA	TCTATATATT	GGGCTATA ⁿ C	CAAGCGTAA	GGCAACGGAC	240
TTTGACTCCG	TCACTCGTTG	GTTCGAATCC	AnCTAGCCC	GCCATTAGAG	nCATTAACTC	300
AGTTGGTA						308

(2) INFORMATION FOR SEQ ID NO: 4384:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4384:

AATTTGGCC	AAAACACCCA	TCCGCTGTAA	CTTCAGAGTG	TCATGGCAT	TTATTACACT	60
ATCTCCAACT	CCTAGTGGAA	CAACCACATC	TCGTCCTTGG	GGTGCATGGA	ATGTTCCGTC	120
AGCCCTGTGA	ATTATTTCTT	GAACCTCCACC	ACCTGGGGCG	TTTCCAGAAC	CTCTATCATT	180
TAATACAGCA	AATGTCGGTT	GCGTTAATGC	TCCTGAATTA	TCGGkAGCTA	CACCCTTCC	240
TGCTAAAGTA	CCAGTAGACA	ATGTAGGTAT	TGGCTTGATG	AGATTTtTAT	CAGTAATGGC	300
TTT ⁿ AGAnAT						309

(2) INFORMATION FOR SEQ ID NO: 4385:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4385:

AAAGGTGAAA	AGCACCCCGG	AAGG ⁿ AGGTG	AAATAGAAC	TGAAACCGTG	TGCTTACAAG	60
TAGTCAGAGC	CCGTTAATGG	GTGATGGCGT	GCCTTTGTA	GAATGAACCG	GCGAGTTACG	120
ATTGATGCA	AGGTTAAGCA	GTAAATGTGG	AGCCGTAGCA	nAACAGGTCT	GAATAGGGCG	180
TTTAGTATTT	GGTCGTAGCC	GA ⁿ ACCAGG	TGATCTACCC	TTGGTCAGGT	TGAATTCA	240
AACACTGAAT	GGAGGACCGA	ACCGACTTAC	GTTGAAAAGT	GAGCG A TGA	ACTGAAGGTA	300
GCGGAGAA						308

(2) INFORMATION FOR SEQ ID NO: 4386:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4386:

TAGAATCTTC ATCAATATGA TCTAACCAAT ATTGATAAAA CCTTGATGTG TTTCGTGTCA	60
ATGACATACC ATATCGACTA GGTACCTTT TAGAATGTTG ATTAATCAnG GCAAATATCA	20
TGGCAAGGTC ATCTTCAAAA TGATTGATT CAAGTGGAAAG GCATATGACG TCTCATCACT	180
ATACCCTTT TCCCATTCTG CAAATCCACC ATAAATACTA CGCGACGC GG AACCCGGACC	240
CATTCGCGGC AATCTCGGtn AATCCTTATC TGGACAGCTG GCATGTCTAG CGGCTGGATT	300
TACAAGCTGG CTGGCTAAAG CTGGCATATG CGCTTGCCGG TTGAAGCCCA ACCTGGCTGG	360
CTGGTGGGn ACAAAATTGGT CGCTTTCAA TTTCnGGCAT	400

(2) INFORMATION FOR SEQ ID NO: 4387:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4387:

TCAATTATG GGGCATTATG ACTTTATATA CCTAAAATAC TATTAAGAAG TCCTGAAAAA	60
TTCACATTAG CAGTTGGATT GTTCAACTTT ATTAATGATA AGATGCAAA TAATTCACA	120
GTGTTGCAG CAGGGCAAT TATGATTGCA GTACCTATAG CAATCGTATT CTTGTTCTTG	180
CAACGCTATT TAGTATCAGG TTTAACAAACA GGTGCGACAA AAGGTTAGTT TGAAATTcNc	240
GnGTGGGGCA GAATTGATAA AGAACCACnA ATGACGATAA AGATTAAAAG GAGGACGTAA	300
TGGATGACGA	310

(2) INFORMATION FOR SEQ ID NO: 4388:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4388:

AACATCATGC TGATGTTGTT GAATATGAAG AAGATACAAA CCCAGGTGGT GGTCAGGTTA	60
CTACTGAGTC TAACCTAGTT GAATTTGACG AGATTCTACA AAAGGTATTG TAACTGGTGC	120
TGTTAGCGAT nCATACAAACA ATTGAAGATA CGAAAGAATA TACGACTGAA GTAATCTGAT	180

TGAACTAGTA GATGAACTAC CTGAGGAACA TGGTCAAGCG CAAGGACCCA TTTCGAGGAAA	240
TTACTGGAAA ACATCATCAT ATTTCTCATC nGGTTAGGn ACTGAAATGG TCACGGTAAT	300
TTTGGCGTGG	310

(2) INFORMATION FOR SEQ ID NO: 4389:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4389:

TTTACCATAT CATCCACTAT TTATTAAACC TAATAAAGAT GAATTAGAAG TGATGTTAA	60
TACAACAGTG AACTCAGACA CAGATGTTAT TAAATATGGT CGTTTGTAG TTGATAAAGG	120
TGCGCAATCT GTTATTGTCT CGCTTGGCnG TGGATGGTGC TATTTATATT GATAAnGAAA	180
TCAGTATTAA AGCAGTTAAT CCACAAGGGA AAGTGGTTAA TACAGTTGGC TCTGGTGATA	240
GTACAGTTGC AGGCATGGTG GCTGGGAATT GCTTCAGGTT TAACGnTTGA AAAGGCATTC	300
CA	302

(2) INFORMATION FOR SEQ ID NO: 4390:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4390:

AAAGAGTGCG TAATAGCTCA CTAGTCGAGT GACACTGCGC CGAAAATGTA CCGGGGCTAA	60
ACATATTACC GAAGCTGTGG ATTGTCCTTT GGACAATGGT AGGAGAGCGT TCTAAGGGCG	120
TTGAAGCATG ATCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG	180
CGAAAGACGG GTGAGAATCC CGTCCACCGA TTGACTAAGGTTCCAGAGG AAGGCTCGTC	240
CGCTCTGGGT TAGTCGGGTC CTAAGTGAGG CCCACAGCGT AGGCGTGGAT ACAGGTTGTA	300
TnCCTTACCA CCTATAATCG nTTAATCGTG GGG	333

(2) INFORMATION FOR SEQ ID NO: 4391:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4391:

AGTGCCTTG TGCACAnACT TGACTGnAAC TTAGTGCAT TGCAGCACCA GCAACCCATG	60
GCGCAATAAG CCCAATGCAG CTATAGGGAT ACCGnCAATA TTATAGCCGA ATGCCAAAA	120
TAGATTTGA CGAATATTAC GAATGGTGC TTTACTTGCA TAAATGGCTT TAGGAATAAG	180
CATCAAGTCG CCACCAAGAA TAGTAATATC AGCTGCTTCA ATGGCAACTT CTGTACCTGT	240
ACCAATGGCG ATACCGATAT CAGCTTAAC TAATGCAGGT GCATCATTAA CACCGTCACC	300
AACCAT	306

(2) INFORMATION FOR SEQ ID NO: 4392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4392:

TACGGTATGC ATATCTTTA AACCTATTC TTTGTTATT AGGACATATA AATTCATCAT	60
TAAGTCGTC ATATTCCAA TTTAAGTGT TGAAAETC ACTTTAACAC TTTCTAGTTT	120
TATCTTAAT AAACATGCCA TACGTAATAA GTGGCGTTT ATTAAAATCA TCTATAATAG	180
CCATATAGTT TTGCTCACTA CCATAACCTG CATCAGCTAC AATATACTCC GGTAAATAAC	240
CGAAGGGATT TTGAATCATT GTTAAAAATG GAATTAAGT TCTAGTATCT GTTGGGTTT	300
GAATAGGGTC ATGGGATAAA CCAAATGnGG AATTGCCCCnC AATTnGTAAA TGGAA	355

(2) INFORMATION FOR SEQ ID NO: 4393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4393:

CATTCCGTAA TAAAATTACG TGGTTACAAA TTATTCAGG TTTCTTCTTT GCATTTGGTG	60
CTTTAACATA TCTTATTTCAT GCACAACCTA ATATGAATGG TTTAGCAACT GGATTATTC	120
TTTCTCAAAC ATCCGTTGTG CTTGCTACAT TAACTGGTAT TTATTTCTTA AAACAACATA	180
AAACGTCAAAGAAGATGGTT ATTACAATCA TCGGCTTAGT ACTCATTAA GTAGCCGCTT	240

CTGTTACAGT ATTTATAAAA TAAGGAGTGT AGATGTCATG AAAAAATCAG CGGTTAAAT	300
GGAACCTATT CCAAAGCCAT CGCGACCAAT GGGTCATTE GATTAnTAAC GATAATGGCG	360
nnGG	364

(2) INFORMATION FOR SEQ ID NO: 4394:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4394:

GATTAAAACG ATTATAGGTG GTACAGGAAT ATCAACCTGT TATCCATCGC CTACGCCGT	60
CGGCCCTCAGC TTAGGACCCG ACTAACCCAG GAnCGGACGA GCCTTCCTCT GGAAACCTA	120
GTCAATCGGT GGACGGGATT CTCACCCGTC TTTCGCTACT CACACCGGCA TTCTCACTTC	180
TAAGCGCTCC ACATGTCCTT ACGATCATGC TTCAACGCCC TTAGAACGCT CTCCTAnCAT	240
TGTGCCAAAG GACATGCCAC AGCTTCGGTG AATATGTTA GCCCCGGTAC ATTTTCGGCG	300
CATGTnCACT CGACT	315

(2) INFORMATION FOR SEQ ID NO: 4395:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4395:

AGCCCCCAAA TGGGTATTGA AATTGAATGG TGGGnCCTGA AnTGGACTCG AACACCAGAC	60
CTCACGCTTA TCAGGGTGC GCTCTAACCA GCTGAGCTAT AGGCCATTAA ATTTGAATGA	120
ACAAACATTC AAAACTGAAT ACAATATGTC ACGTATTCC GCATCTTCTG AAGAAGATGT	180
TCCGAATATA TCCTTAGAAA GGAGGTGATC CAGCCGCACC TTCCGATACG GCTACCTTGT	240
TACGACTTCA CCCAATCAT TTGTCCCACC TTCGACGGCT AGCTCCTAAA AGGTTACTCC	300
ACCGGCTTCG GGTGTTACAA AC	322

(2) INFORMATION FOR SEQ ID NO: 4396:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4396:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTC TCGTTTCGTC	60
AGATTCAAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTGAC	120
GTTTAGACA TAAAAAAAGA nACCTCACGG TCCAAACTTG CCTGGCAACG TTCTACTCTA	180
GC GGAAAnTGA ATTGGCTACC ATCGnCGCTA AAGACCTTC TTGACTTGTG ACAATCGCTT	240
GCTTCTTCC TCTCCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAC TCGTTGCGCT	300
CTT	303

(2) INFORMATION FOR SEQ ID NO: 4397:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4397:

TAAGAATATA AATGATTTG AAAGCATTG MAGCTACAA CATTCTATA AAATTTTCA	60
ATAACAATTG CGCCACTAAA ACTCAAAATT TCCACCACCA ACATCCAAAT TATCAACATC	120
GCAACATAAC CAAATGTTAT AATAAATCTA TTACACAAAG AGATAAATTA CTTATGCAA	180
GGCGGAGGAA TCACATGTCT ATTACTGAAA AACAACGTCA GCAACAAGCT GAATTAA	240
AAAAATTATG GTCGATTGCG AATGATTTAA GAGGGACATG GATGCGAGTG AATTCCGTAA	300
TTACATTTA GGCTTGATTT TCCTATCGCn TCCTTATCTG GAAAAAnCCG ACCAGGATnT	360
GCAGATGCCT GGCCAGG	377

(2) INFORMATION FOR SEQ ID NO: 4398:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4398:

TGCAATAACA GTATCTATGC CTACTTGTTC TGCAATGGCT TGAGCAGTGT TTTTATTATC	60
GCCAGTTAAC ATGGGCAACT TCAATGCCA TATCATGGCA ATTGTTTAT AGCATCTTG	120
GGCATGATnT TTGACAGTAT CTGCCACTGC GATGATACCA GTTAATGAAT AATTAACAGC	180

AATGAGCATA nCAGTTTAC CATCTCGTTC ATATGTGTT AAATCATCAG AAATATGCTT	240
AAGCAACTAA TATCATTGTC AACCATTAAT TTACCGTTAC CAACCAATAT ATGGTGATGA	300
TCnATCCTTC CTC	313

(2) INFORMATION FOR SEQ ID NO: 4399:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4399:

TGGCTATGAT CATCCAAAAT ATGGTGAATC AATTGCTGCA GCCATTATAC TT G CGAAGA	60
TGAACCTCAT TACGCTGAAA TTTTAAATCA ACATATGCGA AGTCGTTAG CAGGTTATAA	120
AGTCCCAGA ATGTATGTAC CAGTGACACA TATGCCGTTA AACAGTACGC AGAAACCAGA	180
TAAACTTGCG ATTGACAAA TGATGAATGA CAAAGTCTCG CAAACACTTT AAAGGTGATA	240
AAAATTTTG ACATTTAGTG TAAGCGTTA CAAATAAAGC GTGTTGTTT TGAATTAAAT	300
GCATTCACA TTAGTATTCA TATTATnTTT AGGAGGAATT TATATGACAT TTGAAAAAGA	360
ACGGGCTTAA AACATTATTC CTGAGATGTA CTAGTATGCT	400

(2) INFORMATION FOR SEQ ID NO: 4400:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4400:

CTCATTAGC TCTACTAAC TCGTTGCCT CTTTCTCGT TTCGTCAGAT TCAAACGTTT	60
TCACCTCGCC AAGCCATTAA TCTTTGTGTT TACTTTTAT TTTGACGTT TAGACATAAA	120
AAAAGAGACC TCgtCTAAC TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTGGC	180
TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCCTTCCT	240
TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTGTT CGCTCTTTC TCGTTTCGTC	300
ArATTCAAAC GtTTCAcTT CGGCCAAGGC ATTTTCTTT GTGGTTACTT TTTAATTGG	360
ACGGTTTAG GCATAAAAAA AAAGGGGACC CTGCGGGCTC nAAAGGGGG	409

(2) INFORMATION FOR SEQ ID NO: 4401:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4401:

TCATGTAGAC TTTCAAGAAT CGACACATGA AAATTCAAAA CATCATGCTG ATGTTGTTGA	60
ATATGAAGAA GATACAAACC CAGGTGGTGG TCAGGTTACT ACTGAGTCTA ACCTAGTTGA	120
ATTGACGAA GATTCTACAA AAGGTATTGT AACTGGTGCT GTTAGCGATC ATACAACAAT	180
TGAAGATACG AAAGAATATA CGACTGACAT mATCTGATT GAACTAGTAG ATGAACTACC	240
TGGAAGAACCA TGGTCCAAGC GCAAGGnCCA ATCCGAGGAA ATTGACTGGA AAACAATCCA	300
TCCATATTC C	311

(2) INFORMATION FOR SEQ ID NO: 4402:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4402:

TTAACGGATT ATTTGGCAAT TCGGTTAGTT GTCGAACAAAT TGCTAGTTGG GATGAGTTT	60
AAGTCAGTCG CTAAAGATTG TGAAAGTAGA TCGGAAAATT GGTTTAAGCA AACTGTTGCA	120
TCATGGTGT ACTACAGTGA TATGCCTAGC GATGTATTAC TACAACATGG ACGTCAATGT	180
AAATTnCAA CGTTTATTCA TTTTGGCAGC AACTATGGAA TAAAAATGTA TTTAAAATT	240
TATGGCTAAT TGCCTGGGA AATGACATAC GAATCTCAGG TTAAAACAGA AAATTAAAGC	300
AGGTCCATGT nAAGTGTGGG CGGGnCGCAT	330

(2) INFORMATION FOR SEQ ID NO: 4403:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4403:

TGnTCACACA TAATTTGCGG CCATATGTTG TTGGCACTGG CCGTTTGAT TATCTGGCAC	60
TTTGGGCCCA TATGTTGnCA AAATACGnGC CAATTGCTTC TTTATAAGTT GTTATTTTT	120

TACTTTTCC ATCGATAAGC CATAACCTCTG GATGATAACAT ATGATGCCCC ATCGCAGACC	180
AATAGCGAAA TTCACCCGTT AAAGTTTCGA GCTCTGATAA TTGTATAGAC CATTGATGAT	240
TTTGAGGTGG TACTTGATAT AAATTTCTT CTCTAAAATA TTCATTAAA ATGGTTCGA	300
TAGCCGCATA CGCTGCCATG TTGTATTAAT CnTTAATTG	340

(2) INFORMATION FOR SEQ ID NO: 4404:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4404:

TTAACATATA TTTTGGGACC TTAGCTGGTG GTCTGGGCTG TTTCCCTnnA CGAACACGGAA	60
CCTTATCACCC CATGTTCTGA CTCCCAAGTT AAATTAATTG GCATTCGGAG TTTGTCTGAA	120
TTCGGTAACC CGAGAGGGGC CCCTCGTGCC AAACAGTGCT CTACCTCCAA TAATCATCAC	180
TTGAGGCTAG CCCTGAAAGC TATTCGGGA GAGAACCCAGC TGATTTCCAG GTTCGATTGG	240
AATTTCTCCG CTACCCTCAG TTCATCCGCT CACTTTCCA ACGTnAATCG GTTCGGTGCC	300
TGCCATT	307

(2) INFORMATION FOR SEQ ID NO: 4405:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4405:

TTTTTTAAG TCTGATGTGA AAGCCCACGG CTCAAACCGTG ATGGGTcATT GGAAACTGGAA	60
AnACTTGAGT GCAGAAAGAGG AAAGTGGAAAT TCCATGTGTA GCGGTGAAAT GCGCAGAGAT	120
ATGGAGGAAC ACCAGTGGGC GAAGGCGACT TTCTGGTCTG TAACTGACGCTGATGTGCGA	180
AACGTGnGGG ATCAAACAGG ATTAGATACC CTGGTAGTCC ACGCCGTAAA CGATGAGTGC	240
TAAGTGTAG GGGGTTCCG CCCCTTGAGT GCTGnCAGCT AAACGCATTA AGCACTCCGC	300
CTGGGGAGT GACGGACCGC AAG	323

(2) INFORMATION FOR SEQ ID NO: 4406:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4406:

AATTATGGGA TGCAATGGGA TACGAACGTG TTAAAACACG TATGGAAGAC GAACTTGGAG	60
ACTTACCACA ATGGATTAGT GATTTAGATG GTGGCTTTA TAAACAAGAT GAGACCATTG	120
AATATGCAAC ACCTATTTCT CACTTCGTAA AAGATGAAC TTTGGATAAA GGTGATGCCA	180
AACTTTCCGT AACTCATGAT GATCA ACT TGT TACTGAAATT ACAAAAGTAAA ATAATGTCA	240
TTACCGATGA ATTCAACGGT GCGTTAGTTG ATGCGATTGA TTTACTGGGA AATGACCCCTT	300
ACnCnAGnAT GGGTA	315

(2) INFORMATION FOR SEQ ID NO: 4407:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4407:

CACCAACCTCC CTACCTACTC GCCCCCCATC ATAAAATAGG TGGAC AG GAA TATCAACCTG	60
TTATCCATCG CCTACCCCTGT CGCCTCAGCT TAGGACCCGA CTAACCCAGA GCGGACGAGC	120
CTTCCTCTGG AAACCTTAnT CAATCGGTGG ACAGGGATTCT CACCCGTCTT TCGCTACTCA	180
CACCGGCATT CTCACCTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT	240
AGAACGCTCT CCTACCATTG TCCAAAGGAA TCnCACAGCT TCGGTAATAT GTTTAGCCCC	300
GGTACATTTC CGGCGCATGT CACTCGACTA nTG	333

(2) INFORMATION FOR SEQ ID NO: 4408:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4408:

ATTTAATGAA GTGCTTGTAA ATGAACCAAG CGCTAAAGAT ACTGTTGAAA TTTTAAAAGG	60
TATTCGCGAA AAATTGAAAG AACACCATCA AGTAAAATTA CCAGATGACG TATTAAAAGC	120
ATGTGTTGAC TTATCAATTC AATATATTCC ACAACGATTA TTACCGAGATA AAGCAATCGA	180

TGTGTTAGAT ATTACAGCAG CACATTTATC TGC ^G CAAAGT CCCAGCTGTC GATAAAGGTT	240
GAAACTGAAA AACGGATTTC TGGATTTnGA AAATGATAAA CGTAAAG ^A G TAAGTGCTTG	300
AAGGGATTTT AAAAAAGCTG AC ^G ACCATT CCAAAATTGG AATCCAAATC nnTTACCAGG	360
TTAAATTG ^G GAAAATGGTT AATTGGT ^G GG ACC	393

(2) INFORMATION FOR SEQ ID NO: 4409:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4409:

GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTAGCTC	60
TACTAAACTC GTTGC ^G C ^T TCT TTTCTCGTT CGTCAGATTC AAACGTTTC ACTTCGCCAA	120
GCCATTTTC TTTGTGTTA CT ^T TTTATTT TGACGTTTA GGCATAAAAAA AAAGAGACCT	180
TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTG ^C C ^T TG GCAACGTTCT ACTCTAGCGG	240
AAGTnAATTG GGCTACC ^A TC GT ^C CTAAAG AC ^T TTCTTG ACTTGTGGAC AATCGCTTGG	300
CnTCTnTCCT CTCCTTCGG	319

(2) INFORMATION FOR SEQ ID NO: 4410:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4410:

AATTAAACAT TTCATTTAA TCAATGAGAC TAA ⁿ ATACGC CTAAC ^T CGT TAACTTTAA	60
AATGTATTAA AATTCTAAAG TTTCTTTGC TTTTTCnATG ATG ^T ATTTT TGTTGGTAA	120
CCAAACATT ^T TCAGCTTGAG TGAATGGATA AATTGTATCT GCCTGCCTGA ACTCTTCCAA	180
TAGGTGCTTC TAATGAAAGG ATTGCACGTC ACTTAATTCA GCTAACAACT GCTGCACCAA	240
CACCAGCTTG CnGTTGTGCT TCTTGACTAC AAACTGACGA CCAGTTTTC AACTGAGCAC	300
AATTGTGCAC ATCGATTGGT GACAG	325

(2) INFORMATION FOR SEQ ID NO: 4411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4411:

GAGTTGGACA ATGCCGAAGC GTGAGCAAAG TTTTACCAT GCATGGTTGC ATTAGCGCA	60
ACATGACCAT AGTTTACTA AAGCACAGCG CCAAGTGATT AAAGGCTTAC CCAATGATCC	120
TGAAATGACG ATAGAGTCAG TATTAACCTCA TTTTCAATA GATCAGGAAG ACTAnCAAGC	180
TTATGTTGAA GGACATCTT TGGCGTTACC GGGTTnGGCA nGTATGTTGT ATTACCGTTC	240
ACCACAGCAT CACTTGAAC CACCTTGTT AACGGGTTAA TTGGCCATTG GGGTAAGTTG	300
TCCGACCATT GCCAAGTGGG TGATGAGTTn AGGCCAGTCC GCAAA A ATT GGGAAAGTAG	360
TCCGGAAAAT GGGTTAACGCC AACCTGTTGC CATCCAGGGG	400

(2) INFORMATION FOR SEQ ID NO: 4412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4412:

GATATATGGC AGCTCAAAGG AATGGGTTTC AGTTGAAGTG AAATTATCAC AGTCACTAGA	60
CCCGAGCACA TTATTCATC TCACTGACAA TGAGGCAGGA GATCGCTTTT ATATGCGTT	20
GAATGATAAT CGAACGTCAT ATTTGGCTA CAAAGCAATT CAATTATTCA AAAATAATT	180
TAAAAATAAA CAATCTATTT TAAAAGACTG GGGAAAATTA AACATAACCA TCACCATT	240
TACCATCCGC nATTCTGGGA ACCATCATCC TTCGAGTTGT TGGAGGGTTC CATTCCAAG	300
CCATAAAATCA GATGATGAAT GCGnGAGTT TGGCCTAAAn CATTGGAAT ACCCGGAGTT	360
TTAATTCCA	369

(2) INFORMATION FOR SEQ ID NO: 4413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4413:

TACCATCCTC GCTAAGAACCC TTTCTTGACT TGTGACAATC GCTTGCTTCTT TTCCTCTCCT	60
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TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGTCTTTTC TCGTTTCGTC	120
AGATTCAAAC GTTTCACTT CGCCAAGCCA TTTTCTTG TGTTTACTTT TTATTTGAC	180
GTTTAGACA TAAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCnACTCTA	240
GCGBAAGTAA GTGGGCTACC ATCGTCGCTA AAGACCTTC TTGGACTTGT GGACAAAnCGC	300
TTGCGTCCTT nCCTC	315

(2) INFORMATION FOR SEQ ID NO: 4414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4414:

GACCATCTCC TAAGGCTAAA TACTCTCTAG TGACCGATAG TGAACCAGTA CCGTGAGGAA	60
AGGTGAAAAG CACCCCGGAA GGAGGTGAAA TAGAACCTGC AAACCGTGTG CTTACAAGTA	120
GTCAGAGCCC GTTAATGGGT GATGGCGTGC CTTTGTAGA ATGAACCGGC GAGTTACGAT	180
TTGATGCAAG GTTAAGCAGT AAATGTGGAG CCGTAGCAGA ACAGGGTCTG GAATAGGGCG	240
TTTAGTATTT GGTCGTAnCC GnAAACCAGG TGATCTACCC TTGGTCCAGT TGAAGTTCA	300
GTTnACACT	309

(2) INFORMATION FOR SEQ ID NO: 4415:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4415:

TTTATTATAAC TTTACATTTC TCGTTTCGTC AGATTCAAAC GTTTCACTT CGCCAAGCCA	60
TCTTTCTTTG TGTTTGCTTT TATTTGACG TTTAGACAT AAAAAAAAGAG ACCTTGCAGT	120
CTCAAATGCG GCTCATCGCA TCCACTTTT GCCTGGCAAC GTTCTACTCT AGCGGAAnTA	180
AGTCGGACT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG	240
TGACCTCCTT GGCTATAGTC ACCAGnACAT ATGAATGTGA AATTTATACA TTCAAAACTn	300

(2) INFORMATION FOR SEQ ID NO: 4416:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4416:

AGAAAAAATAA GCGAACTGnA ATAAATAAAG ATTCAATTAA CGCATCAGTA TTAGGATTCA	60
CTCTAAAACG ATTAATAGTT TTATAAGAAG GTGTTGATC TTGAGCTAAC CACATCATTG	120
GAATACTGTC ATGAAGTAAT TTCTCTATTG TACGACCAGA AAATACAGAT TGAGTATATG	180
CATATAAGAT GATTTTAAC ATCATCTTG GATGATAGGA TGTTGCGCCA CGATGATGTC	240
TGAATTCATC GAATTGCTA TCAGGTATCG TTTCAACAAATTTCATT	286

(2) INFORMATION FOR SEQ ID NO: 4417:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4417:

TTTGATAAAA ATGGGCCATC GTCACGAGCT TCAACAATTG GTTTCGCAAC GTTTTCGCCA	60
AGCCCAGCCT GATATATTAC ATGAGGAGCG GTGCAAATGT TGTTAGAAAT TAAAGATTAA	120
GTGTATAAAG CGAGCGATAG AATCATACTA GATCATATCA GTCTAAAAGT AGATAAAGGC	180
GAGAGTATTG CCATTATAGG TCCATCAGGT AGTGGTAAAA GTACATTTCA AAAGCAAATA	240
TGTAATTGTT TGAGTCCAAC TAGTGGAGAA CTTTATTTA AACGTAAACC CTATAATGAT	300
TATGACCCGG AAGAATTGCG TCAACGAATC CAGTTATTTG GATGCAGCCA AAGTGGACTT	360
GTTTGGTGGGA ACGrATTGGA nGATAACCATT GGATAATTCC	400

(2) INFORMATION FOR SEQ ID NO: 4418:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4418:

GTATTTACAA TCAAACATAAG CAAAAGTATT CAGATGCCTC AGATAAAGCT TGGGCGCATT	60
CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTAGCAA CGCATATAAA AGTGCAAAGG	120
GTTGGCTAAT AGATATGGCT AATAAAATCGC GCTCGAATG GGATAATATT TCTAGTACAG	180

CATGGTCGAA TGCAAAATCC GTTTGGnAAA GGAnCATCGA AATGGTTAG TAACTCATAAC 240
AAATCTTAA AAGGTTGGAC TGGGGATATG TATTCAAGAG CCCACG 286

(2) INFORMATION FOR SEQ ID NO: 4419:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4419:

CTCACTTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT AGAACGTCT 60
CCTACCATTG TCCAAAGGnA TGCrCACAGC TTCGGTAATA TGTTTAGCCC CGGTACATT 120
TCGGCGCATG TCACTCGACT AGTGAGCTAT TACGCACTCT TTAAATGATG GCTGCTTCTA 180
AGCCAACATC CTAGTTGTCT GGGCAACGCC ACATCCTTnT CCACTTAACA TATATTTGG 240
GACCTTAGCT GGGTGGTCTG GGCTGTTCC CTTTCGAACA CGGACCTTGA TCACCCCCATG 300

(2) INFORMATION FOR SEQ ID NO: 4420:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4420:

AGAAAATAGG TGTCCCGTAC CGGCAAACCG CACACAGGTA AnTCAAnATG AGAATTCTAA 60
GGTGAGCGGA GCGAACTCnC GTTAAGGAAC TCGGCAAAT GACCCCGTAA CTTCGGGAGA 120
AGGGGTGCTC TTTAGGTTAA CGCCCAGAAG AGCGCAGTG AATAGGCCA AGCGACTGTT 180
TATCAAAAAC ACAGGTCTCT GCTAAACCGT AAGTGATGTA TAGGGGCTGA CGCCTGCCG 240
GTGCTGGAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAAcT ACGAATCGAA GCCCCAGTAA 300
ACGGcGGCCG TAACTATAAC GGTCTAGACG ATCTGC 336

(2) INFORMATION FOR SEQ ID NO: 4421:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4421:

GGnCACCCCTC GTGCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG GCTAGCCCTA	60
AAGCTATTTG GGAGAGAACCG AGCTATCTCC AGGTTGATT GGAATTCTC CGCTACCCCTC	120
AGTCATCCG CTCACTTTTC AACGTAATCG GTTCGGTCT CCATTCAGTG TTACCTGAAC	180
TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCAGGTCTAC GACAAATACT AAACGCCCTA	240
TTCAGACTCG CTTTCGCTAC GGCTCCACAT TTACTGCTTA ACCTTGCATC AAATCGT	297

(2) INFORMATION FOR SEQ ID NO: 4422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4422:

GTACATCGTC TAATAATAAG TTGACGATAT CTTGCAATGC ATCTTATCT AAATGTAAGA	60
ATTCAACGAT GCCGTTGAAG CGGTTAAGGA ATTCAAGGGCG GAAGAATTTC TTCATTTCGT	120
GCATAATATC TTTTCTTCA GCGTCATTGC CATTGCCAAA GCCAGCATT GATGTACAAA	180
TAATAATTGT ATTTTAAAG TTGATGACAT TACCTTGACC ATCAGTCAAA TTACCATCAT	240
CCATTACTTG TAATAACAAT GTTAAAATTG TGGATTGCTT TTGATTCAAn CAATAAATG	300
ACTGAGAnGG GATACGGCGA CTTTCAGTA AACGGATTGA ATGGCATTCA AnCCACATAC	360
CAGCGTGGAC CATCATTTC GAACAGCGTG GGCACATATC	400

(2) INFORMATION FOR SEQ ID NO: 4423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4423:

AAGTTGAGTC GCATAGCTAG TATGAAACGT GGTGTGCGCA TGGGAACATAT CAAGCTTGA	60
AGATGTGGTA CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT	120
CCATTAAATG AGTGATGCGA TTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT	180
AAAATTGCCT ATAAATTTT AGCACATAAA ATAAGAnGnG CCAACCATTG TTAGACTATA	240
ACAACGGTTG GCTCTTAAT TGAAAAAGA ACCATACG CTATGGTAGT T	291

(2) INFORMATION FOR SEQ ID NO: 4424:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4424:

AACTGCCACC ACCTGGGnC GTTTCCAGAA CCTCTATGCA TTTCAATCAC AGnCAAATGT	60
GCGGTTGACG TTCAATGACT ACCTGCAATT CATCGGTAG CTCACACCCCT TTACCTGnCT	120
AAAGTACCAAG TAGACAATGT AGGTATTGGA CTTGCATGAG CATTGTTATn EGTAATGGG	180
CTTAGATAT TTTATTAATA CCGGCCAACATC ATGCTATTCA AACCGCCAAT AGCTTTATTA	240
GCAACATTT TACCTAAATC AGCCGCAGCT CTTCCCATGT CTTTACCAAT ATCTCTAAC	300
CAATCATATG TTTTGATAA GCCATTTCT AAAACCATTAA AATACTGATT TAGCGTTAGA	360
CCATGCCGAA CTTGAAATTG CATCAAAACG ATCGTGGGCT	400

(2) INFORMATION FOR SEQ ID NO: 4425:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4425:

CTTGACAAT TTGTATACCG TACTATCTG CGCTTATTGA AGTAATGAAT GAAACACCTA	60
AGATGATAAA AGAACACAGGT GGTTTGCGA AAAGTGAAGT ATGGCGTCAA ATGATGTCAG	120
ATATATTTGA CACAGAGTTA GTGGTTCTG AAAGTTATGA AAGTTCATGC TTAGGTGCCT	180
GCGTGCTCGG ACTTAAAGCT GTAGGTGACA TTGAAGATTT TTCAATCGTT TCATCGATGG	240
TCGGTGCCAC AAACAATCAT ACGCCGATTG AAGAAAATGC ACTGTTACCA AGAnTCGAAT	300
CCATTnTTAT CATTAAGCGT CTTAnCAGAG ATATGACAAT	340

(2) INFORMATION FOR SEQ ID NO: 4426:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4426:

CTGAAGATGA TAAAGATGCA GATGGTGGCG AGTTGCACGT AACATTACG GATCATGATG	60
ATTCACACT TGATAACGGA TACTCGAnG AATTATCATC AGACAGCGAT TCAGACTCAG	120
ATAGTGACTC AGACAGCGAC TCAGACTCAG ACAGCGACTC AGACTCAGAC AGTGATTAG	180
ATTCAGACAG CGACTCAGAT TCAGATAGCG ACTCAGATTG GGACAGCGAT TCAGACTCAG	240
ATAGCGACTC AGATTCAAGAT AGCGATTAG ACTCAGACAG CGACTCAGAT TC	292

(2) INFORMATION FOR SEQ ID NO: 4427:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4427:

AACAGTGCTC TACCTCCAAT AATCATCACT TGAGGGCTAGC CCTAAAGCTA TTTCGGAGAG	60
AACCAGCTAT TTCCAGGTTTC GATGGAATT TCTCCGCTAC CCTCAGTTCA TCCGCTCACT	120
TTTCAACGTA ATCGGTTCGG TCCTCCATTC AGTGTACCT GAACTTAACAC CTGACCAGGG	180
TAGATCACCT GGTTTCGGGT CTACGACAAA TACTAAACGG CCCTATTAG ACTCGGCTTT	240
CGCTACGGTT CCCACATTAA CTGGCTAAAC CTTGCATCAA AATCGGTAACCTCGnCGGGTC	300
ATTCTAn	307

(2) INFORMATION FOR SEQ ID NO: 4428:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4428:

GACCATAACAT CGTCATCGTT TGCACCGTCA AATACTGGTG ATGCAACGTG AATAACCAAGA	60
TTTTTAGCAG CCATACCTAA GTGTAGCTCT AATACTTGTC CGATGTTCAT ACGAGATGGT	120
ACACCAAGAG GATTTAACAT GGATATCGAT CGGGACGTCC ATCTGGTGAA GTGAAGGCAT	180
ATCTTCTTCA GGGAACAAAT TTGAGGAAAT GGACACCTTT GTTGACCATG TCGGACCACA	240
CATGCTTATG CACCAACATG GAATTTACG TTTTGGAn GATGATTATT ACACGTnACT	300
AATTGGTTA CACCAGGTGG AnAATGTAT CGTCGGCCTT GCTTCACGAT TGGA	354

(2) INFORMATION FOR SEQ ID NO: 4429:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4429:

GTGnACTATC nGCTTGTCTA TGATAATATT ATTCTTTGTA CTTGTTAAA AGATATTAGA	60
CTAAAACTAA AAACAGCAGT AAGATGATT ATGATTAAAA CTATCTTACT GCTGTTCACT	120
TTTTATAATA CTTCTGAATG TCTCACTTAT ACTTCTAGTC ACAGATTAA ATAATCAAAA	180
GTGCACATTA TTAAAATATC AATTCACAC TCAATGCGGC TCATCGCATT CATTCTTGT	240
CTAGAACGT TCTACTCTAG CGGAACGTAA GTAGCTACCA TCTCGCTAAG GAACTTTCTT	300
GACCTGGTGA CAACCGCTGC GnCTnTCTCT CTTCGGCTCT CGCTTACTCC ATTTAGCTCC	360
ACTAAACTCG TGCGCCCTT CCCGTTCGGC AGATCCAACG	400

(2) INFORMATION FOR SEQ ID NO: 4430:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4430:

ACTGCCATCC TTCAATCGGn ACGACATTT TCTTGTCCC ACATAGTGAG CCCAACCGCC	60
ACCATTACA CCTTGACAGC CACATAACAT AACTAAGTTT AAGATnGGGG GATAAATCGT	120
ATCTGAGTTA AACCAATGGT TATACCCGC ACCCATGATA ATCATTGAAC GCCCTTCAGT	180
ATCGATAGCG TTTGCGCAA ATTCTTCGC TACTTGAATG ACAACACTTT GTTTACGCC	240
TGAAATGGCT TCTTGCCAAG CAGGTGTATA TTTGATTCT GCATCGTCGT AA	292

(2) INFORMATION FOR SEQ ID NO: 4431:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4431:

TGAGCCGnAC ATCGAGGTGC CAAACCTCCC CGTCGATGT GACTCTGG GGGAGATAAG	60
CCTGTTATCC CCGGGGTAGC TTTTATCCGT TGAGCGATGG CCCTTCCATG CGGAACCACC	120

GGATCACTAA GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCATH AAGCTCCCTT 180
ATGCCTTAC ACTCTATGAA TGATTCCAA CCATTCTGAG GGAACCTTGTA GCGCCTCCGT 240
TACCTTTAG GAGGCGACCG CCCAGTCAAA CTGCCCGCCT GACA 284

(2) INFORMATION FOR SEQ ID NO: 4432:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4432:

TATCATTGTG GTACGATAAG GCATATGTTG TACCTATGnA TGGTGGAAAGA GCCTTCAGTT 60
GTCGCTGCAG CTAGTTATGG TGCAAAGCTA GTGAATCAGA CTGGCGGATT TAAAACGGTA 120
TCTTCTGAAC GTATTATGAT AGGTCAAATC GTCTTGATG GCGTTGACGn TACTGGAAAA 180
TTATCAGCAG ACATTAAGC TTTAGAAAAG CAAATTCTATA AAATTGCGGn TGAGGCATAT 240
CCTTCTATTA AGCGCGTGTG GTGGTTACCA CGTATAGCGA TTGATACATT CCTGGCCACC 300
AGTTCTATCT TT 312

(2) INFORMATION FOR SEQ ID NO: 4433:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4433:

CGGTACTCGT TAAGGCTGAG CTGTGATGGG GAGAAGACAT TGAGTCTTCG AGTCGTTGAT 60
TTCACACTGC CGAGAAAAGC CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC 120
AGGTAGTCAA GATGAGAATT CTAAGGTGAG CGAGCGAACT CTCGTTAAnG AACTCGGCAA 180
AATGACCCCG TAACTCGGG AnAAAGGGTG CTCTTAAGG TTAACGCCCA GAAGAGCCGC 240
AGTGAATAAG CCCAAGCGAC TGTTTATCC AAAACACAGG TCTCTGCT 288

(2) INFORMATION FOR SEQ ID NO: 4434:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4434:

GGACCGAAC	GACTTACGTT	AAAAAGTGAG	CGGATGAAC	TAGGGTAGCG	GAGAAATTCC	60
AATCGAACCT	GGAGATAGCT	GGTTCTCTCn	nAAATAGCTT	TAGGGCTAGC	CTCAAGTGAT	120
GATTATTGGA	GGTAGAGCAC	TGTTTGGACG	AGGGGCCCT	CTCGGGTTAC	CAATTCAGA	180
CAAACCTCCGA	ATGCCAATTA	AATTTAACCT	GGGAATTCA	AACATGGGTG	ATnAAGTC	240
TGTTTCGAAA	GGAAACAGCC	CAGACCACCA	GCCAAGTCCC	AAAATATATG	TTAATGGGA	300
AAAGGTGTGG	CCTTTGCCCA	GGACAACCAA	GAAGTT			336

(2) INFORMATION FOR SEQ ID NO: 4435:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4435:

ATTGACGCCG	CATTTTACG	GAATGGGAAT	AAAGCGACAC	AAACCGTCAC	GTCnGTGTTG	60
GTCATGAC	AAGGTAATGC	GAGTGATCTG	ATGTATGGCT	TATCATGGCA	ATCTGTTATG	120
GnCTGACTGA	TCGGACGATG	TATCATTGCG	CAATTGTTT	ACTTGTCGTT	ATTCAGGCAC	180
CCGACTATGT	TGTAGGCAAG	ACTACTCGCG	AATAATGAGC	ATTTGCTAG	GA	240
AATCATTGGC	TGCGTTTAA	TGAGCGTAAT	GAGGAAGGGG	CGTTAAAAAA	GTTGGATTTA	300
ACGA						304

(2) INFORMATION FOR SEQ ID NO: 4436:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4436:

AATATACTCC	GGTAAATAAC	CGAAGAGTTT	TGAATCATTG	TTAAAAATGG	AATTAnAGTT	60
CTAGTATCTG	TTGGGTTTG	AAATAGGTCA	TAGGATAAAA	CAAATnGAGA	ATTTGTCGCT	120
ATTGTAAAT	TGTATCCTGG	CTTAAGTTGG	CCATTTCA	TATGGTCTTC	CTTCATTCTC	180
ATAAAAGTTG	CATCATGGAT	CAGTTTAGA	AAAGCTATT	CTATCTTAA	GAATCGATT	240
TTGTTCTTCA	TATTTATTTT	TTCTTTCGGA	ATAATCATCA	AATTTATnTT	TGGAACCTCT	300

(2) INFORMATION FOR SEQ ID NO: 4437:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4437:

ATCGTTAAA TCAGTTAGTA AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAAATA	60
TTATAGAAAA CATCAAAGGA TGTTAAGAAA TACAATTAT TACCCAGCAT TTAATAATGG	120
TGCTATAGAA GGAATTAATA ATAAGATAAA ATTAATCAAG TGAATTCTT TTGGTTACAG	180
AAATTCAAC AACTTAAAG CACGTATAAT GATGATTTC AGCTTGTACA AGGGGGAnAA	240
AAGGAnGnCA ACCAAGCCC ATAATGGACT GGCCGCCTAA TATTAAAAC TCTAAAGGTT	300
GTATTTAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA CCCGTTAAC	359

(2) INFORMATION FOR SEQ ID NO: 4438:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4438:

ACTTACAGTT ATTAACTT GGnCAGAACAT CATATCCAT AAGTCGAAA TGTTGTAAAA	60
CATAAACCTT GnAACGGCA ACATTTTG GTCCTTCTCC ATCATTAT TTAAAAGCGC	120
ATTATGATCA ATATCATGCC CAATTAACCTT TCCAGCAATT TCCATAGTAT GTTCTGAGGT	180
ATTGTTAAAA AGGAATCGCC CAGTATCACCA GACGATACCA AGATATAAAA CGCTCGCGA	240
ATCTTATTAA ACAATTGCTT CATCATTAAA ATGTGAGATT AAATCG	286

(2) INFORMATION FOR SEQ ID NO: 4439:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4439:

TCGCTTGACT TCTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAnCTCT ACTAAACTCG	60
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TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTCA CTTGCCAAG CCATTTCT	120
TTGTGTTTAC TTTTATTT GACGTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA	180
TGCGGCTCAT CGCATCCATT TTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG	240
GCTACCATCG ACGCTAAGAA CCTtTCTTGA CTTGTGACAA aTCGCTTGCT TCTTCCTCn	300
TCTTCGGTCT CGCTTACTCA TTTAGCTCTA CTAA A TCGT TGCGCTCTT TCTCGTTCG	360
TCAGATTCAA CAGTTTCAT TCGCCAAGCC ATTT	394

(2) INFORMATION FOR SEQ ID NO: 4440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4440:

TAATAGGTTTC GAGGTGGAAG CATGGTGACA TTGGCAGCTG ACGAATACTA ATCGATCGAA	60
GACTTAATCA AAATAAATGT TTTGCGACAA TGCAACTTTT ACTTACTATC TAGTTTGAA	120
TGTATAAAATT ACATTCAATAT GTCTGGTGAC TATAGCAAGG AGGTCACACC TGTTCCCATG	180
CCGAACACAG AAGTTAACAGT CCTTAGCGTC GATGGTAGTC GAACTTACGT TCCGCTAGAG	240
TAGAACGTTG CCAGGCAAAA AATGGATGCG ATGACCGCAT TGAGACCGCA GCnTn	295

(2) INFORMATION FOR SEQ ID NO: 4441:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4441:

TTTCATAAAA AGATTCAAA CGCGTTCATC AA _n CCTCGTC GCAGGTCTTT CGAACACTAG	60
CGATTATTTCT tTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG TTTGCTTGG	120
TAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA CAATTCTTT TTAGTCAAGC	180
GCTCGCATAAC TGCTTTATTT TCATAAGCAA ATCACTTTA ACCAAAAAAT ATTTGAATGT	240
TAAATAAACAA TTCAAAATG AATACAATAT GTCACGTTAT TCCgCATCTT CTGAAGAAGA	300
TGTTCCGAAT ATATCCTTAG AAAGGAGGTG ATCC _n GCCG _n ACCTT	345

(2) INFORMATION FOR SEQ ID NO: 4442:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4442:

AATCATTGTC AAAACTACGT TCTGGTAAAC AAGGACAACC CGTTTGAACC	ATGGCCCAC	60
ACCATTTGAT AGGCAGnCAT GTGCGCAATG GACATCCACA TAGTTGCGTA ATGTTTCATA		120
CGTCATTGCT CAAATCATTC ATGACTAGCG CAACATGATT ACCTTGTGCGT GnGCACCTTC		180
ATTAAAGnAA CTTATGATAG ATTTATTTCC CGGGACATTA AGCATTGCA TCGTTAACAT		240
GCGTATTGCA CCCAATTAG AAGTTCCCTCC GTGCCGTTG GTATATCACA AATTTGTAGT		300
GTATCTTGGA TGC		313

(2) INFORMATION FOR SEQ ID NO: 4443:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4443:

AGCATGGTGT TTCTCAGATT GTCGGATGTA TAAATGTGTA TGTTATGTTT TAATTTTCC	60
CAGTCTTAA AAATAGATTG TTTATTTTA GAATTATTTT TGAATAATTG AATTGCTTTG	120
TAGCCAAAAT ATGACGTTCG ATTATCATTC AAACGCATAT AAAGCGTATC TnCTGCCTCA	180
TTGTCAGTGA GATGAAATAA TGTGCTGGG GTCTAGTGAC TGTGGATAAT TTCACTTCAA	240
CTGAAACCCC ATTCCCTTG AGCTGCCAT ATATCTCTT GGACAATATC GGTCCCTCTA	300
ATACGGnCCG TAGnCCATTC CATTCAATT CTTTC	336

(2) INFORMATION FOR SEQ ID NO: 4444:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4444:

CAGACTGGGA TATTATAAA ACGTTGGCAA AAGCATTTC AGAAATGGCA AAAGACTATT	60
TACCTGGAAC GTTTAAAGAT GTTGTGACAA CTCCACTTAG TCATGATACA AAGCAAGAAA	120

TTTCAACACC ATACGGCGTA GTGAAAGATT GGTGAAAGGG TGAAATTGAA GCGGTACCTG	180
GACGTACAAT GCCTAACTTT GCAATTGTAG AACGCGACTA CACTAAAATT TACGACAAAT	240
ATGTCACGCT TGGGCCTGTA CTTGAAAAAA GGGGAAATT GGAGCACCTG GGGGTAAGTT	300
TCCGTGTCCA GTTGAACCAT TATGGAGGAn TTnAAAAAGT ATGTTAACGG ACCTGGGAGT	360
TGAATAACCA ATGGATnGAT TCCC GTGAAG AGCGAATCC	400

(2) INFORMATION FOR SEQ ID NO: 4445:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4445:

TACGCCACG ACGGATAGGG ACCGAACGT CTCACGACGT TCTGAACCCA GCTCGCGTAC	60
CGCTTGTAAAT GGGCGAACAG CnATCGCCTT GGGACCGACT ACAGCCCCAGGATGCGATGA	120
GCCGACATCG AGGTGCCAAA CCTCCCCGTC GATGTGAACt CTTGGGGAG ATAAGCCTGT	180
TATCCCCGGG GTAGCTTTA TCCGTTGAGC GATGGCCCTT CCATGCGGAA CCACCGGGAT	240
CACTAAGTCC GTGCTTTCGA CCCTGACTAC GGACTTGTnA GGTCTGCGGC ATTCAAGCTT	300
CCCTTGATGG CCTTGACAC TGCTTATGGA ATGnATTG	339

(2) INFORMATION FOR SEQ ID NO: 4446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4446:

CAATTAAAG TGTTGAAAAT GTCACTTTA AACTTTCTAG TTTTATCTT AATAAACATG	60
CCATnCGTAA TAAGTGGCGT TTTATTAAAA TCATCTATAA TAGCCATATA GTTTGCTCA	120
CTACCATAAC CTGCATCAGC TACAATATAC TCCGGTAAAT AACCGAAGGA TnTTTGGAAAT	180
CATTGTTAAA AATGGAATTG AAAGTTCTAG TATCTGTTGG GTTTGAAAT AGGTCATAGG	240
ATAAAACAGG GTGAGAATTt GTCGCTATTT GTAAATTGTA TCCTGGCTTA AGTTGGCCAT	300
TTTnCATAG GTCTTCCT	318

(2) INFORMATION FOR SEQ ID NO: 4447:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4447:

TTTGAAATT CTCTATGTTG GGGCCCGGAC TATAATTGAA AAATGCTTGT TACAAGTGCA	60
TTTTATTC CA GTCAACTACT AACAAATATAA CATTGTGGAG CCCAGAnCTT TGATTAATGT	120
ATATGAAAAT CAAAGTAATG CTTATGTATG ATTATTTCAA ATATTTACA TACATGAAC	180
TTTCCAATGT ACGATACTAT TATTATAAAG CGCTCGCTAA GATTTACGA TGATTAGAGG	240
GTAAAAAAATG AACGATCAAT GGTnAACCA TTTAATTGG	279

(2) INFORMATION FOR SEQ ID NO: 4448:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 302 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4448:

GACACCGGCA TTCTCACTTT CTAAGCGCTC CACATGTCCT TACGATCATG CTTCAACGCC	60
CTTAGAACGC TCTCCTACCA TGTCCAAAG GACAATCCAC AGCTTCGGTA ATATGTTAG	120
CCCCGGTACA TTTCCGGCGC AGTGTCACTC GACTAGTGAG CTATTACGCA CTCTTAAAT	180
GATGGCTGCT TCTAAGCCAA CATCCTAGTT GTCTGGGCA ACGrCACATC CTTTCCACT	240
TAACATATAT TTTGGGACCT TTAGCTGGTG GTCTnGGGCT GTTTCTGA TTGAACACGG	300
GA	302

(2) INFORMATION FOR SEQ ID NO: 4449:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4449:

CGTTGGTATA TAGAGGGCAA CCGTCACCTG ATAAAATGTG GACACAGTTT TTACAAGAGG	60
TTAAGGAAAT GAGTTGGAG GCATACGAGC ATCAAGAATA CCCATTGAA TGTTAGTAA	120
ATGACTTAGA TCAATCACAT GATGCCTCAC GGAATCCATT ATTTGATGTC ATGTTAGTAC	180

TACAAAACAA TGAnACGAAA TCATGCTCAT TTTGGGCATA GTAAATTAA CACACATTCA	240
ACCCCAAATC AGTGACGGGC GGAAATTGG ATTnTCCTT TTCCATCATT GGAAGAAGGA	300
TCGCGGATGA CCTAATAnCA ATCCAATTAT CGGGGTATAA ATACCGGATT TTATAACCA	359

(2) INFORMATION FOR SEQ ID NO: 4450:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4450:

GATGACAAAA TTTGCTTGAA AACCGAAATG GATGGTCATC ATTGACTGnA TCAAGGTACA	60
TCATTCTTG GTGCTTATGC ATTTAGACAT TATACAAAAA CAATACTTTT ATAGGGCAAC	120
CTTATGGGGT TCTATCGGCT ATACATTACC TGCAACATTA GGTTACAAT TAGCAGACAA	180
AGATCGTCGn TAACTTATTA TTAATTGGTG ATGGCTCATT GCCAACTAAC TGTTCAAGCT	240
ATTTCAACTA TGGATTAGAC AGCATATTAA ACCGGTATTA TTTGTGGATT AATAATGACG	300
GCTATACGGT AGAACGACTT ATTCCC	326

(2) INFORMATION FOR SEQ ID NO: 4451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

GAAAACATCA AAGGATGTTA AGAAATACAA TTTATTACCC AGCATTAAAT AATGGTGCTA	60
TAGAAGGAAT TAATAATAAG ATAAAATTAA TCAAGTGAAT TTCTTTGGT TACAGAAATT	120
TCAACAACTT TAAAGCACGT ATAATGATGA TTTTCAGCTT GTACAAAGGA GAnAAAAAGA	180
AGACAACCAA GCCCAATAAT GGACTGGCCG CCTAATAATA AAAACTCTAA AAGTTGTATT	240
TTAAAAATAG GTCTTAAAT TATATACCCC CCCCATTTGG GTGGAGAACCC GGTAAACCAT	300
GCCTAGGTGC CTAACCTCCn ATAATGGnAC CCCTCCTTAC CATTGGGCC ATGGGGCCAA	360
TAAAGCGGGG GGCAATTGGG G	381

(2) INFORMATION FOR SEQ ID NO: 4452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4452:

TTAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG TTATTAATCT TGTGAGTGTT	60
CTTTCGAACA CTAGCGATT A TTTCTTATGA ATTCAAGCTT ATTTAAA ACT CTTTATTCA C	120
TCGGTTTG C TTGGTAAA AT CTATATTTA CTTACTTATC TAGTTTCAA TGTACAATT	810
CTTTTAGTC AAGCGCTCGC ATAAGCAATA TCAC TTAAC CAAAAAATAT TTGAATGTTA	240
AATAAACATT CAAA ACTGAA TACAATATGT CACATn	276

(2) INFORMATION FOR SEQ ID NO: 4453:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4453:

GGCGAAACCG CGTAGCGTT TTTAAGTCTG ATGTGAAAGC CCACGGTCAA CCGGGAGGGT	60
CATTGGAAAC TGGAAA ACTT GAGTGCAGAA GAGGAAAGTG GAATTCCATG TGTAGCGGTG	120
AAATGCGCAG AGATATGGAG GAACACCAGT GAGCGAAGCG ACTTTCTGGT CTGTA ACTGA	180
CGCTGATGTG CGAACGTGG GGGATCAAAC AGGATTAGAT ACCCTGGTGA GTCCACGCCG	240
TAAACGATGA nTGCTAAATG TTAGGGGGTT TCCGCCCTT A@GGCTGCC AGCTAnACGC	300
ATTGAAGCAC TGCCGCCTGG GGAGTGACGA CCGCAAnTTG A	341

(2) INFORMATION FOR SEQ ID NO: 4454:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4454:

ACnCTCCCCA AAGTCATATC GTCGTTAGTA ACGTCCTCA TCGGCTTCTA GTGnCCAAGG	60
CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTCCA CCATTTTAT AAGTCAAACG	120
CTCACATACG GCTTCGTTT CATTATTTA AATGCTCATT TACATAAGTA AACTCTGCTT	180
TAAAATAATT TAACTCATTG TCTGCTAAC GTTTCTTTT ATAAAAAGAT TTAAACGCGT	240

TATTAATCTT GTGAGTGTTC TTTCGAACAC TAGCGATTAT G

281

(2) INFORMATION FOR SEQ ID NO: 4455:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4455:

ATGTCTTCAC TTATACTTCT AGTCACAGAT TTAAATAATC AAAAGTGCAC ATTATTAAAA	60
TATCAATTTC ACACTCAATG CGGCTCATCG CATTCAATTTC TTGTCTAGCA ACGTTCTACT	120
CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACCC TTTCTTGACT TGTGACAATC	180
GCTTGCnTCT TTCCTCTCCT TCGGCTCTCG CTTACTCAT TAGCTCTACT AAACTCGTTG	240
CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCnGT	279

(2) INFORMATION FOR SEQ ID NO: 4456:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4456:

ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT	60
CCATTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGE	120
AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT	180
ACTCATTAG CTCTACTAAA CTCGTTGCGC TCTTTCTCG TnTCGTCAGA TTCAAACGTT	240
nTCACTTCGC CAAGCCATT TCTTGTGTT TACTT	275

(2) INFORMATION FOR SEQ ID NO: 4457:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4457:

ATCCGATTCA CAAAGCACAT CATCATATAC AAGTCAGTCA ACAAGCCAAA GTGAATCCAC	60
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ATCGACATCA ACGTCACTAA GCGATTCAAC AAGTATATCT AAAAGTACGA GTCAATCAGG	120
TTCGGTAAGC ACATCAGCGT CATTAAGTGG TTCAGAGAGT GAATCTGATT CACAAAGTAT	180
CTCAACAAGT GCAAGTGAGT CAACATCAGA AAGTGTCA ACATCACTCA GTGACTCAAC	240
AAGTACAAGT AACTCAGGAT CAGCAAGTAC GTCAACATCG CTCAGTAACT CAGCAAGCGC	300
AnTCCAATCC GATTTGTCGT CAACATCTT AAGTGGATTC AACATCTGCG TCnATGCCAA	360
AGnnGTGAAT CCGATTACCA AAGCACATCA GCATCCTTAA	400

(2) INFORMATION FOR SEQ ID NO: 4458:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4458:

GAGTGCAGT TCTGGAATCT GGACTCACTG ATCTGATTCT GGAGTCGCTA TCTGATTCTG	60
AGTCGCTGTC TGAATCTGAA TCACTGTCTG AATCCGAATC GCTATCTGAT TCTGAGTCGC	120
TATCTGAACC TGAGTCGCTG TCTGAGCCTG AGTCACTGTC TGAATCCGAA TCCGGATCCG	180
GGTCTGGGn TGTTCCGGT TCTGGGTCTG GGACTTGGTT CTGGATCTGG CGTTGGTTCT	240
GGGTCTGGGG TCTGGACTGG TTCTGGGGTC AAACGGCGGC CCTGGAGTGG GGTCTTCGG	300
AATnAACGGC GGAATCACCA TCAAGCAACT TnCAACAACC ATAACGAAAA A	351

(2) INFORMATION FOR SEQ ID NO: 4459:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 271 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4459:

ATCCTGCAGT TGATCAGTAT GGTGATATTA ATTGTTAA TACGAACGCG TCATCTACAA	60
GTGAAATCAT TTACGATTAA ATCTCACATT TTAATGATGA AGCAATTGTT AATAAAGATA	120
TCGCGAGCGT TTTATATCTT GGTATCGTCG GTGATACTGG GCGATTCCCTT TTTnACAATA	180
CCTCAGAACCA TACTATGGAA ATTGCTGGAA AGTTAATTGG GCATGATATT GATCATATG	240
CGCTTTAAA TAAAATGATG GAGAAGGnCC C	271

(2) INFORMATION FOR SEQ ID NO: 4460:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4460:

ACTGTGGATT AATATTATGC CTGGCAACGT TCTACTCTAG CGGAACGTA	60
CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG	120
TATAGTCACC AGACATATGA ATGTAATTAA TACATTCAA ACTAGATAGT	180
GATTTGCTT CGCAnAACAT TTATTTGAT TAAGTCTTCG ATCGATTAGT	240
GCCACATGTC ACCATGCTTC CACCTCGAAC CTATnAACCT CAG	283

(2) INFORMATION FOR SEQ ID NO: 4461:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4461:

CTTCTACAAG TCCTGAATAT ACTTATGAT CTCTCTTTC GTGTATGCAA ACTGACGTTG	60
TAATTTAAAT AACGTCTCAT CTTTCCATTG CGAATCTTGA TATTGTATAT TTTCAAAATC	120
AAAGTCAACT TTATGGTTAT CAATCCACGC TTTATATGGT AATTCTCCAG CAATCGCACC	180
TTTTAAATCA TTATTTCAA TGACTTTATT CTGTTAAAAT CAACAAAnCAT AA ⁿ TTCCnG	240
GATTCAATTG ACCTTTAAAA GCAACATTAC TTCC	274

(2) INFORMATION FOR SEQ ID NO: 4462:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4462:

GGCTGCTAAA AATCTTGGTA TTCACGTTGC ATCACCGATA TTTGACGGTG CAAACGATGA	60
CGATGTATGG TCAACAATTG AAGAAGCTGG TATGGCTCGT GATGGTAAAA CTGTACTTTA	120
TGATGGACGT ACAGGTGAAC CATTCGATAA CCGTATTCA GTAGGTGTAA TGTACATGTT	180
GAAACTTGCG CACATGGTTG ATGATAAAATT ACATGCGCGT TCAACAGGAC CATATTCACT	240

(2) INFORMATION FOR SEQ ID NO: 4463:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4463:

GC GGCTCATC GCATTCATTT CTTGCTAGC AACGTTCTAC TCTAGCGGAA CGTAATTAGC	60
TACCACTCCTC GCTAAGAACCC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCCTCTCCT	120
TCGGCTCTCG CTTACTCATT TAGCTCTACT AAAACTCGTTG CGCTCTTTTC TCGTTTCGTC	180
AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTTTAnTTTGAC	240
GTTTTAGACA TAAAAAAAAGA GACCTCACGG nCTCAACTTG CCTGGCAAAG GTCTAnTCTA	300

(2) INFORMATION FOR SEQ ID NO: 4464:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4464:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCTAA GGTAGCGAAA	60
TTCCCTTGTGCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTTGGGC ACTGTCTCAA	120
CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG GACAGGACGG	180
GAAAGACCCC GTGGGAGCTT TTACTGGTTA GCCTGGATAT TGGAAATTGCG GGCACACTTG	240
GTTACAGGAT AGGTAAGGAG CCTTTGGAA ACGTTGAGCG CTACTTTAnG TTGGGAGGCG	300
CTGGTnGGGA TACTTACCCCT AACTGTTTT GGCTTTCTn AACCGGCACC ACTTATCCTG	360
G	361

(2) INFORMATION FOR SEQ ID NO: 4465:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4465:

CTGTATGTAC ACCACCAATC GGTAGGTT TAGAACGTT TGTCAGAAAG TATAAATTCA	60
ATCATTCCGA AAGAGAAATG GGTAAGGCTT CCTTCACTAT GGGAC A TTT GGTATTACTG	120
AAGGTGCTAT TCCTTCGCA GCCCAAGATC CATTGCGCAT TATACCTGCA AACATCATG	180
GTGCAATGAT TGCATCAGTC ATTGCAGCCA TTGGTGGTGT CGGCGATAGA GTGCGACATG	240
GnGGTCCCAA TCGTGCTGT ATTAGGTGGG TTTTGT _n TTTT TT	292

(2) INFORMATION FOR SEQ ID NO: 4466:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

GCAAACAAAA CAGTATTAGT AGATTATGAA AAATATGGTA AGTTTATAA CTTATCTATT	60
AAAGGTACAA TTGACCAAAT CGATAAAACA AATAATACGT ATCGTCAGAC AATTATGTC	120
AATCCAAGTG GAGATAACGT TATTGCGCCG GTTTAACAG GTAATTAAA ACCAAATACG	180
GATAGTAATG CATTAA _n AGA T _n AGCAAAT ACAAGTATTA AAGTATATAA AAGTAGATAA	240
TGCCnCTGAT TTATCTGAAA GTTACTTGT GGAATCCCGG AAACCTTGAG GGTGGCCCCT	300
AATAnTGG	308

(2) INFORMATION FOR SEQ ID NO: 4467:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 271 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4467:

AAGCAGGCGC TCTCCCAGCT GAGCTAAGCC CCCATAATAA T A CAGTATA TCGGGAAAGAC	60
AGGATTGAA CCTG _n GACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT	120
CCCGTATAAT TAAnGCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA	180
CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTATT GAAAATAGTG CCGAGGACCG	240
GAATCGAACCG GGTACGTGAT CACTCACCGC A	271

(2) INFORMATION FOR SEQ ID NO: 4468:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4468:

TGTGTTAGGT ATTACATCAT CACATTATC TGCCTCAAAG TCCAGCTGTC GATAAAGTTG	60
TAAACTGTAA AAACGCAATT TCTGAATTAG AAAATGATAA ACGTAAAGCA GTAAGTGCTG	120
AAGAnTATAA AAAAGCTGAC GACATTCAAATGAAATCAA ATCATTACAA GATAAATTAG	180
AAAATAGTAA TGGTGAACAT ACTGCTGTTG CTACAGTTCA TGATATTCA GATACTATT	240
AACGATTAAC TGGTATTCCA GTTCTCAAATnGATGATAA CGnTATTGAA CGTTAAAAAA	300
ATATTT	306

(2) INFORMATION FOR SEQ ID NO: 4469:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4469:

GGTTTATTAA CAGCATTCTT ATCAGCATTGTAACGTAA TTGTTTATAA CTTCTGTGTG	60
AAGCGCAATA TTACAATTAA AATGCCAAA GAAGTACCGC CGAATATTTC ACAAGTATT	120
AAGGACTTAA TTCCATTTC AGCGGTAATC ATCATTCTT ATGCATTAGA TTTAGTCATT	180
CGAACAGCT TTAAATCAAATGTAGCGGAA GGTATTTAA AATTATTCGA ACCATTATT	240
ACAGCAGCAG ATGGATGGGT TGGTGGTCAC CATTAAACnT TGGGnGCnTT TGCATTAATC	300
CTGGGTTTGT AGGGTAATCC ATGGGTCCG	329

(2) INFORMATION FOR SEQ ID NO: 4470:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4470:

AACTGGGTGA TAAGGTCTG TTGAAAGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA	60
AATATATGTT AAGTGGAAAA GGATGTGGCG TTGCCAGAC AACTAGGATG TTGGCTTAGA	120
AGCAGCCATC ATTTAAAGAG TGCGTAATAG CTCACTAGTC GAGTGACACT GCGCCGAAAA	180

TGTACCGGGG CTAACATAT TACCGAAGCT GTGGATTGTCCTGGACAAT GGTAGGAGAG	240
CTTCTAACGGA CTTGAAGCTG ATCGTAAGAC TGTGGAGCGn TAGAATGAGA TGCCGTGTGA	300
TAGnAAAGAC GGTGAGATCC CTCCACCGTT GACTAAGTTC CAGAGGAAGC TCTCCGTGG	360
GTTATCCGGT CCTAACGnGAG GCCGACAGCT AGGCATGGnT	010

(2) INFORMATION FOR SEQ ID NO: 4471:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID N: 4471:

TCATTTTAG AAATATTATC TTTTCCACAA ATCATTGAT ATAAAGTGCG ATCATTGCC	60
GCGAGTGCTG CCATTGACAC TAGCTGTTGC GTATCATT TGGCTAGCAC TTCGGGATAC	120
TTTCTTAGCT GAACAGTTAG ATGACCTAAT TGATCTTGA AAATATCATT ATCTTGACCC	180
ATATATGACC ACCAAGCTGT TTCATCACAA ACCATGACAT ACTTAGCTAG TGCTTCATCT	240
TTTCTATAA GCTGACGTA TAATTGTC TGCTGCTCC GTTTTnCATG TACCGCGAGG	300
CGTAAnCTTA AAGGGCCCAA GGnCG	325

(2) INFORMATION FOR SEQ ID NO: 4472:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4472:

CCCGTCTTTC GCTACTCACA CCGGCATTCT CACTTCAG CGCTCCACAT GTCTTACGA	60
TCATGCTTCA ACGCCCTTAG AACGCTCTCC TACCATTGTC CAAAGGACAA TCCACAGCTT	120
CGGTAATATG TTTAGCCCCG TACATTTCG GGGGCAGTGT CACTCGACTA GTGAGCTATT	180
ACGCACCTTT TAAATGATGG GCTGCTTCTA AGnCAACATC CTAGTTGGTC TGGGGCAACG	240
CCACATCCTT TTTCCACTTT AACAnATATT TTGGGA	276

(2) INFORMATION FOR SEQ ID NO: 4473:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4473:

AATTTnCCAA AAAATTCAAA TGGCTCATT ACCAAAAGGT AAACCTCCGC CTTTAAnTTT	60
CTTaATGCAT kGTCTAACAA CCGCTTCCTT TAAAAgAATA GATTGTCAAG CGCTCGCATA	120
AGCAATATCA CTTAACCAA AAAATATTG AATGTTAAAT AAACATTCAA AACTGAATAC	180
AATATGTCAC GTTATTCCGC ATCTTCTGAA GAAGATGTT CGAATATATC CTTAGAAAGG	240
AGGTGATCCA GCCGCACCTT CCGATACGGC TACCTtGTTA CGACTTCACC CCAATnCATT	300
TGTCCCACCT TCGACGGGCT AGCTCCGAAA AGG	333

(2) INFORMATION FOR SEQ ID NO: 4474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4474:

TATAAAATAG CAACGTTATT CCAATTATCT TAATGGTTAT CTTATCCTCA ACTAAATTGG	60
AGGAATCACT ATGACAATTA ATAAAGTAAC CGTTCTGGC GCAGGCACAA TGGGCGCTCA	120
ACTGGCAGCA CTTTTGTGA ATGCTGGACT TAAAGTAAAnA CTATTAGATA TTGTAGTG	180
CAAAAACGAT CCnAATCTCA TTGCGAAAAA ATCTTACGGT TAAATTACAG GTAAGAACG	240
GCCGCTACTA TTCGnCTTAA ATCTAGCGGT CATTACCAT ATGGTATTGTT GATGTGCTTG	300
GTAAATGTGT GCTGTTGAT ATCGA	325

(2) INFORMATION FOR SEQ ID NO: 4475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4475:

TAAC TGCGGC AACATTGCT TGTTTGGTT ATGGTTGGCA CATTGATGTC GGCATTCATA	60
CAATACATCT AGTATTATCT GGTATTTTG ATCGTTATCC AAAGTAAAT AATGATTATT	120
GGACATTGGG GTGAGTTAT CCCATTCTC TTAGAAACGT ATGGATGAAG CTTATTCGCT	180
GACATTnAC CACCCTGTAA GCTATACTTT AAAATAATT TTTAATCACA CCGAGTGGCA	240

TGTTAACGAG CCACAGTTG ATTTAGTCAA GAAAGnAGAGG TATTGTAGAn TCTTATGCGC 300

TGATATCC 308

(2) INFORMATION FOR SEQ ID NO: 4476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4476:

ATGATATGCT GTATATCCC CCAGCGCCTC CACGTAAC TA GCGCTCACGT TTCA~~AGG~~GCT 60

CCTACCTATC CTGTACAAGC TGTGCCGAAT TnCAATATCA GGCTACAGTA AAGCTCCACG 120

GGGTCTTCC GTTCCTGTG CGGGTAACCT GCATCTTCAC AGGTACTATG ATTTCACCGA 180

GTCTCTCGTT GAGACAGTGC CCAAATCGTT ACGCCCTTCG TGCGGGTCGG AACTTACnCG 240

ACAAGGAATT TCGCTACCTT TAGGACCGTT ATAGTTACGG 280

(2) INFORMATION FOR SEQ ID NO: 4477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4477:

GCTAAGAACCC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCTCTCCT TCGGCTCTCG 60

CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTC TCGTTTCGTC AGATTCAAAC 120

GTTCCTACTT CGCCAAGCCA TTTTCTTTG TTTTACTTT TTATTTGAC GTTTAGACA 180

TAAAAAAAGA GACCTCACGG nCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA 240

ATTGGGCTAC CATCGnCGCT AAAGACCTTT CTTGACTTG 279

(2) INFORMATION FOR SEQ ID NO: 4478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4478:

GAGGATCCCC	GAATGTTGAA	CCCATCACTG	ATTCTGGTTC	ATAATTATCC	ACATCCATA	60
ACGTTAAATC	TAAAGCGTGT	GTACCGATAT	CGATTAATGG	TCCTCCACCT	TGAGCTTCTT	120
CGTCTAGAAA	GACACCCCAT	GTTGGnACTG	CTCGACGACG	AATGGCATGT	GCCTTCCGA	180
AGTAAATGTC	TCCTAAGTCG	CCACGTTGCG	CTGCTTGATG	TAAAAATTGA	CTATCTGCTC	240
GGAnACGATT	TTGATAACCT	ATTGTTAATT	TT			272

(2) INFORMATION FOR SEQ ID NO: 4479:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4479:

GAAATTGGGA	ATCCAATT	TTTGTGTTGG	GGCCCATCCC	CAACTTGCAC	ATTATTGTAA	60
GCTGACTTTT	CGTCnCTTAC	TGTGTTGGGG	CCCTCACCCC	AACTCGCATT	GCCTGGTAGA	120
ATTCTTTTC	GAAATTCTCT	GTGTTGGGEC	CCCTGACTAG	AATTGAAAAAA	AGCTTGTAC	180
AAGCGCATT	TCGTTCAAGTC	AACTACTGCC	AATATAACTT	CGTAGAGCAT	AGAATATTGA	240
TTTATGTCCC	AGCCTGAGTT	AATTT				265

(2) INFORMATION FOR SEQ ID NO: 4480:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4480:

ACATAGAAAT	GCCACTTTA	CAAACAAATG	AATATTCGTC	TTTTAC AC C	ATTACGCATA	60
ATAAAAGAAG	CTAACGACA	TGTAAACC GT	TGTCACTTAA	CTTCTTGT	TTCCGATGAC	120
AGCTTCTATT	TAGAGAATGT	CATGATTATT	TTATATT	CAC TTCAATGTTA	TCAATATTAG	180
TGCCATCTAT	GACGTCTGCC	ATACGATGCT	CTGGCAGTTT	TTGGTGGTA	ATTCAAACGT	240
ATATTCCCAC	CGTTTCATT	TAATAACGTT	GTCCnGGACC	CATGTACCGT	AAGATATGTT	300
TTCATAGTGG	TTCCAATTAA	ACCAAnTCTTC	AGGAACCTCn	TAG		343

(2) INFORMATION FOR SEQ ID NO: 4481:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4481:

ACTGCGGCAA TAGCAGCAGC ACCACAAACG GCCTGTGTCC GGACACCTAG GTAATAATGC	60
GCATGTTTT GTCACCAGTC CAAAGTTTG TTGACAAAGA GCATCATTAC AATACTGGAA	120
AATAACGACA CCTACATCGA TGGCTAATAG TTTACTACCT TGACCGATAA TATCGAATAT	180
ATTGAGTTTA AGTCCATATA GGATGATTGC AAATCTTAAT AAATATTTAG ATGAAAACGT	240
AATACCTGAG CTATATTGnT CAGGATATCC TCTAGAGTGA CGATAnAG	288

(2) INFORMATION FOR SEQ ID NO: 4482:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4482:

GAGGCATCCC CGGGCCTTCC TTCCCAACAG TCGCTTCAAA GTTTGGTGGT AACCTGnTA	60
CATCAAATTA TCGGTGCTAC TGTnAGGTAC GTGTAATCTT CGCTATTTA TTAGCCGTAT	120
CACATCAAGT GGCTTCCCTA CTGGAACCAA TTTGCTATTG GCCTTATTAT CAGGTGCAGG	180
ATGGGGATTC GGACAAATCA TTACATTTAA AGCGTTCGAA TTAGTCGGCT CATCTCGTGG	240
CCATGCCAGT CACAAACAGCA TTCCAATTAT TAGGCGCATC TTTATGGGG	289

(2) INFORMATION FOR SEQ ID NO: 4483:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4483:

AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC ATCGCATTCA	60
TTTCTTGTCT AGCAACGTTA TACTCTAGCG GAACGTAAGT TAGCTACCAT CCTCGCTAAG	120
AACCTTTCTT GACTTGTGAC AATCGCTTGC TTCTTCCTC TCCTTCGGCT CTCGCTTACT	180
CATTTAGCTC TACTAAACTC GTTGCCTCT TTTCTCGTTT CGTCAGATTC AAACGTTnC	240
ACTTCGCCAA GnCATTTTC TTTG	264

(2) INFORMATION FOR SEQ ID NO: 4484:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4484:

CTGTACCACC TATAATCGTT TTAATCGATT GGGGGACGCA TAGGATAGGC GAnGTGGCGA	60
TTGGATTGCA CGTCTAACGCA GTAAGGCTGA GTATTAGGCA AATCCGGTAC TCGTTAAGGC	120
TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCAAGTCGT TGATTCACA CTGCCGAGAA	810
nAAGCCTCTA GATAGAAAAA GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG	240
AATTCTAAGG TGAGCGAGCG A	261

(2) INFORMATION FOR SEQ ID NO: 4485:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4485:

ATGCAGCTAT TATTTTGAC AGATTCCATA TCGTTCAACA TTTAAATAGA GAACTTAATA	60
AGTATCGTGT ACAAGTTATG AATGAATACC GTAATAAAA AGGACCTGAT TATACAATT	120
TTAAGAATAA CTGGAAAGTC CTATTGATGG ATACTAGTAA AACCATATT AGTAAATACA	180
GATGGAnTAA ATCTTTAAG GCTTATAAAC GCTCATCTGA CATTGTAGAn GTCATGCTTT	240
CAAAAGACGA TATACTACGA C	261

(2) INFORMATION FOR SEQ ID NO: 4486:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4486:

AGCAACATGA TGCACCTCTC GTGTCTCACC AGATTAGCG ACTAAACTTG TAGACATACG	60
TAAATCTGCT TTAATAAGTA ATTnATGCAC ATGACTTATT GCGAGTAACA TCGGCATTGC	120
AAAGCCATTG CTATCAACTA ATCCACTATC ATCTAACACT AGAnTTGAG CGCCTTGCTT	180

TACAGCATTC ACTGCTTCTC GGCCTAATGC TTCTAACGCA TCTTCCAAAT CCCCTTCATA	240
TACCGTTGAT AAATAAGTTA	260

(2) INFORMATION FOR SEQ ID NO: 4487:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4487:

ATGAGGTGCA TAGGGATAAAA ACAGnnAGCA GCAATTGTC GCTATTGTA AATTGTATCC	60
TGGCTTAAGT TGCCATTTC TCATATGGTC TTCCTTCATT CTCATAAAAG TTGCATCATG	120
ATCAGTTTA GAAAAGCTAT TTCTATCTT AAGAATCGAT TTTTGTCTT CATATTTATT	180
TTTCCTTCG GAATAATCAT CAAATTATT TTTGAACCTC TTAATCTTAG TTCTTTTA	240
CGGGTCTGTT TTCCAATTG AGTACTATCC TCGTTCCC@ ATAGAATGAA TTAAACCTT	300
CCGATTCCT TTAAnC	316

(2) INFORMATION FOR SEQ ID NO: 4488:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4488:

CACTTTACT GCTAAAACGT CAATTGTTGA TGAGTCGTGT TTTATCTCAA GATGTGTTAC	60
TCAAAAAGTT ATAGAAGAAG CTACTAAAGT TAAAACAGAG ATTGATACTG CCAGAAGA@	120
ACTGTATCTC TCCATCTACT GTAAGTCCGT ATTAGAACTA AAGCGGCTAA TTCATTACGA	180
ATTAACCCCT TTAATTGTTT GCCAGACACA TCGCTATGGA TGAATTAAA GCGTnAAAAT	240
GTACTGGATC ATGAGTTCAT TTTTATAGnT ATGTACnCAT GTGTATAGTA TTTAGAAATA	300
GACTCAA	307

(2) INFORMATION FOR SEQ ID NO: 4489:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4489:

TTGGCAAATG TCATATAACT AGTAACATGA TCATCGACAT CAAATTAGT ATGATCAAAT	60
GTTCCCCAAT CATTAATTG ATT CGGTGT TTGCTCAATT GATTATATGT TTTCCCTAGC	120
ACTTCATGCG GCACCATATC TTTACCTAGT AGCCCACAA AGATAAGTCT AACAA GTGGC	180
ACCATAATCG ATAAA CTACC GCCACCTGCA CGCTTATGGT AAAACACCCA GCCAGCACTT	240
ACGCTACGCA TCGCTGTACA CGTGCTACTA AGGTTACCAC CACACTGATT CAATGCTTT	300
TAGCAGTATG CCACnCCGGn GACGATATGG TAGCGACGTA AnAA	344

(2) INFORMATION FOR SEQ ID NO: 4490:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4490:

CCCAACCGGC ACATTGTTGT AAGCTGACTA TATGTCACTT CnTGTGTTGG GGCCCCTGTC	60
TTCGACTGGC ACTGCTCCCT CAGGAGTCTC GCCATTAATA CTACGTATTA ACATGTAATT	120
TTACTTTAA ATACTTTAAA AAAATAAGAC ACTTTGGTCC AACTTAAGCC AGGGATAACAA	180
TTTACAAATA GCGACAAATT CTCAATTGT nTTATCCTAT GGACCTATTT CAAAACCCAA	240
CAGGTACTnA GTAACTTGA ATTCCATTAA TTAACAATGG ATTGCAAAAT GACCTTACGG	300
TTCATTTGAC CGG	313

(2) INFORMATION FOR SEQ ID NO: 4491:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4491:

AGGTCTGACT CTAGAGGATC CCCGATGAGT TAAAGAAAA ATATCAAACA CCTGAATTAT	60
ATTTTAAAGC TTGGCAAGGT TTTTACCAACG AGGTTCACAA TGAGCCAGAA CGTGATGAAG	120
TAATGCGTTA TATTCTGACT TTCTTAAATA ACAGCGTCAA TACAATGGC TTTATTGTTG	180
AAGATGACGA AATTGTAGAA ATTAAATATT CTAAAAAGGT TGGGACATAA ATCCCTAAA	240
AACAGCAGTA AGATAATTAA CCATTAGAAA ATATCTTACT GCTGTGCnCn A	291

(2) INFORMATION FOR SEQ ID NO: 4492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4492:

GCCGTCTAG CCTTGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAATACT	60
ACGTATTAAC ATGTAATTTC ACTTGAAAT ACTAAAAAAA ATAAAACACT TTGCCCAACT	120
TACACTACCA ATAGAAACTG CTGTTAGAAT TCCTCAAAAT GATATTTCGC GATATGTTAA	180
TGAAATTGTT AAAAAGATAG CTGATAGCGA GATTCGATGG AATTCAAGACA TCATCGTGGG	240
CGAACACATCC TATCATCTAA AAATGATGTT AAAAATCACC TGCATATTGC ATATACTGCA	300
ATCTGGAATT TTCTGGGCCG TGAGAATGAG AAAATnGAC nTCATGAACA GTGATTGCGA	360
ATGGATGTGG GTTAAGCTnC AAGATTCAAA CACCTTGCGnT	400

(2) INFORMATION FOR SEQ ID NO: 4493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4493:

TGATCCAGAG ATTTCCGAAT GGGGAAACCC AGCATGAGTT ATGTCATGTT ATCGATATGT	60
GAATACATAG CATATCAGAA GGCACACCCG GTAGAACTGA AACATCTTAG TACCGGAGG	120
AAGAGAAAGA AAATTCGnTT CCCTTAGTAG CGCGAGCGA AACGGGAAGA GCCCAAACCA	180
ACAAGCTTGC TTGTTGGGGT TGTAGGACAC TCTATACGGA GTTACAAAGG AnGACATTAG	240
ACGAATCATC TGGAAAGGTG AATCA	265

(2) INFORMATION FOR SEQ ID NO: 4494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4494:

CATTACTAAA AAAGATAATC AAGGTATGAT TTCACGCGAT GTTCAGAAT ACATGATTAC	60
TAAGGAAGAG ATTCCTTGA AAGAGCTTGA TTTAAATTG AGAAAACAAC TTATTGAAAA	120
ACATAATCTT TACGGTAACA TGGGTTCAAGG ACAATCGTT ATTAAAATGA AAAACGGTGG	180
GAAATATAACG TTTGAATTAC ACAAAAAACT GCAAnGAGCAT CGTATGGCA GACGTCATAG	240
ATGGGCCCTA TATTGATACC ATTGGAGGTG AATnTAAATA ACCATGCAC TCT	293

(2) INFORMATION FOR SEQ ID NO: 4495:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4495:

ACTTACAAAG TTCTGTGAAC CAAGTACCAT CAACTGCTGG TATGACGCAA CAAAGTATTG	60
ATAACTATAA TGCAGAGAAG CGTGAAGCAG AAACTGAAAT AACTGCAGCTAACGTGTTA	120
TTGACAATGG CGATGCAACT GCACAACAAA TTTCAGATGA AAAACATCGT GTGCGATAAC	180
GCATTTAACCA GCATTnAACAC CAAGCGAAAC ATGAnTTTAA CTGCAGATTA CACATGCCTT	240
AGGAGCAAGC AGTGCA	256

(2) INFORMATION FOR SEQ ID NO: 4496:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4496:

GTCATCAGAA ACCCTTGTCA CACAAGGCTT GTATTTTTA TACTTATTAA TTAAATTAAA	60
TTCATCATTAA TCTAATTAA ACAATATAC TAAACGTTTC ATAATTATCG CCTGTACAAT	120
ACGCACAAAA ACATGTCTTG AAACGCCTT CATTACTCTA AnATACCCAA TATACTTTT	180
ATATCGTTCG GATTCTGAGT ATTTCAAGACG ATTTCTGCA TAnAAATAAA CGTGTTCAA	240
GGCAATATAT TGCA	254

(2) INFORMATION FOR SEQ ID NO: 4497:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4497:

AATCGGCTGT	CTGATTCTGA	ATCGCTATCT	GAGTCCGAAT	CGnTATCTGA	ATCCGAGTCG	60
CTATCCGAGT	CTGAGTCGCT	ATCTGAATCC	GAGTCACTGT	CGGAGGGAA	ATCACTATCT	120
GAATCCGAAT	CACTCGCTGA	ATCCGAATCA	CTGTCTGAGT	CTGAGTCACT	GTCGGAATCT	180
GAGTCACTGT	CGGAATCTGA	ATCGCTATCT	GAATCCGAAG	TCACTGGTCG	GGAATCTGAG	240
TCACTGTnGG	AATCTGAATC	GCTATCTGA				269

(2) INFORMATION FOR SEQ ID NO: 4498:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4498:

CACCCCGGCA	CTATAAAAAT	GGAGCAGAAG	ACGGGATTG	AACCCGCGAC	CCCAACCTTG	60
GCAAGGTTGT	ATTCTACCGC	TGAACTA	CTGCATATGC	GGGTGAAGGG	AGTCGAACCC	120
CCACGCCGTA	AGCTTAGnAT	ACCTCAAGTC	TAGTGCCTCT	GCCAATTCCG	CCACACCCGC	180
AAATGGTGAG	CCATAGAGGA	TTCGAACCTC	TGACCCTCTG	ATTAAAAC	TCAGATGCTCTA	240
CCAAC	TAAATGGCTC	TTnCAGGTGC	CGG			273

(2) INFORMATION FOR SEQ ID NO: 4499:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4499:

GTAGTAAAAC	GCATTTAGTG	ATTGAAACAG	GCAAGATAGA	CGCGGGATAT	CACGGCAATT	60
TAGGGATTAA	TATCAAGAAT	GACGCTATTG	CATCGAATGG	TATATCACA	CCAGGTGTTT	120
TTGAATATTA	AAAGGAGAAT	CGATTTGAAG	TGCnnCATAA	GACAATACGG	ACTTATCAA	180
TCAACGAAGG	AGACAAACTA	GCTCAATTGG	TTATCGTGCC	TATATGGACA	CCTGAAC	240
AGCAAGTGG	GGAATTGAA	GTTGTTCAAnA	CGTGGAGAAA	AGGCTCGGAG	AGCGGGTGAA	300
AGCATCTTAG	TCGA					314

(2) INFORMATION FOR SEQ ID NO: 4500:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4500:

ATTGTAAGGC TATCATGTCA AAGATTATAA CAATAAATCT GGTTGAGATT TGGTGGCGGG	60
GCGATGGAAG CTATCTATTT GACCATCCAT TTGGCAAAGG TTTGGGAGTT ACACAGGTGG	120
ACTTAACTTT AATGGCGGTC GTCACTATGG TATCGACTTT GGTATGCCATA CAGGAACGAA	180
CCATTTATGC TGTTAAAAGG CGGTATAGCT GATAAAGTAT GGnCTGATTA CGGTGGCGGT	240
AATTCTATAC AAATTAGGAC CGGTGCTAAC GAATGGAnCT GGTATATGCA TTTATCTAnG	300
CATT	304

(2) INFORMATION FOR SEQ ID NO: 4501:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4501:

TTCCTTCATT CTCATAAAAG TTGCATCATG ATCAGATCAG TTTTAGAAAA ACTATTTCTA	60
TCTTTAAGAA TCGATTTTG TTCTTCATAT TTATTTTTTC TTTCGGnATA ATCATCAAAT	120
TTCTTTTGAA ACTTCTTAAT CTCAGTTATT TTTTACGGG TCTGTTTCT AATTTGAGCA	180
CAATCTCGT TCTCAATAAG AATGATTAA ATCTnCGATT TCTTTATCTA AATGGACTAC	240
CAATTAAATC TAT	253

(2) INFORMATION FOR SEQ ID NO: 4502:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4502:

AGTCGGTCC CTATCCGTCG TGGCGTAGG AAATTTnGA GGAGCTGTCC TTAGTACGAG	60
AGGACCGGGA TGGACATACC TCTGGTGTAC CAGTTGTCGT GCCAAnGCAT AGCTGGGTAG	120

CTATGTGTGG ACGGGATAAG TGCTGAAGAT GCTTAAGCAT GAAGCCCCCC CAAGATGAGA 180
TTTCCCAACT TCGGTTATAA GATCCCTCAA AGATGATGAG GTTAATAGGT TCGAGGTGGA 240
AGCATGGTGA CATGTGG 257

(2) INFORMATION FOR SEQ ID NO: 4503:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4503:

ATACGTTAA TACACAAAAA ACTGCAAAGC ATCGATGGCA GACGTCATAG ATGGCACTAA 60
TATTGATAAC ATTGAAGTGA ATATAnAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA 120
TCGGAAAAAC AAGAACGTTAA GTGACAAGnT TTACATGTTG CTTAGCTTCT TTTATTATGC 180
GTAATGATGT AAAAAGACGA ATATTCAATT GTTGTAAGA GTGGCATTTC TATGTCTTAA 240
AAGTGACGAA ACTTCAAATG TGCCAAGTGT 270

(2) INFORMATION FOR SEQ ID NO: 4504:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4504:

TACCTTGACC GAAGTTCTTA CCTACATCAC CAAATTAAT GACATGTCCA CCAGTCATAT 60
ACTCTAATCC ATGGTCGCCG ATACCTTCAA CGACAACATC TACACCACTA TTTCTAATAC 120
AGAATCTTTC TCCTGCCTA CCGTTAATAA ATGCCTTACC ACTTGTCGCA CCATAGAATG 180
AGACGTTACC AGCAATAATT TCATTTGTC GTTCTTCAAAGGTGCTTG ACAATGACCG 240
TACCAACCnT 251

(2) INFORMATION FOR SEQ ID NO: 4505:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4505:

AGAAGTTAAC	CTCCTTAGCG	TCGATGGTAG	TCGAACCTAC	GTTCCCGCTA	GAGTAGAACG	60
TTGCCAGGCA	AATGACAAAT	CGGAGAATT	GCTCAGCTGG	GAGAGCATCT	GCCTTACAAG	120
CAGAGGGT	CGGGTTCGAA	CCCGTCATT	TCCACCATT	ATTCTTAGAT	ATAGCAGGCC	180
TAGCTCAATT	GGTAGAnCAC	TGACTTGTA	TCAGTAGGTT	GGGGGGTCAG	TCCTCTGGCC	240
GGCACCATCT	TTTGnCCATA					260

(2) INFORMATION FOR SEQ ID NO: 4506:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4506:

TTCTTAGTA	GATACTAAGG	CGTTATTAGA	CGCATTAGAC	AATGGTGTGA	TTAAAGGTGC	60
AGCACTTGAT	ACGTATGAAT	TTGAACGCAA	ACTTTCCC	AGTGATCAAA	GGGGCAAAAC	120
ACTGAACGAT	CCATTGTTAG	AATCGTTGAT	TGACAGGGAA	GATGTCATAT	TAACACCACA	180
TATTGCGTTT	TATACTGAAG	CTGCAGTTAA	AAATCTATTG	TCGTGCATTA	GGTGCAACAT	240
TAGGTGTATT	GCAGCTTGGG	GAACTTnGnT	ACGTTAAAT	TTAAAATCGG	CTGTGGGTAT	300
TTTGGnTTTT	GGG					313

(2) INFORMATION FOR SEQ ID NO: 4507:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4507:

GnCAATACGG	CCAATTCTA	AGATTGCTAC	TTCTGGGTGG	ATTGATAACT	GGAGTGAACC	60
ATTGTCCACC	AGCTGnAAC	GATATTACTG	ATTGTGCATG	TAGCACCTTT	CATTCATCG	120
GCTGTTAATT	TACCATCACG	TGGCTTTAAC	AGCTAATTCA	TTAATTTCAT	CTGAAATTG	180
GGAAAATAGA	CTTACGGATC	AGCATGTTA	ACAAACAGGTA	CTAATAATCC	TCTATCAGTG	240
TCTGCTGCAA	TT					252

(2) INFORMATION FOR SEQ ID NO: 4508:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4508:

CATCGAACCA GATGTACTCG CACTTGTGA GTCTGATGTT GAATCACTAA CACTATCAGA	60
TAATGACGTT GAATCACTCA TACTTGTGA TGTACTTGTC GAAAGCGACA TACTTTGTGA	120
ATCACTAGTA CTTGTACGCA TCGAAGTACT AGTTGAAGCT GATGTACTAC GAGAGTCACT	180
TGTTGATGTT GATGTACTTG CTGATCCTGA TGCACTTGTA CTTCTTGATG TGCTTTGTGA	240
ATCGGATTTC GCTCGTGCnT GGTACTnG	268

(2) INFORMATION FOR SEQ ID NO: 4509:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4509:

CGAGAGTGCG TTAATTCGGT TACTGCTATC ACgTAAGGGG CGGAAACCCC CTAACACTTA	60
GCACTCATCG TTTACGGCGT rGACTACCAG GGTATCTAAT CCTGTTGATCCCCACGCTT	120
TCGCACATCA GCGTCAGTTA CAGACCAGAA AGTCGCCTTC GCCACTGGTG TTCCTCCATA	180
TCTCTGCGCA TKTCACCGCT ACACATGGAA TTCCACTTTC CTCTGCTGGC ACTCAAGTTT	240
TCCAGTGTCC AATGACCCTC CACGGTTGAG CCGTGGGCTT nCACATCACA CTTAnA	296

(2) INFORMATION FOR SEQ ID NO: 4510:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4510:

TTACTACTTA CTGAGTGACC TGTACCTGCT TTGGAGTAA TTGTGATTGA TGAATTTGGT	60
TTTATAGTAT TGGCATTGAA CGTCACTTTA CCAGTTGTG CATCTAACGT TACATAGTCA	120
GGCTTATTGCA CAATTGTCCA TTGnTTATT TGACCAACGAA CAACATTAAT TGTCTTACTA	180
TGTTGCTGCA CCATTACCCA CTTnTCAAGT GTAAGCAATA TCCATTGCTT GAGTTGGGAT	240

(2) INFORMATION FOR SEQ ID NO: 4511:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4511:

AAAATCACAT CAGCCTGCAT TAACGACGTC GTTAATTAT ATACATCTCC TGTAGTATCT	60
AGATAATTCT TTCCAACGCT AAATTCTAAT TCAAGTTCTC GTAAATCCAT CAACTCTATT	120
TGATGTCCCT CATTGATGAC TTCTAGTTCA TTTTTAAAT CATCCATAGC AATTCTCGTT	180
TTAGAACCTA CTGTGGAACC TGACAATAAT ACAATATTCA nGAnGACGCC CCTCCTATTT	240
TGATAAATGC	250

(2) INFORMATION FOR SEQ ID NO: 4512:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4512:

AGCTGGnTTC GAACCAACGA GTGACGGAGT nAAAGTCCGT TGCCTTACCG CTTGGCTATA	60
GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTGAACTG CCGAACCGA AGAGCGGATT	120
TACAGTCCGC CGCGTTAGC CACTTCGCTA CCCCTCCAGC TTATTCATAT AATTTAATAA	180
TCAAAATGGT GGAAGAATGA CGGTTGAA ACCGCCGACC CTCTGCTTGT AAGGCAGATG	240
CTCTCCCCAG CTG	253

(2) INFORMATION FOR SEQ ID NO: 4513:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4513:

GnCGACCCTT AATAACTTAA TCTATGTTTC CACCATTTT ATAAGTCAA CGTTAACATG	60
nAAGTTACGT TCTTTATAA AAAGATTTAA ACGCGTTATT AATCTGTGC AGTGTCTTT	120

CGAACACTAG CGATTATTC TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG	180
TTTGCTTGG TTAAAATCTA TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAAATAATG	240
GTTGGAGACTA GC	252

(2) INFORMATION FOR SEQ ID NO: 4514:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 244 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4514:

GTCATTGAAT ATGGAAACTT TAGAATTACA AGGCGCTAAA TTACGATACC ACCAAGTCGG	60
ACAAGGACCC GTGCTCATCT TTATTCCTGG TGCAAACGGT ACCGGAGACA TTTTCTGCC	120
TCTTGCAGAA CAGTTAAAAG ACCATTTAC TGTGTAGCC GTTGATCGTC GTGATTATGG	180
AGAAAGCGAG TTAACTGAAC CACTCCCTGA TTCCGCTTCA AACCCTGACA GTGATTATCG	240
TGTC	244

(2) INFORMATION FOR SEQ ID NO: 4515:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4515:

TATTAGGCAA ATCCGGTACT CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT	60
TCGAGTCGTT GATTCACAC TGCCGAGAAA AGCCTCTAA TAGAAAATAG GTGCCCGTAC	120
CGCAAACCGA CACAGGTAGT CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA	180
AGGAACTCGG CAAAATGACC CCGTAACCTTC GGGAGAAGGG GTGCTCTTTA GGGTTAACGC	240
CCA	243

(2) INFORMATION FOR SEQ ID NO: 4516:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4516:

ACTAGTCGAG	TGACACTGCG	CCGAAAATGT	ACCGGGGCTA	AACATATTAC	CGAAGCTGTG	60
GATTGTCCTT	TGGACAATGG	TAGGAGAGCG	TTCTAAGGGC	GTTGAAGCAT	GATCGTAAGG	120
ACATGTGGAG	CGCTTAGAAG	TGAGAATGCC	GGTGTGAGTA	GCGAAAGACG	GGTGAGAAC	180
CCGTCCACCG	ATTGACTAAG	GTTCAGAG	GAAGGCTCGT	CCGCTCTGGG	TTAGTCGGGT	240
CCCTAACCT	GAGGCCGCAA	nnGTAGG				267

(2) INFORMATION FOR SEQ ID NO: 4517:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4517:

TTGAATCTGA	CGAAACGAGA	AAAGAGCGCA	ACGAGTTAG	TAGAGCTAAA	TGAGTAAGCG	60
AGAGCCGAAG	AGAGGAAAGA	AGCAAGCGAT	TGTC&AAGT	CAAGAAAGGT	CTTAGCGAC	120
GATGGTAGCC	AACTTACGTT	CCGCTAGAGT	AGAACGTTGC	CAGGAAAAAA	ATGGGATGCG	180
ATGAGCCGCA	TTGGAGACCG	CAGTCCTnTn	TnTTTTTTA	TGGCCTTAAA	ACGTCAAAAT	240
TAAAAAGTTA	AACACAAAGA	AAATGGCCTT	TGGCGAGTGG	AAACGTTTG	AATCTGGACG	300
GAACGAGAAA	GAGCGCACG					319

(2) INFORMATION FOR SEQ ID NO: 4518:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4518:

GGTATAATAG	ATGACTATGT	ACTATTCG	GTACATCCTT	GGCAATATCA	GCATATTCTG	60
CCGAACGTCT	TTGCGAAAGA	GATTAGTGAA	AAGTTGGTTG	TACTATTACC	GTTAAAATTT	120
GGAGATTATC	TGCGTCTTC	AAGTATGCGT	TCATTAATTG	ATATTGGCGC	ACCGTATAAC	180
CATGTCAA ⁿ G	TACCATTGCA	AATGCAGTCA	TTAGGCGCAT	TAAGGCTAAC	GnCTACGGTT	240
ACATGAAAAAA	CGGGGAACA					259

(2) INFORMATION FOR SEQ ID NO: 4519:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4519:

ATAGGGTGT	GCTGAATAGG	GCGTTAGTA	TTGGTCGA	CCGnnAACCA	GGTGATCTAC	60
CCTTGGTCAG	GTTGAAGTTC	AGGTAACACT	GAATGGAGGA	CCGAACCGAC	TTACGTTGAA	120
AAGTGAGCGG	ATGAACTGAG	GGTAGCGGAG	AAATTCCAAT	CGAACCTGGG	AGATAGCTGG	180
TTCTCTCCGA	AATAGCTTTA	GGGCTAGCCT	CAAGTGATGA	TTATTGGAGG	TAGAGOATG	240
TTTGGACGAG	GGG					253

(2) INFORMATION FOR SEQ ID NO: 4520:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4520:

AACTCGTTGC	GCTCTTTCT	CGTTTCGTCA	GATTCAAACG	TTTTCACTTC	GCCAAGCCAT	60
TTTTCTTGT	GTTTACTTTT	TATTTGACG	TTTAGACAT	AAAAAAAGAG	ACCTCACGGT	120
CTCAACTTGC	CTGGCAACGT	TCTACTCTAG	CGGAACGTAA	GTTGGCnACC	ATCGTCGCTA	180
AAGACCTTTC	TTGACTnGTG	ACAATCGCTT	GCTTCTGTCC	TCTCCTTCGG	CTCTCGCTTA	240
CTCAT						245

(2) INFORMATION FOR SEQ ID NO: 4521:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4521:

GGGCCTAAGT	GGACTCGAAC	CACCGACCTC	ACGCTTATCA	GGCGTGCCT	CTAACCCAGCT	60
GAGCTATAGG	CCCATTAATT	TGAATGAACA	AACATTCAA	ACTGAATA	ATATGTCACG	120
TTATTCCGCA	TCTTCTGAAG	AAGATGTTCC	GAATATATCC	TTAGAAAGGA	GGTGATCCAG	180
CCGCACCTTC	CGATACGGCT	ACCTTGTAC	GACTTCACCC	CAATCATTG	TnCCACCTT	240

(2) INFORMATION FOR SEQ ID NO: 4522:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4522:

nATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGT TGATGGCGTG	60
CCTTTGTA AATGAACCGG CGAGTTACGA TTTGATGCAA GGTAAAGCAG TAAATGTGGA	120
GCCGTAGCGA AACGATGTCT GAATAGGGCG TTTAGTATTT GGTCGTAGAC CGAAACCTGG	180
TGATCTACCC TTGGTCAnGT TGAAGTTCA GTAACACTGA ATGGAGGACC GAACCGACTT	240
ACGTTTGAA	249

(2) INFORMATION FOR SEQ ID NO: 4523:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4523:

TCCCTATCCG TCGTGGCGT AGGAAATTG AGAGGGAGCTG TCCTTAGTAC GAGAGGACCG	60
GGATGGACAT ACCTCTGGTG TACCAATTGT CGTGCCAnG CATAGCTGGG TAGCTATGTG	120
TGGACGGGAT AAGTGCTGAA GATCTnAAGC ATGAAGCCCC CCTCAAGATG AGATTTCCA	180
CTTCGGTTAT AAGATCCCTC AAAGATGATG AGGTTAATAG GTTCGAGGTGGAAGCATGGT	240
GACAGTGG	248

(2) INFORMATION FOR SEQ ID NO: 4524:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4524:

AACGTTAAGA TCCCTATTAA ATTATCTTAG GAATCATCAT GGGCATTAT GATGTCTTAA	60
AGCTGGATAT CGACATACTT ATATATGGTT ACGGTGTCCC ATGGCTTACA TATTTTATA	120

AAATTAGTAA TCTGAATCTG CTTCTAAACC TTGTCATAAT TTGAnCGGCT GTGGCTCGnA	180
CCAATACGGG TCGGACCTGC TTnAACCAATT TTATTGGAAA TCTTCTAAAT TACGGACGGC	240
ACCCGGATGC TTTTACTTCT ATATCAGCAC CTACTGTATC TTTCATTAAT TAAACGGCTT	300
CTGCAGTCGG ACCGGCAACT GCAAAA	326

(2) INFORMATION FOR SEQ ID NO: 4525:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4525:

AAGAGCACCC TTCTCCGAGT TACGGGGTCA TTTGCCGGTT CCTTAACGAG AGTCGCTCGT	60
CACCTTAGAT TCTCATCTTG ACTACCTTGT CGGTTTGC GG TAnGGCACCT ATTTTCTATC	120
TAGAGGTTTT CTCGGCATGT GAAATCAAACG ACTCGAGACA CAATGCTTC TCCCATCACA	180
GTCAGCCTTA ACGAGTACCG GATTTGCCTA ATACTCAGCC TACTGCTTAG nGGCATCCAT	240
CGCAGTTnGC TATCCACTGG TCCCCCTCGA TTAAACGATT ATAGGTGGTA CAGATATCAA	300
C	301

(2) INFORMATION FOR SEQ ID NO: 4526:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4526:

TGATATTATG AGCTGTGTTT TTAGCTTAG AACCGAAGTC CCCTGCTTT TTACCAAGAT	60
TTTCAGTAAC TTGTnCCATC CATTTCCT TTTTCGTACC ACCATGGAAT TTTGGCAAAA	120
CACCCATCCG CTGTAACCTTC AGAGTGTAC TGGCATTAT TACACTATCT CCAACTCCTA	180
GTGGAACAAAC CACATCTCGT CTTGGGGTG CATGGAATGT nCCGTCAGCC CTGTGAATTA	240
T	241

(2) INFORMATION FOR SEQ ID NO: 4527:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4527:

CGATCACACT CTTCCGTCGT CATGCCATT GGCTTTCAC ACAATACATG GACACCATGG	60
TGTCAATGCT TCTATAGAAA GATCAGCATG GAATTATTAA GGGTACAAA TGACCACCGC	120
ATCAACAAGT TTAAACAGCT CGCTAGGTGT CTCAACTGCA TGAGGTATAT TGAAAGCGCT	180
TCGCAACCAT nCAATCATCT GGCAGTGTAA TTGAATATCT TGTGACTGGC AACTTAATGA	240
GnACTGTGTC TTTGGAGTT TCCAGnCAAT GCCGGGAATT ATGGACGGGT CTTGGTGGCA	300
ATACCACCCA ACACCT	316

(2) INFORMATION FOR SEQ ID NO: 4528:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4528:

GTCCCAAGGG TTGGGCTGTT CGCCCATTAA AGCGGTACCG ACGACTGGT TCAGAACGTC	60
GTGAGACAGT TCGGTCCCTA TCCGTCGTGG GCGTAGAAAT TTGAGAGGAG CTGTCCTTAG	120
TACGAGGAGG AnCGGGATGG ACATACCTCT GGTGnACCAG TTGTCGTGCC AACGGCATAG	180
CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAAGCAT CTAAGCATGA AGCCCCCCTC	240
AAGATGAGAT T	251

(2) INFORMATION FOR SEQ ID NO: 4529:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4529:

AGTACGTGAC GTTCACTACT CTCACTATGG CCGTATGTG CCAATTGAAA CACCTGAGGG	60
ACCAAACATT GGATTGATTA ACTCATTATC AAGTTATGCA CGTGTAAATG AATTGGCTT	120
TATTGAAACA CCATATCGTA AAGTTGATT AGGATACACA TGCTATCACT GATCAAATGA	180
CTATTAACAG CTGACCGAGAA GATAGCTATG TTGTAGCACA AGCAAACCTCT AATAGATGAA	240
ATGGTCGTTA AGGTGATGAG TGTATGCGTT CGGGnACnAT CAGTATGCAA GAAAAGGTTT	300

GTGACCGCAG AGTGTnA

318

(2) INFORMATION FOR SEQ ID NO: 4530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4530:

TAGCTGTGTG ATAAATTGCA AGTGCAGCAC CACATAAGCC GAACATCATC GTAATAAAAC	60
GGCCTGACAT ACAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGA TCACCAAAGTT	120
GAGCAAAGAn GATGTTCTnC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC	180
CAAAGTGCCGT CTGCCAAAC GGTAAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACCA	240

(2) INFORMATION FOR SEQ ID NO: 4531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4531:

CGGCTTTCT GGGACGTTAA CCCTAAAGTG CACCCTTCT CCCGAATTAC GGGGTCATTT	60
TGCCGAGTTC CTTAACGAGA TTGACTCGn TCACCTTAGA ATTCTCATCT TGACTACCTG	120
TGATCGGTTT GCGGTTAGGG GCACCTATTT TCTATCTAGA GGCTTTCTC GGCAGTGTGA	180
AATCAACGAC TCGAAGACAC AATGTCTTCT CCCCATCACA GCnCAGCCTT AACGAGTACC	240
GGATTTGCCT AATA	254

(2) INFORMATION FOR SEQ ID NO: 4532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4532:

CATTACGTAT AAATGGCAAT CGTGATACTA CAGGTACAAA TGACGCAAAC TGGTCAGCTA	60
TGAATAAACCG GAATGTGGCT AAAGTCGTTA ACGCAAATA TGACGTCATC TATAACGGAC	120

ATACTTTGC AACATCTTA CCAGCGnAAT TTGTAGTAAA AGATGTGCAA CCAGCGAnAC 180
CAACTGTGAC TGAAACAGCG GCAGGAGCGA TTACAATTGC ACCTGGAGCA AACCAAAC 238

(2) INFORMATION FOR SEQ ID NO: 4533:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4533:

GGTCATTAAT AAAATATCTA AAGCCATTAC TGCATAAAAA TCTCATCAAG CCAATACCTA 60
CATTGTACTA CTGGnCACTT TAGACAGGnC ~~A~~GGGTGTAG CTACCGATAA TTCAGGAGCA 120
TTAACGCAAC CGACATTGGA CTGTATTAAA TGATAGAGGT TCTGGAAAAC GCCCCAGGTG 180
GTGGAGTTCA AGAAATAATT CACAGGGCTG ACGGAACATT CCTGCACCCC AAGGACGAGA 240
TGTGGTTGTT CCACTAGGAG TTGGAA 266

(2) INFORMATION FOR SEQ ID NO: 4534:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 4534:

TACTCAGAGG ATACCCCGAC GTAATGCATT CAATTCAATT TTTAACGTA TTATTCATT 60
GAGCAGAAAG AAAATTATGG CACCAAACCTT TAATATTTTT TTCAATGTCA TTCTTTGAn 120
GGGAGTGGGA CAGAAATGAT ATTTTCGCAA AATTTATTTC GTCGTCCCAC CCCAACTTGG 180
CATTGTCTGT AGAAATTGGG AATCCAATT CTCTTTGTnG GGGCCCATCC CCAACTTGCA 240
CATTATTGTA AGCTGACTTT TCGT 264

(2) INFORMATION FOR SEQ ID NO: 4535:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4535:

GCGAATGGAT AACAGTTGAT ATTCTGTAC CACCTGATAA ATCGTTTAA TCGATGGGGG 60

GACGCATAGG nATAGGCGAC TGCCGAT~~E~~ ATTGCAC~~T~~C AAGCAGTAAG GCTGAGTATT 120
AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA 180
GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AAATAGGTGC CCCGTACnGC 240
AAACCGACAC 250

(2) INFORMATION FOR SEQ ID NO: 4536:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4536:

AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 60
AATTCTCCGA TTTAAA~~ACT~~G CCTGGCAACG TTCTACTCTA GCGGAAnTAA TTCGA~~ACT~~AC 120
CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180
TATAGTCACC AGACATATGA ATGTAATT~~T~~A TACATTCAAA ACTAnATAGT AAGTA 235

(2) INFORMATION FOR SEQ ID NO: 4537:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4537:

TGCATCTTCA CAGGTACTAT GATT~~C~~ACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60
TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TT~~C~~GCTACCT TAGGACC~~G~~TT 120
ATAGTTACGG CCGCCGTTA CTG~~G~~GGCTTC GATT~~C~~TAGC TT~~C~~GCAGAAG CTAACC~~A~~CTC 180
CTCTTAACCT TCCAGCACCG GGCAGGCGTC AGCCCTATAC ATCACCTTAC GGTT 234

(2) INFORMATION FOR SEQ ID NO: 4538:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4538:

ACCCCTCTGCT TGTnAGGCAG ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACACTGC 60
CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGACTACC ATC~~A~~CGCTA AGGAGCTTAA 120
CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 180
TGTAAATTAT ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTGCTTC GCAAACCATT 240
TA 242

(2) INFORMATION FOR SEQ ID NO: 4539:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4539:

TCATTAACAC CATCACCATATAATAAACCT TCCATATCTG TTCCTGTGCC AATAAAGCCA 60
TATTGCGTTT GGnCTGTCGT GCCAGTGCAA GATTCCAAC GATAATTCT AGGCGTCACT 120
GCTGGCGAAC CATCTAATGG ATAATCATAA TCCATCGTGC GTCCAAGAAG TACTTGnTTT 180
ATTTAAAGTT TGTATTGTGG AATCCTGTGC ACATGTTCTC ACTCCTCTGT ACCT 234

(2) INFORMATION FOR SEQ ID NO: 4540:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4540:

ACACAAAGAA AAATGGCTTG GCGAAGTGAA AACnGTTGAA TCTGACGAAA CGAGAAAAGA 60
GCGCAACGAG TTTAGTAGAG CTAATGAGT AAGCGAGACC GAAGAGAGGA AAGAACGnAG 120
CGATTGTCAC AAGTCAAGAA AGGTTCTTAG CGAGGATGGTAGCTAACTTA CGTTCCGCTA 180
GAGTAGAACG TTGCTAGACA AGAAATGAAT GCGATGAGCC GCATTGAGTG TGAAATTGAT 240
AT 242

(2) INFORMATION FOR SEQ ID NO: 4541:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4541:

GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA GTCAAACGCT CACATACGGC	60
TTCGTTTCA TTATTTAAA TGCTCATTAA CATAAGTAAA CTCTGCTTTA AAATAATTAA	120
ACTCATTGTC TGCTAACGT TTTCTTTAT AAAAGATT AAACGCGTTA TTAATCTTGT	180
GnAGTGTCT TTCGAACATA GGCGATTATn TCTTATGAAT TCAAGCTTAT TTAAACTCT	240

(2) INFORMATION FOR SEQ ID NO: 4542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4542:

AAGCTAGCAA TGATGTCAAG CAATGGCAAC ATGTGCTCAn TTAGCTAATA TGCAAGCACA	60
TGGTGAATAT GACGAGGTTG CAACTTCAAC GGCGAGGnTG ATGAATGCCT TACGTTGCG	120
TGAGACAGTA GCTATGGGCC GCGGTATTAC AGGTGGTAAT GGCATACTGA GCTGACGATT	180
ATGATATTGT CACGTTTCT TCTCTGTATG CAGAAGGGAT TTACACGTAC GAGGTACACA	240
TG	242

(2) INFORMATION FOR SEQ ID NO: 4543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4543:

TGGTGAGCCA TAGAGGATTC GAACCTCTGA CCCTCTGATT AAAAGTCAGA TGCTCTACCA	60
ACTGAGCTAA TGGCTCTTCC ATGGTGCCGG CCAGAGGACT TGAACCCCCA ACCTAQTAT	120
TACAAGTCAG TTGCTCTACC AATTGAGCTA GGCGGCAAT ATGTAAGATT AAATGGTGGAA	180
GAntGACGGG TTCGAACCGC CGACCCTCTG CTTGTAAGGC AGATGCTCTn CCAGCTGAG	239

(2) INFORMATION FOR SEQ ID NO: 4544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4544:

ATAGAGGATT CGAACCTCTG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC AACTGAGCTA	60
ATGGCTCTTC CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA	120
GTTGCTCTAC CAATTGAGCT AGGCCGGCAA TATGTAAGAA TAAATGGTGG AGAATGACGG	180
GTTCGAACCG nCGACCCCTCT GCTTGTAAGG CAGATGCTCT nCCAGCTGAG CTAAATTCT	239

(2) INFORMATION FOR SEQ ID NO: 4545:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 233 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4545:

AATTCATGCT TTCAAAAGAC GATATACTAC GACACTCCTA CGAACTTGTC CAAGGATTAC	60
GAAAAGACCT AAGGTTATGT AATTGGCCTA AATTATTAA TCGTTAAAT TCAGTTAGTA	120
AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAnATA TTATAGAAAA CATCAAAGGA	180
TGTTAAGAAA TACnATTAT TACCCAGCAT TTAATAATGG TGCTATAGAA GGA	233

(2) INFORMATION FOR SEQ ID NO: 4546:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4546:

ACTTTGTTGT CTTCCATCAA CTTGAGACTT CATAACGTTT TGCATCTTCG CCACCTTCAC	60
CACTATTACT CTTTCCACCT AATTGGTTCA TGGCTTGTGC TAnTTTTCA TGTGCTTCCG	120
CTGAAATCGA TCCATAACTC ATCGCCCCGT TATTAAGCG TTTGACAATG TCACTTACCG	180
GTTCAACTTG GnCGATGTCA ATCGGTGTAC ATGCTTAAA TTCAAGTAAA TGTCTAATGT	240
GATCTGT	247

(2) INFORMATION FOR SEQ ID NO: 4547:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4547:

GAGGAAATT	CTGAAAACAA	TCATCATATT	TCTCATTCTG	GTTTAGGAAC	TGAAAATGGT	60
CACGGTAATT	ATGGCGTGAT	TGA A AAATC	GAAGAAAATA	GCCACGTGGA	TATTAAGAGT	120
GAATTAGGTT	ACGAAGGTGG	CCAAAATAGC	GGTAATCCAG	TGCATTGAG	GAAGACACAG	180
AAGAAGTTA	AACCGAAATA	TGnAACCAAG	GTGGGCATTA	TCGTTGGTTA	TCGATTTCG	240
ATAGTGTACC	TCAAATTTCA	TGGGTCCAAA	TTAATGGTTA	ACCCATCCATTGAnGnAGG		300

(2) INFORMATION FOR SEQ ID NO: 4548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4548:

TTGCTATAGT	CACCAGACAT	ATGAATGTAA	ATTATACATT	CAAAACTAGA	TAGTAAGTCA	60
AAGTGATTT	GCTTCGCAAA	CATTTATTT	GATTAAGTCT	TCGATCGATT	AGTATTGTC	120
AGCTCCACAT	GTCACCATGC	TTCCACCTCG	AACCTATTAA	CCTCATCATC	TTTGAGGGGA	180
TCTTGATAAA	CCGnAAGTTG	GGGAAATCTC	ATCTTACGG	GGGGGCTTCA	TGCTTAGGAT	240
GGCTTTnCAG	CACTTATGC	CCGGTnCCAC	ACATTAGGCT	TACCCAGCCT	ATGCCCGTT	300
GGCACG						306

(2) INFORMATION FOR SEQ ID NO: 4549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4549:

ATTCGATT	GTGATTTGA	ATACTTTCT	TCCACACAAA	TGTATACCTA	TTGGCATTAG	60
CTTCTACTTT	TGTACCATCA	ATAAGATTT	GCTTAAACA	TTGACTATGA	AACTGGATAA	120
ATAAAAGATT	AATTAACGCA	TCAGTATTAG	GATTCACTCT	AATACGATTA	ATAGTTTAT	180
AAGAAGGTGn	TTGATTTGA	GCTAACACACA	TCATTCGAAT	ACTGT A TGn	AG	232

(2) INFORMATION FOR SEQ ID NO: 4550:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4550:

CTGGGTTCA	AACGTCGTAT	GnAGTTCGGA	TCCCTATCCG	TCGTGGCGT	AGGAAATTG	60
AGAGGAGCTG	TCCTTAGTAC	GAGAGGACCG	GGATGGACAT	ACCTCTGGTG	TACCAGTTGT	120
CGTGCCAnG	CATAAGCTGG	GTAGCTATGT	GTGGACGGGA	TAAGTGCTGA	AACATTCTTA	80
AGCATGAAGC	CCCCCTCAAG	ATGAGATTTC	CCAACTTCGG	TTATAAGATC	CCTCAAAGAT	240
GATGAAGTTA	ATAAGTTC					258

(2) INFORMATION FOR SEQ ID NO: 4551:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4551:

TTACAGGCAT	GCGAGTTGGG	GTGAGGGCCC	ACACAGAAC	TGACGAAAAG	TCATGACAAT	60
AATGTGCAAG	TTGGGGATGG	GCCCACAAAG	AGAAATTGGA	TTCCCAATT	TACAGACAAT	120
GCAAGTTGGG	TGGGACGACG	AAATAAATT	GCGAAAATAT	CATTCTGTn	CCCTCCCTCA	180
AAAGATGACA	TTGAAAAAAT	ATTAAAGTTG	GTGCCATATT	TTCTTCTGCT	CATGAATATA	240
CGTTAAAATT	GATTGATCAT	CGCGAATTGA	TATTATTCTC	ATATAAAA	TACTTATTAC	300
ACTTACCGTA	TGATAGTTG	nTATATACTC	TGATAAAGTC	AAACCTAATA	GCGTTCTAG	360
CTGTGnGTGT	TTCATAATTA	TATACATTAT	CAGGCTTTAA			400

(2) INFORMATION FOR SEQ ID NO: 4552:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4552:

ATAGGAAACT	GCCAATTGGA	CGGTTGCCGC	ATTCAAACCC	AGCACGATTA	CGGCGAATTG	60
CACGTGAAAnC	ATTTCTACAG	CTTGATCTTG	ACCTATGATT	TTACTTCTTA	AACGATTAGA	120

AATATTTTTT AAACGTTCAA TATCGTTATC ATCCATTGG AGAAACTGGG AATACCATTG 180
AATCGTTGnA ATAGTATCTG GAAATATCAT GGAACGTGAG CAACAGCAGT GTGTTGCACC 240
ATTnACTGAT TTTGCTAATT TATCTTGGTG AATGGATTTG GATTTGCATT TTGGAATGTG 300
CGTGCAGCTT TT 312

(2) INFORMATION FOR SEQ ID NO: 4553:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4553:

AGCAGCGATC AAAAATAATC CGCAATACGC TGGCAAACTA CCAATACCAA ACCATAGAAC 60
AACAAATGGT GCCCATGCTA TCGGAGATAT CGGCCTAA^C AATTGAAATA GCGGTTCGAT 120
AGCGTTGTAT AGCCAACGAT TCCTTCCAAG CAAGAAGCCC AATGGAATAG CAACCAACAA 180
TGCACACA ACA AAGnCCGCTA CAAATCTCCA TGAACTAATT GCTAAATGTG GnGAATTCT 240
CCAGTAACAA TGGA 254

(2) INFORMATION FOR SEQ ID NO: 4554:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4554:

GGTCTGAATC GCTATCTGAG TCTGAATCGC TATCTGAGTC TGAATCACTG TCTGAGTCⁿ 60
AGTCACTGTC TGAATCTGAC TCACTATCTG ATTCTGAGTC GCTATCTGAT TCTGAGTC^{CG} 120
TGTCTGGAAT CTGAATCACT GTCTGGAATC CGAATCGCTA TCTGGATCTG AGTCGCTATC 180
TGAACCCGAG TCGCTGTCTG AGCCTGAGTC ACTGTCTGAA ATCGAAATCG GAACCCGGGⁿ 240
CTGGGGCTTG G 251

(2) INFORMATION FOR SEQ ID NO: 4555:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4555:

TACACAAAGA GATAAATTAC TTATGCAAAG GCGGAGGAAT CACATGTCTA TTACTGAAAA	60
ACAACGTCAG CAACAAGCTG AATTACATAA AAAATATGG TCGATTGCGA ATGATTAAAG	120
AGGGAACATG GATGCGAGTG AATTCCGTAA TTACATTTA GGCTTGATTT CTATCGCTTC	180
CTATCTGAAA AAGCCnACC AGAATATGCA GTGCCCTGTC AAGnGAAGAC ATCACGTTCC	240
AGAACGCATGG C	251

(2) INFORMATION FOR SEQ ID NO: 4556:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4556:

AGCTACCCCCG GGGATAACAG GCTTATCTCC CCCAAGAnTT CGCATCGACG GGGAGGTTG	60
GCACCTCGAT GTCGGCTCAT CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT	120
TCGCCCATTA AAGCGGTACG GAGGCTGGGT TCCGAACGTC GTGAGnCCGT TCGGTCCCTA	180
TCCGTCGTGG CGTAGGAAT TTGAGAGGAG CTGTCCTTAG TACGAGAGGA CCGGGTGGAC	240
ATA	243

(2) INFORMATION FOR SEQ ID NO: 4557:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 235 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4557:

TAACTTAAC TATGTTCCA CCATTTTAT AAGTCAAACG CTCnGGGGGG GGCTTCGTT	60
TCATTATTT AAATGCTCAT TTACATAAGT AACTCTGCT TTAAAATAAT TTAACTCATT	120
GTCTGCTAAA CGTTTCTTT TATAAAAGA TTTAAACGCG TTATTAATCT TGTGAGTGT	180
CTTCGAACA CTAGnCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTG	235

(2) INFORMATION FOR SEQ ID NO: 4558:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4558:

CCGTTAAGCA CTAAATCCGC TTAATAACGG CTTCTATCG CGCGAACAT	TCGTTGAC	60
TGCTTTTCT TTCAAAGCTT GACGTTATCA TATTTTTCT TACCTCGTGC	ACACCAAGTA	120
ATACTTTACA ATGTCCATGC TTCAAATAAA GCTTAACGG ACAATCGAAT	AACCAAnCTC	180
ACGTGTTGA TCACCCAATT TAATGATTTC ACGCTTGTGC AATAATnATT	TTCGAGACGA	240
GAGGATCGGA TTAAAACGAT CCCCTCCTCG TATGG		275

(2) INFORMATION FOR SEQ ID NO: 4559:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4559:

TTATATGGAT GTATGCCGA AGCAAGTTGT TTCAGCAGCG ACAnATGTAT	TCCGATGACT	60
CAAACCGTGC ATTGATGGGT GCGAACATGC AACGTCAAGC AGTGCCTTG	GATGAATCCA	120
GAAGCACCAT TTGTTGGTAC AGGTATGAA CACGTTGCAG CACGTGTATT	CTGnGTGCAG	180
CTATTACAGC TAAAGCACAG AGGTCGTGTT GAACATGTTG GAATCTAATG	AAAT	234

(2) INFORMATION FOR SEQ ID NO: 4560:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4560:

TTATTTGAC GTTTAGACA TAAAAAAAGA GACCTCACGG TCTCAACTTG	CCTGGCAACG	60
TTCTACTCTA GCGGAAAnTAA nTGGCTACCA TCGTCGCTAA AGACCTTCT	TGACTTGTGA	120
CAATCGTTG CTTCTTCCT CTCCTCGGC TCTCGTTAC TCATTTAGCT	CTACTAAACT	180
CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTT CACTTCGCCA	AG	232

(2) INFORMATION FOR SEQ ID NO: 4561:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4561:

TCAAAGGACG CATAACCATTA CGGGTCTGCT ACTTGTAAGC ACACGGTTTC AGGTTCTATT	60
TCACTCCCCT TCCGGGGTGC TTTTnACCTT TCCCTCACGG TACTGGTTCA CTATCGGTCA	120
CTAGAGAGTA TTTAGCCTTA GGAGATGGTC CTCCCAGATT CCGACGGAAT TTCACGTGCT	180
CCGTCGTACT CAGGATCCAn TCAAGAGAGA CAACATTTTC GACTACAGGA TTATTACCTT	240
CTTTGATTCA TCTTGTC	257

(2) INFORMATION FOR SEQ ID NO: 4562:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4562:

TACCTAATAA GTTGTGAATT TGAACAGCGG CTGCTTTACA nTGGAACTGC TGATTCAGTT	60
GCCACAATTA CCATACCAAT TTTCTTTTG TCTTCGTCTG TnATAATGTC CTTAGCAGCG	120
TTAGCTCCGA TTGAAACGAT GTCTGGTTT ACAGGACTAA CAGCATTTC AGTTTGACCA	180
ATTCCAATTA AAAATTGTT TGGGTCTACT TGGCGTGGCT TCCTGCTGAA TTTAGCCATG	240

(2) INFORMATION FOR SEQ ID NO: 4563:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4563:

CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC	60
TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACCTAAC CTATGTTCC ACCATTTTA	120
TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTATTTT AnATGCTCAT TTACATAAGT	180
nGACTCTGCT TTAAAATAAT TTAACTCATT GTCTGCTAAA CGTTT	225

(2) INFORMATION FOR SEQ ID NO: 4564:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4564:

TGTTAATTGG nGAATTTGGA TACTGGTTAT ATTCAAGCTGC ACCGCAAGCA ACTTCTATTG	60
ATGGCCTAAC TGCCTTTTA CCTCAAGCAA TGGGTATGGT AATTGTTGCA GTCATTTATG	120
GCTTTATGAA TATGAAAGCA GAGGAATCCC ATTCCCGTAA TAAAATTACG GTGGTTACAA	180
AATTATTTCA GGTTTCTTTC TTTTGCATTG GGGTGCTTTA ACCATATCTT nTT	233

(2) INFORMATION FOR SEQ ID NO: 4565:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4565:

AGCTCAGATA GCGCTCAGAC TCAGACAGCG ACTCAATTG AGATAGCGAT TCAGACTCAG	60
ACAGCGACTC AGACTCAGAC AGCGACTCAG ACTCAGATAG CGACTCAGAT TCAGATAGCG	120
ATTCAGACTC AGACAGCGAC TCAGATTCAAG ATnGCGATTC GGAAnTCAGAC AGCGATTCAAG	180
ATTCAGACAG CGACTCAGAC TCGGATAGCG ATTCAAGATTC AGATA	225

(2) INFORMATION FOR SEQ ID NO: 4566:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4566:

CCAActGGAG CTAATGGCTC TTCCATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC	60
TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAAATGG	120
TGGAGAAnTGA CGGGTTCGAA CCGCCGAnCC TCTGCTTGTG AAGGCAGATG CTCTCCCAGC	180
TGAGCTAATT CTCCGATTTA AAACTGGCCT GGGCAACGTT CTACTCTAGC GGGAACT	237

(2) INFORMATION FOR SEQ ID NO: 4567:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4567:

GTTGGAGATA GTGTAATAAT GCCAATGAGC CACTCTGAAG TTACAGCGGA TGGGTGTTT	60
GCCAAAATTG CATGGTGGTA CGAAAAAGAA AAAATGGATG GAAACAAGTT ACTGAAAATC	120
TTGGTAAAAA AGCAGGGGAC TTCGGTTCTA AGCTAAAAC ACAGCTCATA ATATCAAAA	180
GGTGCAGAGG AAATGGTTGA nnGGCAGCGG ATAAATCAAG ATGGTGCACT TGGTTAGCGT	240
TAAATCGCGA TGTGTGGTT AnTACACATC CGGGAACTAG TAATAAGTAT GTCAGTTAA	300

(2) INFORMATION FOR SEQ ID NO: 4568:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4568:

ATCCC GTGGA GGTTCAAGTC CTCTCGGCCG CATAAAATT CTTAATTAA AAAGCGGGT	60
GTAGTTAAC GGCAAAACCT CAGCCTTCCA AGCTGATGTT GTGGGTTCGA TTCCCATCAC	120
CCGCTCCATA GATAATTTA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT	180
TCCAAAAACG TAACTATAAG TTACAAACAT TnATTTAGT ATTGATGGA GCCTnAATCC	240
AAACATTCCA	250

(2) INFORMATION FOR SEQ ID NO: 4569:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4569:

GATCCCCTAG CTTTACGTTC AACTTTATAT GGGTATAACT CGAATATAAT TTGGCGCTCT	60
ATGTCATGGG ACAACGAGTA GACATTTAAT AACGGATCAG GTTCTGGTGA CGGTATCGAT	120
AAACCAGTTG TTCCTGAACA ACCTGGTAG CCTGGTGAAA TTGAACCAAT TCCAGAGGnT	180
TCAGATTCTG ACCCAGGTTC AGATTCTGGG CAGCGnTTCT AATTCAAGATA GCGGT	235

(2) INFORMATION FOR SEQ ID NO: 4570:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4570:

AATCTATTTC TTCTATTGTT AAATCGCTAT CTCCATCTTC TTTTATCTCT GGTATTATTT	60
TTTCTTCAAC TAAGTCACGA TATAATGTTT TTGAATTTC GTTCAATTG GATTCTGTGAT	120
TTTGAATACT TTTCTTCCAC ACAAAATGTAT ACCTATTGGC ATTAGCnTCT ACTTTTGTA	180
CAAnCAATAAG ATTTTGCTTT AAACATTGAC TATGAAACTG GGA	223

(2) INFORMATION FOR SEQ ID NO: 4571:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4571:

CATGATATTG TGAACCGCAT GGTTAAAGTT GCAAAGACGG TCTTGCTGTC ACTTATAGAT	60
GGATCCGCAG TGCATTAGCT AGTTCGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG	120
CCGACCTTAG AGGGTGATCG GCCACACTGG nACTAAGACA CGGTCCAGAC TCCTACGGGA	180
GGCAGCAGTA GGGAAATTTC CGCAATGGGC GAAAGCTGTA CGGCAGAACG TCGTGTGnAG	240
TGCTGCAGGT TCTTCGGATC GTATAAT	267

(2) INFORMATION FOR SEQ ID NO: 4572:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 221 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4572:

AATnCAACTT TTACTTACTA TCTAGTTTG AATGTATAAA TTACATTGAT ATGTCTGGTG	60
ACTATAGCAA GGnGGTCACA CCTGTTCCA TGCGAACAC AGAAGTTAAG CTCCTTAGCG	120
TCGATGGTAG TCGAACTTAC GTTCCGCTAG AGTAGAACGT TGCAGGCAT AATATTAATC	180
CACAGTAGCT CAGTGGTAGA GCTATCGGCT GTTAACCGAT C	221

(2) INFORMATION FOR SEQ ID NO: 4573:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4573:

GCAGAAATGC CAGCCGCATT GAGTGAACAC AGAGTTACAG GGTATTCTGT AGCCGAACCA	60
TTCGGTGCAn TGGGGGAAAA GTTAGGCAAA GGTAAGACTT TGAAACATGG TGATGACGTT	120
ATACCTGATG CGTATTGCTG TGTGCTAGTA CTnAGAGGGG AATTGCTTGA TCAACACAAG	180
GATGTAGCGC AAGATTTGTA CAAGGTTATA AAAAGTCTGG CTTTAAAATG	230

(2) INFORMATION FOR SEQ ID NO: 4574:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4574:

TCACATATCG ATAACATGAC ATAACATCATG CTGGGTTTCC CCATTCGGAA ATCTCTGGAT	60
CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCCT CATCGGCTTC	120
TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACTTAAT CnATGTTCC ACCATTTTA	180
TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTAnTTT AAATGGCTCA	230

(2) INFORMATION FOR SEQ ID NO: 4575:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4575:

CTTACAATAG TGTGCAAGTT GGGGTGGAGC CCCGACAG AGAAATTAGC TCCTCAATT	60
CTACAGACAA TGCAAGTTGG CGGGGCCCA ACACAGAAGC TGGCGAAAAG TCAGCTTACA	120
ATAGTGTGCA AGTTGGGTG GGACGACGAA ATAAATTTG CGAAAATATC ATTTCTGTCC	180
CACTCCAAA AAGACCGCAG TAGGATAATT CCATTTGAA ATACCTTACT GCCnGTTTT	240
AAAGTAATAG CnAATATTTT GGAATTAnGT TTCCTAGTTA ACCATACCAA CTAATGGCCT	300

CCTTAAATT

309

(2) INFORMATION FOR SEQ ID NO: 4576:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4576:

TGATTCTAGG AATTCAAGCT TATTAAAAC TCTTTATTCA CTCGGTTTG CTTGGGTAAA	60
ATCTATATT TACTTACTTA TCTAGTTTC AATGTACAAA TAATGGTGGG CCTAAGTGGA	120
CTCGAACAC CGACCTCACG CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCC	180
ATTTTTGA ATGTTAAATA AACATCnAAA CTGGnATACC ATATGTCACG GTAATCCGCA	240

(2) INFORMATION FOR SEQ ID NO: 4577:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4577:

CTTCGTGTTA AAATTGATG CACAATGGTC ATCATTTTA TCTTTCCAAT AAGTACTGTC	60
TGGGTAAAAA TnTATTAATT GGGTGGTCG TGAAATGCAA TCTTTTAAC GACTTCAGGG	120
TAATCTTTA ACACATGCAT CGCAACGATT GAACCTnAAC TTGAACCTAA TATATAGACA	180
GGTCATCAC TTAATGACTT TGCAAGTCG GCAATGTCCT GTGCGTCGCG TTT	233

(2) INFORMATION FOR SEQ ID NO: 4578:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 4578:

TAGGCATACC AAAGTCGATA CCATAGTGAC GACCGCCATT AAAGTTAAGT CCACCTGTGT	60
AACTCCAAA CCTTGCCAA ATTGGATGGT CAAATAGATA GCTTCCATCG CCTCCGCCAC	120
CAAAATCTTC AAACCACGAT TTACTTTGnC TACTAATTTC TTTTGAGCA ATGAGTACGC	180

GCCTTAGCAA TTTTAnGTAG CGTAGTCCGC TCCAAAATAA TATTAAACTG ACATAACTTAT 240
TACnAGTTCC CTGGATGTGT ACATAATCCA CACATCGCGA TTTATCGCTA ACAGAGCACA 300
CTTGATTACG CGCGCTCAAC ATTC 324

(2) INFORMATION FOR SEQ ID NO: 4579:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4579:

AATGTAAAAA CTGATTCTA TTAATTATT GATAGAAATC ACTTTTTGT ATTTTATAAT 60
GTACAGCTCG TTGCATTCAAT ATAGCTTGAA GTCACGTTA AAACCATATC TATCATTATG 120
GTATGCATAT CGTTAAAAC CTATTCTTT GTTAnTAGGA CATATAAATT CATCATTAAT 180
TCGTCATATT TCCAATTTG AGTGTnAAAA ATGTCACHTT TAAACTTTC 229

(2) INFORMATION FOR SEQ ID NO: 4580:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4580:

CGGGGACTCn AACCCGTGTT GACCGCCGTG GAAAGGGCGG TGTCTTAACC GCTTGnACCA 60
AGGAGCCATG GCTCCACAGG TAGGACTCGA ACCTACGACC GATCGGTTAA CAGCCGATAG 120
CTCTACCACG GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA 180
CGTAAGTTCG ACTACCACG ACGCTAAGGA GCTTAACHTC TGTGTTCGGC ATGGGAACA 239

(2) INFORMATION FOR SEQ ID NO: 4581:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4581:

CCGnACGAAT TTACACGTGT TCCGTCGTAC TCAGGATCCA CTCAAGAGAG ACAACATTT 60
CGACTACAGG ATTATTACCT TCTTGATTC ATCTTCCAG ATGATTGTC TAATGTCGTC 120

CTTTGTAAC CCGTATAGAG TGTCTACAA CCCCAACAAG CAAGCTTGTT GTnTTGGCCT 180
CTTCCCCTT CGCTGCCGC TACTAAGGGA ATCGAATTTC CTTCTCTTC CTC 233

(2) INFORMATION FOR SEQ ID NO: 4582:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4582:

TTAGTAAAAA GTCTGTGAGT AAGGGTGTAT GGAAAGTGGT TAAATATTAT AGAAAACATC 60
AAAGGATGTT AAGAAATACA ATTTATTACC CAGCATTAA TAAEGTGCT ATAGAAGGAA 120
TTAATAATAA GATAAAATTA ATCAAGTGAA TTTCTTTGG TTACAGAAAT TTCAnCAnCT 180
TTAAAGCACG TATAATGATG GATTTTCAGC TTGTACAA 218

(2) INFORMATION FOR SEQ ID NO: 4583:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4583:

TAATAAACAT GCCATACGTA ATAAGTGGCG TTGTATTAAA ATCATCTATA ATAGCCATAT 60
AGTTTGCTC ACTACCATAA CCTGCATCAG CTACAATATA CTCCGGTAAA TAACCGATGG 120
ATTTTCCAAT CATTGTTAAA AATGGAATTA AAGTTCTAGT GATCTGTTGG GTTTTGGAAA 180
TAGGTCATAG GGTrAAAACn TTTTGAGAA TTTGTCGCTA TTTGTTAAAT TGTATCCGG 240
CTTGAAGTTG G 251

(2) INFORMATION FOR SEQ ID NO: 4584:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4584:

TTTAGGACCG TTATAGTTAC GGCGCCGTT TACTGGGGCT TCGATTGTA GCTTCGCAGA 60

nTAACCCACT CCTCTTAACC TTCCAGCACC GGGGCAGGCG TCACCCCTAT ACATCACCTT 120
ACGGTTAGCA GAGACTGTGT TTTTGATAAA CAGTCGCTnGGCCTATTCAA TGGGGGCTCT 180
TCTGGGGGTT AAACCTAAAG AGCAACCCTT CTCCCGAAGT TACGGGGTC 229

(2) INFORMATION FOR SEQ ID NO: 4585:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4585:

TTATAAAAAG ATTTAACCGC GTTATTAATC TTGTGAGTGT TCTTCGAAC ATAGCGATTA 60
TTTCTTATGA ATTCAAGCTT ATTTAAAACCT CTTTATTACAC TCGGTTTGCG TTGGTAAAAT 120
CTATATTTAC TTACTTATCT AGTTTCAAT GTACAATTnC TTTTTAGTCA AGCGCTCGCA 180
TACTGCTnTA TTTTCAAAAAA ATCAAATGCT CATTACA 218

(2) INFORMATION FOR SEQ ID NO: 4586:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4586:

GGGGGGGGGC CTTCGCCACT GGTGTTCTC CATATCTCTG CGCATTTCAC CGCTACACAT 60
GGAATTCCAC TTTCCCTCTTC TGCACTCAAG TTTTCCAGTT TCCAATGACC CTCCACGGTT 120
GAnCCGGGGC TTTTCACATC AGACTTAAAAA AACCGCCTAC GCGCGCTTGT ACGCCAATA 180
ATTCCGGATA ACGCTTGCCA CCTACGTATT TACCGCGGGC TGCTGGCACG TATTnAGCCG 240
T 241

(2) INFORMATION FOR SEQ ID NO: 4587:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4587:

CAGCCACCTG TTGCCACCAAG CTACACTTGC ATTGTTTGCT ACGACACGCC CAAACAATGC 60

TGAAGTGAAT AAGAAATCAA TCATTTGCTC TTCTGTTAAA TCATGTGTTT TTTCTAATT	120
AAAAAGTGCA CCGGGATGG TACCCGAGGA ACCAGCTGTT GGCGTTGCAC AAATAAACCC	180
CATCGCAGCA TTGACTTCAT TGTTGCAAGG CACCnTTGAC TGCGGCAATC ATTCATATCC	240
GACnAAGCAG ATG	253

(2) INFORMATION FOR SEQ ID NO: 4588:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4588:

ATGAACGGGT GGTAGCGAGT GGACGAAAAA CATCAATGAA AAGCTAGCTG TAGTTGCAAG	60
AGAAACTGGC TTACGATGCC ATTGGATCAA CACATGCGGC ATTGAGAAAT CCACGCATGG	120
CTGAGACGTT TACGATTGCG CGAAAAATGA ATCCTGAAGG CATTAGCA ATGTTGGTGC	180
GGACGTACCA GTAGAAAAGG CTTTGGAAAGC AGTTGAAT	218

(2) INFORMATION FOR SEQ ID NO: 4589:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4589:

GCCATGGCTC CACAGGTAGG ACTCGAACT ACGACCGATC GGTTAACAGC CGATAGCTCT	60
ACCACTGAGC TACTGTGGAT TAATATTATG CCTGGCAACG TTCTACTCTA nCGGAACGTA	120
AGTCGACTA CCATCGACGC TAAGGAGCTT AACCTCTGTG TTCGGCATGG GAACAGGTGT	180
GACCTCCTTG CTATAGTCAC CAGACATATG nATGTA	216

(2) INFORMATION FOR SEQ ID NO: 4590:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4590:

AGATTAAAT AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC 60
ATCnCATTCA TTTCTGTCT AGAACGTT TC ACTCTAGCG GAACGTAAGT TAGCTACCAT 120
CCTCGGCTAA GAACCTTCT TGACTTGTGA CAATCGGCTT GCTTCTTCC TCTCCTTCGG 180
CTCTCGCTAC TCAATTAGC TCTACTAAC TCGGTTGCGG CTCTTTCTn GTTT 234

(2) INFORMATION FOR SEQ ID NO: 4591:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4591:

AATTGACTGA CTTCGTTTA CCGCGTGTAA AATATTGTTA TACATATATT CTAATTGCAC 60
ATTAAACTT CGTAAATGCC AATGTGnGTG GGACAGAAAT GATATTTCG CAAAATTTAT 120
TTCGTCGTCC CACCCCAACT TGnACATTA TTGTAACCTG ACTTTCCGCC AGCTTCTATG 180
TTGGGGCCCC GCCAACTTGC ACATTATTGT AAGCTG 216

(2) INFORMATION FOR SEQ ID NO: 4592:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4592:

ATTCCGGATA ACGCTTGCCA CCTACGTATT ACCGCAGGCTG CTGGCACGTn TTAGCCGTGG 60
CTTTCTGATT AGGTACCGTC AAGATGTGCA CAGTTACTTA CAC~~A~~TGTT CTCCCTAAT 120
AACAGAGTTT TACGATCCGA AGACCTTCAT CACTCACGCG GCGnTGCTCC GTCAGGCTTT 180
CGCCATTGCG GAAGATTCCC TACTGCTGCC TCCCCG 216

(2) INFORMATION FOR SEQ ID NO: 4593:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4593:

TTGGACTAGA ACCAATGAAG GACGTTACTA ACGACGATAT GCTTAAAGGA GCTGTAAGTA 60

AGCTTTGATC CAGAGATTTC CGAATGGGGA AACCCAGCAT GAGTTATGTC ATGTTATCGA	120
TATGTGAATA CATAGCATAT CAGAnGGCAC ACCCGGAGAA CTGAAACATC TTAGTACCCn	180
GTGGAAGAGA AAGAAAATTC GATTCCCTTA GTAGCGGCGA GCAGAACG	228

(2) INFORMATION FOR SEQ ID NO: 4594:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4594:

CAATCGTTGA AGGAAATGTA CCAGCAGCAA TCAAAGACAA AGAAATTATT TCTGTAGACA	60
TTTCATCATT AGAACGCTGGA ACGCAATATC GTGGTGCTTT TGAAGAAAAT ATTCAAAAAT	120
TAATCGAAGG TGTTAAATCT TCACAAAATG CCGTACTATT CTTTGATGAA ATCCATCAA	180
TTATCGGTT AGGTGCCACA GnAAGTGGAT TCCAGGTTAGCCAAAGGGGT TAATCTGGAT	240
TAATTTTTT Tn	252

(2) INFORMATION FOR SEQ ID NO: 4595:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4595:

ACTCTCTAGT GACCGATAGT GAACCAGTAC CGTGAGGAGA AGGTGAAAAG CACCCCGGAA	60
GGAGnTGAAA TAGAACCTGA AACCGTGTGC TTACAAGTAG TCAGAGCCCG TTAATGGGTG	120
ATGGCGTGCC TTTTAGAA TGAACCGGCG AGTTACGATT TGATGCAAGG TTAAGCAGTA	180
AATGTGGAGC CGTAGCAGAA GCACGGTTCT GGAATAGGG CGTTTAGTT ATTTGGGTC	240
GTTACCCGGG AGnAAAGG	258

(2) INFORMATION FOR SEQ ID NO: 4596:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4596:

CCTACCGCTG CAGCCGCTGG ATCTGCTGGA GTTGCATTAG GATCTGCCGG TGCCGCACGT	60
CTACTTCTCT TTTTCGGTCT ATTAGATGCT GGTCAGCAA TTGCAACTAG CTCTGGTTA	120
TTTGAAGAACATC TTCTTGAAATT TCCTTAAAG TAGATGTCCT CCTGAACCAT	180
TnCATTGTTC AGTTGGGTAC ATTAATGCnG TATTATGAC ACTACATCA	229

(2) INFORMATION FOR SEQ ID NO: 4597:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4597:

GCTCACCTTA GAATTCTCAT CTTGCACTCA CCTGGTGGTC GGTTTGGCGG GTAGGGTCAC	60
CTATTTCTA TCTAGCAGGC TTTTCTCCGC AGTGTGAAAT CAACGACTCG AAGnCACAAT	120
GGTCTTCTCC CCATCACAGC TCAGCCTAA CGAGTACCGG ATTTGCCTAA TACTCAGCT	180
TACTGCTTAG ACgtGCAATC CAATCGCACG CTTCGCCTAT CCTACTGnGG TCCCCCCCATC	240
GATTAA	246

(2) INFORMATION FOR SEQ ID NO: 4598:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4598:

AAGAAAATAA AGAATGCTAC AATTACGATT GCAATCAAAC CAAAGAACCA TAATGATGTG	60
TACCAAGTGC TGCACCTTTA GTAATGACAA CGTTAAACT TAGCAACATA ACTACTAGAA	120
CAATTAGCCC TGCAACGTCA AATTATGTG TATTGGTAAT TTCTGATTTC GTTTCAGGCG	180
TCCCTTGAT GAGTAGCATT GAAAGTACGG nAACGATGnG TTG	223

(2) INFORMATION FOR SEQ ID NO: 4599:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4599:

nTnTCACTGT TTGACCCGGT ACCGTGTAG ATAATCCCGC ACGCAATGCA ATCGTTCGTG	60
CAATGTTTG GCCTTGTAAAT CCTTCTGGAA AACCCGTACC AACAAATGACA TCTTCAATCA	120
TATTCTTATT GAATTTCCG TCAATACGTT TCAATACGCC TTGTAATACT TTGGCTGCGA	180
CATCATCAGG TCTTTCGTGG AATAATGCCG CTGCTTTGC	219

(2) INFORMATION FOR SEQ ID NO: 4600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4600:

AAGGTAAAGA GGAGTGGTTA GCTTCTGCGA ATACCGAATC GAAkCCCCAG TAAACGGCGG	60
CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCCTTGTC GGGTAAGTTC CGACCCGCAC	120
GAAAGGCGTA ACGATTGGG CACTGTCTCA ACGAGAGACT CGGTGAAAAT CATAGTACCT	180
GTGAAGATGC AGGTTACCCG CGGACAGG	208

(2) INFORMATION FOR SEQ ID NO: 4601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4601:

AGTGCAGTG ATTAACTGCA TTTTCAATA GATCAGGGAA GACTACCAAG CTTATGTTGA	60
AGGACATCTT TTGGCGTTAC CGGTTGGCA GGTATGTTGT ATTACCGTTC ACAACAGCAT	120
CACTTGAACA ACATTGTTA ACGGATTATT TGGCAATTG TTATTGTCGA ACAnTGCnAG	180
TTGGTGAGAT TTAATCATCG CTAAAGATGT GAAATAGATC GAAAATGGTT TAAGCAAACG	240
TTGCTCAGGT GTTACTACGT GATATGCCTA GCGAGTATAAC TACAAC	286

(2) INFORMATION FOR SEQ ID NO: 4602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4602:

ATATGGCTAT GGTATTCACA TATCGATnAA CATGGACATA ACTATGCTG GGTTTCCCCA	60
TTCGGGAAAT CTCTGGGATC AAAGCTTACT TACAGCTCCC CAAAGCATAT CGTCGTTAGT	120
AACGTCCTTC ATGGCTTCTA GTGCCAGGCA TCCACCGTGC GGCCTTAATA ACTTAATCTA	180
TGGTTCCACC CATTTTATA GGTCAAACGG TAACATGAGG TAGGGTCTTT TATAAAAAGG	240
nTTAAACGGG GTATTAATCT TGTG	264

(2) INFORMATION FOR SEQ ID NO: 4603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4603:

GAAACGTTAG CACAAGCCAT GAACCAATTA GGTGGAAAGA GTAATAGTGG TGAAGGTGGC	60
GAAGATGCAA AACCGTTATG AAGTACAAGT TGATGGAAGC AACAAAGTAA GTGCGATTAA	120
ACAAGTTGCT TCTGGCGTT TTGGTGTAnC TAGTGATTAT TTACAACATG CCAAAGAATT	180
CAAATTAAAG TTCGCCAGGT GCAAGCCCTG GTGAGGTGGT CATTACCTGG TACTAAGGGA	240
TATCCn	246

(2) INFORMATION FOR SEQ ID NO: 4604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4604:

ATTAACTAAC ATGGGCATCT ACGATGGAAA CAGACGTGGTATCCTCGCTA TTATCCAGCT	60
AnGCCATGC TGGCTCGTTT TTCAAATCAA GCCATTTAA ATTTGGAAA GGTGTATGGA	120
CCAAGCCCTA TGACATTGCA TTCACCGATT GAACACGATG TTATGCCAT GTCTCATGGA	180
GAAAATCAAG AGCATCATTC AGCAGTATCG CGATGCTACA TTACGCGCGA TTAAAGCAGn	240
TTTGATGG	248

(2) INFORMATION FOR SEQ ID NO: 4605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4605:

CAAGTTTCC AGTTCCAAT GACCCTCAC GGTTGAGCCG GGACTTnTCA	CATCAGACTT	60
AAAAAACCGC CTACGCGCCG TTTACGCCA ATAATTCCGG ATAACGCTTG CCACCTACGT		120
ATTACCGCGG CTGCTGCAC GTATTAGCCG TGGCTTCTG ATTAGGTACC GTCAAGATGT		180
GCACAGTTAC TTAACACATG ATGTTCTTCC CCTAAATGAA CAGAGTTTG TTTTGTnTn		240
TGGGTT		246

(2) INFORMATION FOR SEQ ID NO: 4606:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4606:

CTTCTTACCA GTCGTTGTAC CTGTGCGATT CAATTGTGC ACTGCTTGCT CTAAGGCATG	60
TGTATCTGCA GTAAATCAT GTnTCGCTTG GTTTAATGCT GTTAATGCGT TATCGACACG	120
ATGTTTTCA TCTGAAATTG TTGTGCAGT TGCATGCCA TTGTCAATAA CACGTTGAGC	180
TGCAGTTATT TCAGTTCTG CTTCACGCTn CT	212

(2) INFORMATION FOR SEQ ID NO: 4607:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4607:

TAGTCAAGAT GAGAATTCTA AGGTGAGCGA GCGAACTCTC GTTAAGGAAC TCGGCAAAT	60
GACCCCGTAA CTTCGGGAGA GGGGTGCTCT TTAGGGTTAA CGCCCAGAAG AGCCGCATGA	120
ATAGGCCCAA GCGACTGTTT ATCAAAACA CAGGTCTCTG CTAAACCGTA AGGAnTGTAT	180
AGGGGCTGAC GCCTGCCGG TGCTGGAAGG TTAAGAGGAG TGGTTAGCTT CTGCGAGTAC	240
GGAATCGAAG CCCCAGTAAA CGGCGG	266

(2) INFORMATION FOR SEQ ID NO: 4608:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4608:

TTCAGTACGT AAATACGCAC GTGAAAAAGG TGTТАnATTA AAGCAGTTTC TGGATCTGGT	60
AAAAATGGTC GTATTACAAA AGAAGATGTA GATECATACT TAAATGGTGG TGCACCAACA	120
GCTTCAAATG AATCAGCTGC TTCACTGACA ACTGAAGAAG TTGCTGAAAC TCCTGCAGCA	180
CCTGCAAnCAG TGAACATTAG AAGGCGACTT CCCAG	215

(2) INFORMATION FOR SEQ ID NO: 4609:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4609:

GGGTTCATAC ATGTCAATAG TAACCGTCTT AACCTGTTGT CGATTTTTA AA T GAATCG	60
CTCGAAATAG GCACGCAAGA ATCTTGAGT TCTATTTCT AAAATATCTA TAACATCATG	120
GTATCATTAT CTATAAAAAT GAAACTCATT GATCCAGTTA CATTAAAC GCTTTAAAT	180
TCATCCATAG CGATGTGGTT CCTGCCAACC ATTAAAGGGG TTAATT ⁿ GA AT ⁿ GATTAGC	240
C	241

(2) INFORMATION FOR SEQ ID NO: 4610:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4610:

ATTCATTTCT TGTCTAGCAA CGTTCTACTC TAGCGGAACG TAAGTTAGCT ACCATCCTCG	60
CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC	120
TTACTCATT AGCTCTACTA AACTCGTTGC GCTCTTTCT CGTTTCGTCA GATTCAAACG	180
TTTCAnTTCG CCAAGCCATT TTTCTTGGT G ⁿ TTA	215

(2) INFORMATION FOR SEQ ID NO: 4611:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4611:

GTGCCATCTT TCTTCATCAA TTCATTAATA ATTGCTGGGA CGCCACCAAGC TTCATGCACA	60
TCATGCATTG AATACGATGA ACTAGGTGCT ATTTTGATA AATATGGCGTGCCTTGGCA	120
ATAGCATTAA TGCGCTCTAA GTCATAATCA ATACCAGCTT CATTGGCAAT GGCTAACGTA	180
TGCAGTACCG TGTTTGTGA ACCACGGCAC ATCTTCGCCA ATTTCTTCTT TAAACAAGTT	240
TAAATTATCT TGTGATTTCAG GTAAATCCAT CTTGTTAGCT ACTACGATTT GAGGTCTATC	300
TTCTAACGT TGCTCGTACG GCGGCTAATT CTGGATTAAT GACTTATAA TCTTCAATAG	360
GGTCTCTACC TTCAGAACCG CTCCATATCC ATCCTGTGGA	400

(2) INFORMATION FOR SEQ ID NO: 4612:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4612:

AATACTATTAA AGAAGTCCTG AAAAATTACAC ATTAGCAGTT GGATTGTTCA ACTTTATTAA	60
TGATAAGTAT GCAAATAATT TCACAGTGT TGCAGCAGGG GCAATTATGA TTGCAGTACC	120
TATAGCAATC GTATTCTTGT TCTTGCAACG CTATTTAGTA TCAGGTTAA CAACAGGTGC	180
CGACCAAAGG GTTAGTTGA ATTTAGGAGT GGGGCCAGAT TGGTTAAGGA CCnCCTAATG	240
ACCGTTAAGG TTnAAAGG	258

(2) INFORMATION FOR SEQ ID NO: 4613:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4613:

GACTTCGTTT CAGTGTAAAA TTTTTCTAAT GTAACAGATA TGCTATTATT CATTGGAATG 60
ATTAGTGCTT CATCTTTTT ACCCCAATAT TTTATAAGTG CAATTCTAT GTGCACGTGC 120
TTGCCACTT TTAATCAACG CTTAACCTCC TAAATTCTCA ATCCAAGTAT GTGCTGCACC 180
AGCTTTTTC TACAGCTTT ACAATATTnn 210

(2) INFORMATION FOR SEQ ID NO: 4614:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4614:

TAGCGTATTA ATCGGGCGAT CGGCTGAGCG TATCTGAGTC TGAATCGCTG TCTGAGTCTG 60
AGTCGTATCC GAGTCTGAGT CGCTGTCTGA nTCTGAATCA CTGTCTGAAT CCGnATCGCT 120
ATCTGAATCT GAATCGCTAT CGAGTCTGA GTCGCTGTCT GAATCTGAAT CGCTGTCTGA 180
GTCCGAATCG CTATCTGAAT CTGAGTCGCT GTCTGAGTCT GAATCGCTAT CTGAA 235

(2) INFORMATION FOR SEQ ID NO: 4615:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4615:

ATGTGCGTGG TTTATTTAA TAGGTTAGTA ATATATTAGG TCATGTTATG TTTAAnTTA 60
TAATGAATAA ATAATTTAGA AATATGCTTC CGATTGTTCG A~~E~~CTTTAAT TCAGTTAGAA 120
GCATCATAGA ATGCATGATT ACTGTTGTAAGATACGTAAGTTTGAT TGACTGTATG 180
TCnTTGGATA GAGTTACAAA CTTATTTG 209

(2) INFORMATION FOR SEQ ID NO: 4616:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4616:

ATGCGCAAGA TATGGAGAAC ACCATCGCGA AGCGACTTTC TGGTCTGTAA CTGACGCTGA 60

TGTGCGAnAC nTGGGGATCA AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT 120
GAGTGCTAAG TGTTAGGGGG TTTCCGCCCG TTAGTGCTGC AGCTAACGCA TTAAGCACTC 180
CGCCTGGGGA GTACGACCGC AAGTTGGAAA CTCAAAGGAA TT 222

(2) INFORMATION FOR SEQ ID NO: 4617:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4617:

CAGTTTGCAA CACCCCAATT CTTGCCAGTC AGCATGATTC TGTCATTTC TGCGATTCT 60
TTGTCGATAT TTTCAAATCT TGTTGGACTT GATCTAAATC AATTGGTGCT TCTTCTTCGA 120
ATGTATCAAC ATATCGCGGT ATGTTTAAGT TGTAATCGTT ATCGGnGATC TCTTGTAATG 180
TCGGCCTGTG GCTATATTAA TCAATCGTGG CTTTACGCT ATATGGGCT ATAATACGTT 240
CGACCTTGGG CAACCGnT 258

(2) INFORMATION FOR SEQ ID NO: 4618:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4618:

TCTAATTGAT AGTGAATATA ATTAGAGTTn GAGGCTGGGA CATAAATCCC TAAATTTCAAn 60
CAGTAAGATA ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTAA TACAATACT 120
CATTGGAATG GCTTCGCTTT CCTAGGGTGC CGTCTCAGCC TCGGTCTTCG ACTGGGCACT 180
GCTCCCTCAG GGGTCTCGCC ATTAAATACT ACGTAT 216

(2) INFORMATION FOR SEQ ID NO: 4619:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4619:

ATGTATCGCG CCGAGCAACA CAAGATAAGC ATTGTAGATG TGGATGCCTT AACTGGCAA	60
GCGATTnGTC GTCCTAAAAC AGGTACATAT GCGCTATCTG ACCTAGTCGG TTTAGATATT	120
GCAGTGTCTG TAATTAAAGG CATGCAACAA GTACCTGAAG AAACACCCnT ATTTTCATGA	180
TGGTCAAAAT TTGTAAATAC GTTGTGTTGA CAATGGGCGC ACCTCGGACC GTAAAACG	238

(2) INFORMATION FOR SEQ ID NO: 4620:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4620:

AACCATTGAA GCACCCCCATT ACGTTTGGC TGACACGNAC GTATATGCC TGCCCAAGCA	60
GATGCAGCCT TATTAACACC TGAACCACCT CGAACGCCAC TACCTTAAG TGACTTCAAC	120
CATTTTCCT GGATCTTAG CTGTATGCAT TGCCCTGGAT GCGACCCTTG nCATCAATTG	180
GGAAATGTAA GTGTGCTCCT GCTAACGAAA TTACCTGTAG CACCTGGATT TCCCATCAG	240
TTGACCAGC	249

(2) INFORMATION FOR SEQ ID NO: 4621:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4621:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCA AGAAAGAACG	60
TAAATTTAAT CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG	120
TGAGAAGACA ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA	180
AGGTGAATCG AAGAGAAATC ACAAAAGTCCG TTnTGGnTTA CAGGTACGGC AGAACGATAC	240
ACAGTCTCGG GCGATTGTCG AGTCCAC	267

(2) INFORMATION FOR SEQ ID NO: 462:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4622:

CAAAAGGTAG TTTAAATTAG GAGTG G GAA ATTGATAAGA CCACTAATGA CGATAAAGAT	60
TAAAAGGAnG ACGTTATGAT GACGATTAAA GTGGATCAT TGGGTGTGGT GGTATTCCAA	120
TGGCAAGCAC ATGCCAAGTT TACAAAAAGT TGAAATGTTG AAATGAnCGC ATTTTGTGAC	180
GTAGACATT CGAACGAGCG AGTGC G GCAG AACGATACGG ACTGACAATG C	231

(2) INFORMATION FOR SEQ ID NO: 4623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4623:

CGAAACCGGC CCGACCCGGA CCnACCCGAG GAAAGGTACC CnAAAGnTGA AGCCC G GGAA	60
AACCACCCAA AC G GCCACC CAAACCACCC AGAAGTACCC AAAGTGAAGC CCGGAAAACA	120
CCCAACACCC ACCCGGACAC CAGAAGTGCC GGAGTGAGCC AGAAACTCCA ACACCGCCAA	180
CACCAGAGGT ACCAGCTGAA CCTGGTAAAC CAGTACCACC TGCAAAGAA GAACCTAAAA	240
AGCCTTCTAA ACCAGTGGAA CAAGGTAAAG TAGAACACC TGTTATTGAA ATCAATGAAA	300
A	301

(2) INFORMATION FOR SEQ ID NO: 4624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4624:

CGAGGTGCTG CAGAAGGTGT C A TCGTCGT TATTAATTG AAGAAAAGAA CTACTTAGAA	60
GCTGTGATTG GTTGCCAGC GAATATTTTC TATGGGACAA GTATTCCAAC ATGTATTTA	120
GTATTTAAAA AATGTCGCCA ACAAGACGAC AACGTACTAT TTATCGATGC ATCCAATGGT	180
TTGAAAAAG GGGnAAATCA TAATCATTnG GCGATGCCA AG	222

(2) INFORMATION FOR SEQ ID NO: 4625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4625:

TGGAAAGTGA	ATCAAAGAGG	TAATATCCGT	AGTCGAAATG	TTGTCTCTCT	TGAGTGGATC	60
CTGAGTACGA	CGGAGCACGT	GAAATTCCGT	CGGAATCTGG	GAGGACCATC	TCCTAAGGCT	120
AAATACTCTC	TAGTGACCGA	TAGTGAA <u>CC</u>	AGTACCGTGA	GGGAAAGGTG	AAAAGCACCC	180
CCGGAAGGGG	AAGTGAAATT	AGGAACCCTG	AAAACCGTG	TGCTTACCA	AAGTTAnGTT	240
CAAGAGGCC	CGTTAAATT	GGGGTnnAAT	TGGCGGTGCC	CTTTTTGGT	AGGAATTGAA	300
A						301

(2) INFORMATION FOR SEQ ID NO: 4626:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4626:

GAATGAAGGA	AGACCATAATG	AAAAATGGCC	AACTTAAGCC	AGGATACAAT	TTACAAATAG	60
CGACAAATTC	TCAATTGTT	TTATCCTATG	ACCTATTTCA	AAACCCAACA	GATACTAGAA	120
CATTAATCCC	ATTTTAnCA	ATGATTCAAA	ATACCTTCGG	TTATTTACCA	GAGTATATTG	180
TAGCTGATGC	AGGTTATGGT	AGTGAGCAAA	ACTATATGGC	nAT		223

(2) INFORMATION FOR SEQ ID NO: 4627:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 221 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4627:

TTGTTGGGGC	CCCGCCnGCG	nCATTGCCTG	TAGAATTCT	TTTCGAAATT	CTCTGTGTTG	60
GGGCCCTGA	CTAGAATTGA	AAAAAGCTTA	TTACAAGCGC	ATTTCGTTC	AGTCAATTAC	120
TGCCAATATA	ACTTCGTAGA	TCATAGAAC	TTGATTTATT	TCCCAGCCTA	TTCTTTCAT	180
AAAAAAAAAGA	CGGATTAATT	ATCCGCTTT	TCCTTATATC	T		221

(2) INFORMATION FOR SEQ ID NO: 4628:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4628:

ATATATTCTGT ATTTATAGTA AAATTAAATA AAGAGnATTA TATAACACGA GGTGTAGTAA	60
GTATGAAATT TGAGnAAATA TATAGATCAC ACTTTATTGG AAGCCTGAGT CAACACGTAC	120
GCAAATCGAT CAAATCATCG ATGAAGCGAA GCATACCAAT TTTAAATCTG TATGTGTGAA	180
TCCACCACAT GTTAAATATG CAGCAGAG	208

(2) INFORMATION FOR SEQ ID NO: 4629:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4629:

ACAATAATGC ATCATAATGC GCAACAACAA TCAATACTGC GAAAACAGAA GCACAACAAG	60
TGATTAATAA TGAGCGTGCA CACCACAACA AGTTTGAC GCACTAACTA AAGTTCGTGC	120
ACACAACCAA GATTGATCAG CTAAAGCTTA CTTCAAAATA AAGAGATATA GCCATTAGTA	180
ACGTTAAAAT AACTTACAAG nTCTGTGACC AGTACCTCAC TGTGGTATGA CGCACAAAGTA	240
TTGATACTnT ATCGAGAGCG TGAGnGAACt GAATACTGCG CTCACGGTAT TACATGCGTG	300
CACTG	305

(2) INFORMATION FOR SEQ ID NO: 4630:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4630:

TCGACTACCA TCGACGCTAA GGAGCTAAC TTCTGTGTTG GGCATGGGAA CAGTGTGACT	60
CCTTGCTATA GTCACCAAGAC ATATGAATGT AATTATACAT TCCAAACTAG ATAGTAAGTA	120
AAAGTGATTT GCTTCGCCAA ACATTTATTT TGATTAAGTC TTGATCGAT TAGTATTG	180
CAGCTCCACA TGTCACCATG CTTCCAnCTn GAA	213

(2) INFORMATION FOR SEQ ID NO: 4631:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4631:

GAnGTGAAAT AGAACCTGAA ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA	60
TGGCGTGCCT TTTGTAGAAT GAACCGGCAG GTACGATT GATGCAAGGT TAAGCAGTAA	120
ATGTGGAGCC GTAGCAAAAA CnAAGTTCTG AATAGGGCGT TTAGTATTTG GTCGTAGCCG	180
GAAACCAGGT GATCTACCCCT TGGTCAAGTT GAA	213

(2) INFORMATION FOR SEQ ID NO: 4632:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4632:

GCTTTAAAT CAAATGATAG CGGAAGGGnA TTTAAAATT ATTGAAACCA TATTTACAG	60
CAGCAGATGG ATGGATTGGT GTCACAATTA TCTTGGTGC CTTGCATTA TTCTGGTTG	120
TAGGTATTCA TGGTCCGTCA ATTGTAGAGC CAGCAATTGC AGCCATTACA TATGCGAATA	180
TCGAAGCGAA CTTCAAGTTG CTTCA	205

(2) INFORMATION FOR SEQ ID NO: 4633:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4633:

AGTTATATTG ACAGTAGTTG ATGGGGCCCC AACATAGAGA AATTGGAACA CCAATTCTA	60
CAGACAATGC AAGTTGGGT GGGCTCTAAC ATAAAGAAnT ACTTTTCTn TAGAAATTAG	120
TATTTCTTAT ACATGGGTTT TACTCAGTAT TTCCTATTCT TAAGTGCACA TTAGCAGCGG	180
CTAATGTGTT AAGAACTACT ACAT	204

(2) INFORMATION FOR SEQ ID NO: 4634:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 226 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4634:

GCCGATGGAT TAGAGTATAT GACGTGGTGG CATGTCATTA ATTTAGGTGA TGTAGGTAAG	60
AACGTTnGGG CAAGGTATGA GTGGTGGTAT TGCCTTACGT TAGCCCGTCT GATGTAGAAG	120
CTTTGTTGA AAATAATCAA CTAGATACGC TTTCGTTTAC AAAGATTAA CACCAAGAAG	180
AAAAAGCATT CATTAAGCAA ATGCTGGAAG AnCCATGTGT CACACA	226

(2) INFORMATION FOR SEQ ID NO: 4635:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4635:

CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA ATATACTCTG GTAAATAACC	60
GAAGAGTTGT TGAATCATTG TTAAAAATGG GATTAATGTT CTAGTATCTG TTGGGTTTG	120
AAATAGGTCA TAGGATAnAA CnGTACGGAG AATTTGTCGC TATTTGTAAA TTGTATCCTG	180
GCTTAAGTTG GCCATTTTC ATATGGTC	208

(2) INFORMATION FOR SEQ ID NO: 4636:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4636:

TTTTCTTG TGTTTATTT TATTTGAAC GTTTAGGAC ATAAAAAAA GTAGACCTTG	60
CGGTCTCAAT CGGGCTCATC GCATCCATT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA	120
CGTAAGTTGG CTACCATCGA CGCTAAGAAC CTTCTTGAC TTGTGACAAT CGCTTGCTTC	180
TTTCCGCTTC TTCTGCTCGn GCTTACTCAT TGAGCnCTAC TAAACTCG	228

(2) INFORMATION FOR SEQ ID NO: 4637:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4637:

CATGGTTCAA AAGTGAAAGA CGGTCTTGC GTCACTTATA GATGGATCCG CGCTGCATTA	60
GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA TAGCCGnCCT GAGAGGGTGA	120
TCGGCCACAC TGGAGCTGAG ACACGGTCCA GACTGCTACG GGAGGCAGCA GTAGGGnATC	180
TTCCGCAATT GGCGAAAGCT GTACGGGCAA CG	212

(2) INFORMATION FOR SEQ ID NO: 4638:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ IDNO: 4638:

ATnTnATTAA ATAGAGAACAA GCAGTAAGAT ATTTTCTAAT TGAAAATTAT CTTACTGCTG	60
TTTTTAGGG ATTTATGTCC CAGCCATTTC TGTATTCTATA TTTAAATTTC GATAATTTC	120
CAGGAAGCAT TTTAATTTC CTAATGAAGC CATATTTTA GATTAACCAA AATTAATATT	180
TACATTTCCCT AACCAATTTC ATGTAACATT TACAGTTCCA AAAATGGGGG TAATAATCCA	240
GGTTAGGATA AAGAGGG	256

(2) INFORMATION FOR SEQ ID NO: 4639:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4639:

AnAGnAACCA CTACATAATA AATCATTAGT GGCTCTTAT CATTCTGTC CCACTCCCCT	60
GAGAAGTTTA AAATTTATA TGTTGGCTTG TTATGTAAG GGAATTAACA TGGTTGTCTT	120
GTTTATATTA TGTGATTCCA ACATTACTAG TCCTGGTAAA TCTAATTCCG TAAAATGCTA	180
AATCTAACCA TCTATTAAAT TTTAAAACC	209

(2) INFORMATION FOR SEQ ID NO: 4640:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4640:

nGnAAAGGTG AAAAGCACCC CGGAAGGGAG GTGAAATAGA ACCTGAAACC GTGTGTTAC	60
AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA CCGGCGAGTT	120
ACGATTGAT GCAAGTTAAG CAGTAAATGT GGAGCCGTAG CAGAACATG GTCTGAATAG	180
GTGCCGTTAG TATTTGGTCG TAGCCCCAG AACCAAGGTG ATCT	224

(2) INFORMATION FOR SEQ ID NO: 4641:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4641:

CACTCACnCA GATTTTAAG TCCTGTCCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA	60
AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCAACC TTGGCAAGGT TTTATTCTAC	120
CGCTGAACTA CTTCTGCATA TGCGGGTGAA GGGAGTCGAA CCCCCACGCC GTAAGCTAnG	180
ATCCTAAGTC TAGTGCCTCT GCCAA	205

(2) INFORMATION FOR SEQ ID NO: 4642:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 235 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4642:

AGCTGACATG ATCAGTCAGC TTACAACAAT GTGCCGGTTG GGGTGGCTGG ACACGGCACC	60
CTGAGGGAAG GGCACCCGTC ATCAAAATT CTATTTATAG AATTTACAG TAATGTGACA	120
GACGGGCAA GCGAACCAATT CAATACGAAG TATTGTATAA ATAGAGAACCA GAGTAAGAT	180
ATTTCTAAT TGAAAATTAT CTTACTGCTG TnTTTTAGG GATTTATGTn CCCAG	235

(2) INFORMATION FOR SEQ ID NO: 4643:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4643:

AGnAAGGTGG GGATGACGTC AAATCATCAT GCCCCTTATG ATTTGGCTAC ACACGTGCTA	60
CAATGGACAA TACAAAGGCA GCGAAACCGC TAGTCAAGCA AATCCCATAA ATTGTTCTCA	120
GTTCGATTGT AGTCTGCGAC TCGACTACAT GAAGCTGGAA TCGCTATAAT CTAGATCAGC	180
ATGCTACGTG ATAGTTCCGG GTCTnTACAC ACGCCCGTCA CACCACGGAG GGTTTTACAC	240
CGAAGCCGTG ATACTTTAG	260

(2) INFORMATION FOR SEQ ID NO: 4644:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4644:

CAGCAGGCCA CCAAAATTGT GTCCGAGAT GTTCATATAA AACTTTATAT AATTCACTAG	60
TTCCTAACAT TTACACCCCTC CATTAGAG GGAGTGGGAC AGAAATGATA TTATCGTAAA	120
ATTTATTCG TCGTCCCACC CCAACTTGCA TGTCTGTAGA AATGGGGATC CAATTChCTT	180
GTTGGGGGCC CGCGGGCAAG GTnACTAGAA TGAAAAAAGC CTGTTACAG CGATTTTCGG	240
TTCAGTCCAC TACTGGCAAT ATAACTTGTA GAGCTAGGAC ATTGG	285

(2) INFORMATION FOR SEQ ID NO: 4645:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4645:

GCTATTACTC TGCTATCAAT GTACCTAAAG CTACCGATGA TTTCCGAGAC ATAGACCGTG	60
CGCTTGTnTG GGGGTTCAAC TGGAAACTTG GTCCATTCCA ATTATGGGAT GCAATGGGGn	120
TACGAACGTG TTAAAACAGT ATGGAAGACG AACTTGGAGA CTTACCACAA TGGGTTAGTG	180
ATTTAGATGG TGGCTTTGA TAAACA	206

(2) INFORMATION FOR SEQ ID NO: 4646:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4646:

ACAGTTACCG ATACAAC TGA AGATGATAAC GATGCAGATG CTGGCGACGT TGACGTCACA	60
CTTACGGATC ATGATGATT CACACTTGAT AACGGATACT TCGAGATGAT ACATCAGACA	120
GCGATTCA GA CTCAGATAGT GACTCAGACA GCGACTCAGA CTCAGACAGC GACTCAGACT	180
CnGACAGTGA TTCAGATTCA GACAGCGACT CAGATTChGA TA	222

(2) INFORMATION FOR SEQ ID NO: 4647:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4647:

GTACTATTG TGTGTGACAA TGTTCCTCCA GCATTTGCT AATGAATGCT TTTTCTTCGT	60
TTAATCTTG TAAACGAAAG CGTATCTAGT TGATTATTTT CAACAAAAGC nTCTACATCA	120
GnCGGGATAA CGTAAGCAAT ACCACCACTC ATACCTTGAC CGAAGTTCTT ACCTACATCA	180
CCGAAATTAA TGACAGTCCA	200

(2) INFORMATION FOR SEQ ID NO: 4648:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ IDNO: 4648:

CCACCATTAA TTTAATACCT ATTTGGGGC TTAGCTCAGC TGGGAGAGCG CCTGCTTG	60
ACGCAGGAnG TCAGCGGTTTC GATCCCGCTA GTCTCCACCA TTATTTGTAC ATTGAAAAC	120
AGATAAGTAA GTAAAATATA GATTTACCA AGCAAAACCG AGTGAATAnA GAGTTTAAA	180
TAAGCTTGGA ATTCAATTAAAG A	201

(2) INFORMATION FOR SEQ ID NO: 4649:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4649:

AGTAAATACA GATGGAATAA ATCTTTAAG GCTTATAAAC GCTCATCTGn CATTGTAGCA	60
ATTCATGCTT TCAAAAGACG ATATACTACG ACACTCCTAC GAACTTGTCC AAGGATTACG	120
AAAAGACCTA AGGTTATGTA ATTGGCCTAA ATTCAATTAT CGCTTAAATT CACTTAGTAA	180
AAAGTCTGTG AGTAAGGGTG TATGGAAAGT GGTnAAAT	218

(2) INFORMATION FOR SEQ ID NO: 4650:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4650:

GTGGCGGTGC GACTGTCAGA AGCACGTTAA ATTAATGAAA GATACAGTAG GTGCTGATGT	60
AGAAGTAAAA GCCATCAGGT GGCGTACGTA ATTTAGAAGA TTTCAATAAA ATGGTGAAG	120
CAAGTGCACACGTATTGGT GCGAGCGCAG GTGTTCAAAT TATGCAAGGT TTAGAAGCAG	180
ATTGATTA CTAATATnTA TG	202

(2) INFORMATION FOR SEQ ID NO: 4651:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4651:

AGCGGCGGAC GGGTGAGTAA CACGTGGATA ACCTACCTAT AAAACTGGnA TAACTTCnGG	60
AAACCGGAGC TAATACCGGA TAATATTTA AACCGCATGG TTCAAAAGTA AAAGACGGTC	120
TTGCTGTCAC TTATAGATGG ATCCGCGCTG CATTAGCTAG TTGGTAAGGT AACGGCTTAC	180
CAAGGCAACG ATGCATAGCC GACCTGAGA	209

(2) INFORMATION FOR SEQ ID NO: 462:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4652:

TGAAGATGCA GGTTACCCGC GACAGGACGG AAAGACCCCG TGGAGCTTTA CTGTAGCCTG	60
ATATTGAAAT TCGGCACAGC TTGTACAGGn TAGGTAGGAG CCTTGAAAC GTGGAGCGCT	120
ACTTGAN TGG TTAGGCCTG GTGGGATACT ACCCTAGCTG TGTTGGCTTT CTAACCCTGA	180
CCACTTATCG TGGTTGGAGA CA	202

(2) INFORMATION FOR SEQ ID NO: 4653:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4653:

CCGTGCGACC CCTTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC GTTCCCGGTA	60
TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGCTCT	120
ATCCAATTGA GCTACGGGCG CATATGTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG	180
AACCGGTACG TGATCACTCA ACnGn	205

(2) INFORMATION FOR SEQ ID NO: 4654:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4654:

AGACGAAACG TTGTTGTTGC GAAGATAAAAT CGCACAGCGA TTGAGCCTAT CTGCTGCACC	60
ATTAACCTGGT GAAGAACAC CATTATCAGA AGTGCCTGAT CAAGTGTCA GCGAAAAAAT	120
GATGGTGACG GTATCGCTAT CAAACCTTCA CAAGGTGAAG TTCGTGCACC ATTCAACGGT	180
AAAGTACCAA TGATTCCCCA ACCAACATG CCATTGGTCC TGTATCAGAT AGTGGTTAGn	240
CTATTAATCC ACACGGGTTA GAnG	264

(2) INFORMATION FOR SEQ ID NO: 4655:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 211 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4655:

GACGATTACA TATCATCGCT AATAACTTAG CATTAAAACC GGTGATGCG CCACCACAAG	60
CCCCACATTC AAGTGATGCA TGATGTGGAT TATTGTGAGA ATGACTAGCA TGGCCCTGCT	120
AACACAAACGA ACTGGGnACA TGCTTCGGTT AAATCCATCA ATTTCAACGC TTGTnACGCG	180
AAATCAGTTT GCTCTTGGCT GCAGTAAATC G	211

(2) INFORMATION FOR SEQ ID NO: 4656:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4656:

TTTACATTTA TCGGTTTAGT CAGATTCAAA CGTTTCACT TCGCCAAGCC ATCTTTCTTT	60
GTGTTGCTT TTATTTGAC GTTTTAGACA TAAAAAAAGA GACCTTGC GG TCTCAATGCG	120
GCTCATCGCA TCCACTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTCGACT	180
ACCATCGACG CTAAGGnGCT TAACTGnTGG GT	212

(2) INFORMATION FOR SEQ ID NO: 4657:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4657:

TGGGTTCGAA nTCCACTTAG GACCCACCAT TAACTTAATA CCTATTTGGG GGCTTAGCTC	60
AGCTGGGnAG AGCGCCTGCT TTGCACGCAG AGGTCA GC GG TTGATCCCG CTATCTCCAC	120
CATTATTTGT ACATTGAAAA CTAGATAAGT AAGTAAAAA TAGATTTAC CAAGCAAAAC	180
CGAGTGAATA AAGAGTTTA	200

(2) INFORMATION FOR SEQ ID NO: 4658:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 185 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4658:

TACAGTATAT CGGGAAGACA GGATTCGAAC CTGCGACCCC TTGGTCCCAA ACCAAGTGCT	60
CTACCAAGCT GAGCTACTTC CCGTATAATT AACCGGCCCG ATAGGAGTCG AACCCATAAA	120
CTCTTGATCC GTAGTCAAAC GCTCTATCCA ATTGAGCTAC GGGCGCATAT GTTTTTATTG	180
AAAAn	185

(2) INFORMATION FOR SEQ ID NO: 4659:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4659:

AAGTGTAGG GGGTTCCGC CCCTTAGTGC TGCCAGCTAA CGCATTAAGC ACTCCGCCTG	60
GGGAGTACGA CCGCAAGTGT ATAACCTAAA GGAATTGACG GGGACCnCA CAAGGTTGGA	120
GCATGTGGTT TAATTCGAAn CAACGCGCAG TAACCTTACC AAATCTTGAC ATCCTTGAC	180
AACTCTAGAG ATAGAGCCTT CCCCTTCG	208

(2) INFORMATION FOR SEQ ID NO: 4660:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 365 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4660:

ACGTCGCGAG AACGCAATTA GCTGAAAAAG ATTACAACAT TAGAACAAAGA TTTAAAGTCA	60
CATTTAGTGA ACATCAAAGG CCGAATAACA TCATAAATTA CGATTAGATA TAACAAAAGA	120
GCTTGGGACA TAAGTCCTAA AGTCTTAGGC AAGTAAAAAA GTGATTCTA TTATTTATTT	180
GATAGAAATC ACTTTTGAT ATGTATTTnT ATGTACAGCT CGTTGAGCnC TATTTCCCTT	240
ATATTAGTGC CATAATACAA ACCTAGCTCT TGTTAACCTT TATTATTCCG AACTGACATC	300

GGTGAACCCA ATAGCCTCAT AAGCAAACAG CTTACATCAT TTTCTTGAnT GGTTTCGTT 360
CTGTC 365

(2) INFORMATION FOR SEQ ID NO: 4661:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4661:

AAAGTATTTC TTTATGTTGG GGGGCACCCC ACTTTGnCAT TGTCTGTAGA AATTGGGAAT 60
CCAATTCTCC TnATGTTGGG GCCCCGCAGT TCAACTACTG CCAATATAAGT GTTGTAGTGT 120
CTAAGACATA AAAGTCATC TCAGTCACAA TTACTTTATA GCCTATCCAT CATCTTTCT 180
ACATGAAATT TTTCCAAGTG ATATATTTT 209

(2) INFORMATION FOR SEQ ID NO: 4662:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4662:

TTATGGCACT TAAAACCAGC GATGACGATT GCAGTATCAC ATGGTATCTT CAACATAACA 60
AATACTTTGA TTCAATTACC ATTTGTAGCA GGTTTAGCAT GGATTGTTAC AAAGCTTGTC 120
CCAGGTAAAG ATATTGCTGA TGACTATAAA CCTCAGCACT TAAACCAAGG CTGTTATCA 180
CGCACCTGGT GTTTGCATAC CAGGAACTCC AAAAGGATTA CCAAATGTnG GGGCAGAnTG 240
GCCTAA 246

(2) INFORMATION FOR SEQ ID NO: 4663:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4663:

AATGGTGTAT TATGAGTAGT AATAATTAGC AAAGAGGTAA ATTAAGTGAT GTCGCGTCAT 60
TTAAGGAAGC GATTACAAT CGAGAACAC AAAGTACAAC TGGTATCGGC GAAGGTATnG 120

CCATTCCACA TGCCAAAGTG GCCGCAGTTA AGTCACCAGC TATTGCGTTT GGTAAATCTA 180
AAGCAGGC GT AGATTATCAA AGnTTTGTT ATGCAACCAG CACACT 226

(2) INFORMATION FOR SEQ ID NO: 4664:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4664:

TTCCGTCTCG GCACCATT TT ACGGCCGTAG CTCAATTGGA TAGAGCGTTT GACTACGGAT 60
CAAGAGGTAT GGGTCGACT CCTATCGGGC GCGCATT TT AAATTAATTG AATAACGGGA 120
GTAGCTCAGC TTGGTAGAGC ACTTGGTTTG GGACAAGGGC GCAGGTTCGA ATCCTGTCTC 180
CCGATTACTT CTAAATCCAT TTATGGGGCT ACTCACTGGG nACGCCTTT nCAC 234

(2) INFORMATION FOR SEQ ID NO: 4665:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4665:

GTACATCTAA AATCATCCAT GAAGGTTGT TACCTGAATT ACGGAATGAT TCAACAAC TT 60
CTAAACGTTT AATTnACCAG TAAGTCTTG CCAAGTAGCT GATTCCAAC TATCGCGTAC 120
AATTAAAGTC TTCGTCAAGA TCAATCCTCT TCAAGTAAAT CTTTAATAAC CTTCTGCACC 180
CATTTTGCA CGAATT 196

(2) INFORMATION FOR SEQ ID NO: 4666:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4666:

CCGCCGAACA ACTACTTGT TTGTTGATTC TCTCCACCTG TTTCAGTAGT TCAGATTCT 60
TAGATTGTGG TTTTTAGTT GGTGCCATGC TTTAACCTTT TCATTGATT CAATAACAGG 120

TGTTACTACT TACCTGTTCC ACGGTTAGA AGGCTTTAG GTTCTTCTTG GCAGTGGTA_n 180
GGTTTACCAAG TTCAGCGGTA CCGCGGTGTT GGnCGTGTG GATTTC 226

(2) INFORMATION FOR SEQ ID NO: 4667:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4667:

GTTCTGAATA GGGCGTTTAG TATTTGGTCG TAGCCGAnAA CCGGTGATCT ACCCTGGTC 60
AGGTTGAAGT TCAGGTAACA CTGGAATGGG AGGACCGA~~A~~ CGACTTACGT TGAAAAGTGA 120
GCGGATGAAC TGAGGGTAGC GGAGAAATTC CAATCGAACCC TGGAGATAGC TGGTTCTCTC 180
CGAAATA 187

(2) INFORMATION FOR SEQ ID NO: 4668:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4668:

CTAAGTGGAG TTGTCACAAC ATCTTAAAC GTTCCAGGTA AATAGTCTTT TGCCATTTE 60
GAAAATGCTT TTGCCAACGT TTTATAAATA TCCCAGTCTG AACGCGATTC CCATAACGGA 120
TCAATGGCAG GATTGAAAGG ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATG_n 180
TT 182

(2) INFORMATION FOR SEQ ID NO: 4669:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4669:

AGTTACGTTA AAAGATGAAA ACGACAAAGT TTTAAAAACA GTTACAACAG ATGAnAATGG 60
TAAATATCAA TTCACTGATT TAAACAATGG AACTTATAAA GTTGAATTG AGACACCATC 120
AGGTTATACA CCAACTTCAG TAACTTCTGG GAAATGATAC TGCAAAAAGA TTCTAATGGT 180

(2) INFORMATION FOR SEQ ID NO: 4670:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 185 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4670:

GGGGCAAAGT CATTnCATAG ATTAATGGTT CTCCGATACC TAGGAAACCA ACTGGCAATG	60
CACCTTTAA AGTATTACGT AATGTTGTGT TGCCTTACA TCTTACCCAA AGTGCTAATG	120
CGGCACCTAC TTGTCCAGCA CCAGCCATCG CTGCAATTGG CAATAAGTAA GTAG A CCTG	180
ATTGG	185

(2) INFORMATION FOR SEQ ID NO: 4671:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4671:

CTGACGAACG AGAAAAGAGC GCAACGATT AGTAGAGTAA ATGAGTTAAG CGAGACCGAA	60
GAAGAGGAAA GAAGCAAGCG ATTGTCACAA GTCAAGAAAG GTTCTTAGCG TTCGATGGTA	120
GCCAACCTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAA AAAAATGGAT GCGATGACCG	180
CATTGAGACC GCAAGGnTnT	200

(2) INFORMATION FOR SEQ ID NO: 4672:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4672:

CCCGGGGTAC AGTTATTCCC CAGAGTCAAC GCGGGGGTTG GACTCGATGT CGGTCATCGC	60
ATCCTGGGCT GTAGTCGGTC CCAAGGTTG GGCTGTCGC CATTAAAGCG nACGnTGCTG	120
GGTCAGACG CGTGAGCAGT CGGTCCCTAT CCGTCGTGGG CGTAGGAAAT TTGAGAGGGC	180

TGTCCCTAGT ACGAGAGGCC GGGATGGCAT ACCTTGGTGT ACCATTGTCG TGCCACGCAT 240
AGTGGGTAGT ATGTGTGGAC G 261

(2) INFORMATION FOR SEQ ID NO: 4673:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4673:

ATAGGGCGTT TAGTATTGG TCGTA_nCCAG AAACCAGGTG ATCTACCCTT GGTCAGGTTG 60
AAGTTCA_nGT AACACTGGAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA 120
ACTGAGGGTA CGGGAGAAAT TCCAATCAA_n CCTGGAGATA GCTGGTTCTC TCCGAAATAG 180
CGTT 184

(2) INFORMATION FOR SEQ ID NO: 4674:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4674:

CCCAGTCAAA CTGCCCGCCT GACACTGTCT CCCACCACGA TAAGGTCGTG GTTGAGAAA 60
GCCAACACAG CTAGGGTAGT ATCCCACCA_n CGT_nCTCCAC GTAAGCTAGC GCTCACGTT 120
CAAAGGCTCC TACCTATCCT G_nAACAAGnT GTGCCGAATT TCAATATCAG GCTACAGTGA 180
AAGCTCCACG GGGTTCTTTC CGT 203

(2) INFORMATION FOR SEQ ID NO: 4675:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4675:

nnGTTTGTAA ATAATATGGT GGAGACTAGC GGGATCGAAC CGCTGACCTC CTGCGTGCAA 60
AGCAGGGCGCT CTCCCAGCTG AGCTAAGCCC CCATAATAAT T_nAGTATAT CGGGAAGACA 120
GGATTCAAC CTGCGACCCC TTGGGTCCCA AACCAAGTGC TCTACCCAGC TGGAGCTTAC 180

TTTCCCGGTA TTATTTAACG CGGCCCGATA GGGAGTCGGA ACCCATTAA

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(2) INFORMATION FOR SEQ ID NO: 4676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4676:

TCTAAAAATC GCGCACTTAA ACCGCTTATG ACAATCATTA TTACCTCAAT ATGCTTGTCA	60
TCACTTGCCT TTATCGTCGT TCATTGGCTA TATAGTTAAT ATGAAAAGAC GCTCAAACAC	120
TTACAAATT AGTGTGCnGA GCGTCTTATT TTTATACTTT AAAAGTCGTA TTGGTTGT	178

(2) INFORMATION FOR SEQ ID NO: 4677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4677:

GCAAGTAAGC ATAATGTGGA GCCGTAGCGA AACAGTCTGA ATAGGGCGTT TAGTATTTGG	60
TCGTAGACCG GAAACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG TAACACTGAA	120
TGGAAGGACC GAACCGACTT ACGTTGAAAA ATGAGCGGAT GAACTGAAGG TAACCGGAGA	180
AAATCCAAT CGAACCTGG GAGATAAGCT TGGGnTCTCC TCCCAAAAT AAGCCTTTA	240
GGGGCTTAAG CCTCCAAAGT GGATGATTAA ATTGGAAG TAAAAn	286

(2) INFORMATION FOR SEQ ID NO: 4678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4678:

CACACGGCTT ATGGTAACAA AAAATTCCCTT TGGAGCATTA TGGAGCGGAA GATAGGTTA	60
CACCTATACC TCGTTCCGGA AGGAnTGTTC TAAAAGTGAA CTACTCCGC AATATTAAAT	120
ATGGAGCGGA GATAGGATTAC ACACCTATAC CTCATTCCAG AGGATGTATT CTAAGAGTG	180

AATACTCCCC ATATATTAAA TATGGAGCGG AGATAGGATT GACCATAⁿ

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(2) INFORMATION FOR SEQ ID NO: 4679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4679:

ATGACTGCTT TTTATTATAC TTTACATTTC TCGTTTCGTC AGATTCAAAC GTTTTCAC	60
CGCCAAGCCA TCTTTCTTTG TGTTTGCTTT TATTTGACG TTTAGACAT AAAAAAAGAG	120
ACCTTGCGGT CTCAATG ⁿ GG CTCATCGCAT CCACCTTTG CCTGGCAACG TTC	173

(2) INFORMATION FOR SEQ ID NO: 4680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4680:

AAAAGTAACA AGAGAAGGAC AAAAAGGTGA GAAGACAATA ACGACGCCAA CAAAAATCCA	60
TTAACTGGAG AAATTATTAG TAAAGGTGAA TCGAAAGAAG AAATCACAAA AGATCCCATT	120
AATG ⁿ TTAA CAGAATACGG ACCAGAAACG ATAACACCAG GTCATCGAGA CGAGTTGAT	180
CCC	183

(2) INFORMATION FOR SEQ ID NO: 4681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4681:

CGGTGCTTTC ACTTTCTAC AGACTGGTTA CTATCGGTCA GAGAGAGATT TAGC ⁿ TTAGG	60
AGATGGTCCT CCCAGATTCC GACGAATTTC ACGTGTTCG TCGTACTCAGGATCCACTCA	120
AGAGAGACAA CATTTCGAC TACAGGATTA nTACCTTCTT TGATTCACT TGCCAGATGA	180
TTCGTCTAAT GTCGTCTTT GTA	203

(2) INFORMATION FOR SEQ ID NO: 4682:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4682:

GGGTCACACC	TGTTCCCATG	CCGAACACAG	AAGTTAACGCT	CCTTAGCGTG	CGATGGTAGT	60
CGAACTTACG	TTCCGCTAGA	GTAGAACGTT	GCCAGGCAAA	AAGTGGGATG	CGATGGAGCC	120
GCATTGGAGA	CCGCAAGCCT	CTGTTCTTG	ATGTCTAAAA	CGTnCAAAAT	AAAAGCGAAC	180
ACAAAGA						187

(2) INFORMATION FOR SEQ ID NO: 4683:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4683:

GGCTACACTG	GTCATGATGC	TGCTAAACTA	CGTGATTATn	ATGAAACACA	TCATGCTTG	60
TCTGGATATG	AAATGATTGA	CCGAGCAAAG	GTGCCATTGC	AACAAATGAA	GTCAATGCTG	120
CGATGGGTAT	ATTTGTGCAA	CGCCAACAAAC	TGGTTCCCTCC	GGTACCATCC	CGGTGCAGTT	180
TTAAATT						187

(2) INFORMATION FOR SEQ ID NO: 4684:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4684:

AGTGCCAAGG	CATCCACCGT	GCGCCCTTAA	TAACCTAAC	TATGTTCCA	TCCTACAGGA	60
AACCGTTATT	AATCTTGTGA	GTGTTCTTC	GAACACTAGC	GATTATnTCT	TATGAATTCA	120
AGCTTATTTA	AAACTCTTTA	TTCACTCGGT	TTTGTAAAAT	CTATATTT		68

(2) INFORMATION FOR SEQ ID NO: 4685:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4685:

ACGGGAAGTA GCTCAGCTTG GTAGAGCACT TGGTTGGGA CCAAGGGGTC GCAGGTTCGA	60
ATCCTGTCTT CCCGATTACT TCTTAAATTC CATTTATGG GGGCTTAGCT CAGCTGGGAG	120
AGCGCCTGCT TTnCACGCAG GAGGTCAAGCG GTTCGATCCC GCTAGTCT	168

(2) INFORMATION FOR SEQ ID NO: 4686:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4686:

ATGATTCAAG CTTATTAAA ACTCTTATT CACTCGTT TGCTTGGTAA AATCTATATT	60
TTACTTACTT ATCTAGTTT CAATGTACAA TTTCTTTTA GTCAAGCGCT CGCATACTGC	120
nTTATTTCA AAAAATCAAA TGCTCATTAA CAAAAGTAAA CTCCGCTTTT AATT	174

(2) INFORMATION FOR SEQ ID NO: 4687:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4687:

TGTTGTTGAA TATGAAGAAG ATACAAACCC AGTGGTGGT CAGGTTACTA CTGAGTCTAA	60
CTTAGTTGAA TTTGACGAAG AGTCTACAAA AnGTATTGTA ACTGGCGCAG TGAGCGATCA	120
TACCACAGTT GAAGGTACGA AAGAATATAC AACTGAAGTA ATCTGA	166

(2) INFORMATION FOR SEQ ID NO: 4688:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4688:

AGAACCTTAC CAAATCTTGA CATCCTTG ACAAATCTAGA GATAAGGCCT CCCCTTCGG	60
GACAAATGAC AGTGGTGCAT GGTTGTCGTC ACTCGTGTCT GAnATGTTGG GTTAAGTCCC	120
GCAACGAGCG CAACCCTTAA GCTATTGCCA TCATTAAGTT GGGCATCTAA TTGACTGCCG	180
GTGACAAAC	189

(2) INFORMATION FOR SEQ ID NO: 4689:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4689:

TAACCACTCC TCTTAACCTT CCAGCACCGG GCAGGGCGTCA CCCCTATACA TCACCTTACG	60
GTTCAGCAGA GACCTGTGTT TTTTGATAAC AGTCGCTTnG GGCTATTACAC TGCGGCTCTT	120
CTGGGCGTTA ACCCTAAGAn ACCCTTCTCC CGAAGTACGG GGGCATTGG CGAGTCCTAA	180
CGAGGTCGTC GTCACTTAGA TTCTCATTT GATACTGTGT GGTTGCG	227

(2) INFORMATION FOR SEQ ID NO: 4690:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4690:

AGATAATGCA CCATCAACTA ATGGATATTG ATGCCAGTT GGGGGCCAGA AATCATAAAC	60
GTCTTCAGTG TAAGCAACAG CATCTTCATT TnGCAGCAA AATGCTTGGG TTATGTGCAA	120
TAACCATCGC AACTGCGCCA CACCTGTGT TGGCTCGCCG CCTGAAGGG GGTG	174

(2) INFORMATION FOR SEQ ID NO: 4691:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4691:

TTTTTTTTA AAAAAGGGA AGGGAAAAnA AAAAGGGAAA AAAATTAAAC CCAAGGGTTT	60
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TTAAAGGGGG CCCAATTTT CCCAAAAAAA AAACCCTTG GGTAAATT TTTTAAAAA 120
CCCAACCAA AAnTTTTTA AAAAGGGTTT TGGGCCCCC TTGGGAAAAA TTTTCCC GG 180
GTTAAATT TTTAAAAGG GTTCCCTTT AAATTTGGG AAAAACCCC TTTTTTTT 240
TTAAGGAAT TTAAAAAATT TAAGGCCCTC CCCTAAATTA AAATTAAAGG TGGGAAAAA 300
AAAATTAATT AAAnAACCA TTTTTTTT TTAATT TTAACCAAAGG GGGTAATTG 360
GCC 363

(2) INFORMATION FOR SEQ ID NO: 4692:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4692:

TAGTGTCAAT TTTATTGATA TTTGCAATTA AACTGAAATT TAATTTTCG GATGTATT 60
nTTTACTTAA AGTAAAATAG AACACGATT TGATGTCTGG GAATAGTGGA AATGATAAAA 120
ACTACTAATG ATTGATTAAG TAGTGGTTCT TAACATTAGC CTC~~A~~CTAAT TGTTACTTAA 180
AAATAGGAAT ACATGAGTAA AACTCAAnTGG 210

(2) INFORMATION FOR SEQ ID NO: 4693:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4693:

ATAGTAGTAA AGTATTTCT TCCAAACATT TATTTGATT AAGTCTTCAT CATTAGTATT 60
CTCAGCTCCA CATGCACCAT CTTCCACCTC AACCTATTAA CCTC~~C~~ATCATC TTTAGGATCT 120
TATAACCAAT TGGAAATCTC ATCTTGAGGn nGCTTCATCT TAGATGCTTT CACACTTATC 180
CCTCCACACA TAGCTACCCA GCTATCCGT 209

(2) INFORMATION FOR SEQ ID NO: 4694:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4694:

GCACATTAAC CnAAGCACCA GGCCATATAG CAATTGTTGA TACAGTATTT AAATATTTAG	60
CATGTGACGG AATAGTTACA TATGTATTCA CTAAGGCCAT AATGACAAAT CCATTAAGAA	120
GTTGGATGCT TATTCGACCC TGCTAGATGA TCTGATGAAC GGAACGCATA TTAAATAAGT	180
ACGTGGTTAT GGATCAGTAA GATACTCTAC CAGTTACCAG nG	222

(2) INFORMATION FOR SEQ ID NO: 4695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4695:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTAT CTAAATGACT ACCAATTAAA	60
TCTATTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT	120
TCTTCAACTA AGTCACGATA TAATGTTTT GAATTTTCG	159

(2) INFORMATION FOR SEQ ID NO: 4696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4696:

AATATGGTAG TTTTTAACCTT ATCTATTAAG GTACAATTGA CCAAATCGAT AAAATAATA	60
ATACGTATCG TCAGACAATT TATGTCAATC CAAGTGGAGA TAACGTTATT GCGCCGGTTT	120
TAACAGGTAA TTTAAACCA AATACGGATA GTAnTGCATT A	161

(2) INFORMATION FOR SEQ ID NO: 4697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4697:

CCAAACTCAA TATGGCTTTA TTGGCACAGG GAACAGATAT GGAAGGTTTT ATTTATGGnT	60
---	----

GATGGGTGTT AATGAACATG GCGTTGCCAT TTCAACACAA TATTTCGAG GTTATAGTTC 120
ATATGGGATC AACACACAAA GCCGGACGCA GTGAATATTA CGCAAAATGA 170

(2) INFORMATION FOR SEQ ID NO: 4698:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4698:

CCACGGCTAA CTACTGCCAG CAGCCGCGTA ATACGTAGTG GCAAGCGTTA TCCGGAATTAA 60
TTGGGCGTAA ACGCGCGTAG GnGTTTTTA AGTCTGATGT GAAACCCACG GTCAACCGGA 120
GGGTCATTGG AAACCTGGAAA CTTGAGTCAG AAGAGGAAGT G 161

(2) INFORMATION FOR SEQ ID NO: 4699:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4699:

TAAATCTTCA TCAATATGAT CTAACCAATA TTGATAAAAC CTTGATGTGT TTCGTGTCAA 60
TGACATACCA TATCGACTAG GTACCTTTT AGAATGTTGA TTAATACAA CAAATATCAT 120
GGGCAAGGTC ATCTTGCAAA ATGGATTCGA TTCAAGTGGG AGGGnCGATG ATGGACGTGC 180
TGCATGCACT GATGACCCTT TTTGCCATT CTGGCAAATC CCACCATGAA ATGACTGACG 240
CGGACGCh 248

(2) INFORMATION FOR SEQ ID NO: 4700:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

CCCGACGAAG CGAACGTTG GCACGTCTC AACGAGAGAC TCGGTGAAAT CATAGTACCT 60
GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 120
GATATTGAAA TTCGGCACAG nTTGTACAGG ATAGGTAGGA GCCTTGAAA CGTGG 175

(2) INFORMATION FOR SEQ ID NO: 4701:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4701:

TACAGGGTAG	TGAGATTTCG	AAACAATATG	GAGAAGCAGG	ACTTCCTGGA	AAATACAATT	60
AATGTTTATA	CGAATGGTCA	TGCTGGTCAA	AGTTCTTGCA	GGCATATGCA	CCGAAAGCTT	120
AATGATTCCAT	CATACTGGAG	ATGCGAATGA	CTATGTTGGG	TAAAGGATTT	ATCTGGT	177

(2) INFORMATION FOR SEQ ID NO: 4702:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4702:

CGATTGGATT	GCACGTCTAA	GCAGTAAGGC	TGAGTATAG	GCAAATCCGG	TACTCGTTAA	60
GGCTGAGCTG	TGATGGGGAG	AAGACATTGT	GTCTTCGAGT	CGTTGATTTC	ACACTGCCGA	120
GAAAAGnCTC	TAGATAGAAA	ATAGGTGCC	GTACCG			156

(2) INFORMATION FOR SEQ ID NO: 4703:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4703:

CTTGAAAAAG	ATGGTTATT	TGTTGAAGTA	ATTGACTTAC	GTACTGTTCA	ACCAATGAT	60
GTTGACACAA	TTGTAGCTTC	AGTTGAAAAA	ACTGGTCGTG	CAGTnGTCAG	CAAGACGCAC	120
AACGTCAAGC	TGGTGTGGT	GCAGCAGTTG	TAGCTGAATT	AAGTGA		166

(2) INFORMATION FOR SEQ ID NO: 4704:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4704:

GGGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGnCT CGAACCTACG	60
ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGATTAA TATTATGCCT	120
GGCAACGTTTC TACTCTAGCG GAACGTAAGT TCG	153

(2) INFORMATION FOR SEQ ID NO: 4705:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 163 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4705:

AGGTAGAGCA CTGTTGGAC GAGGGGCCCG TCTCGGGTTA CCGAATTCAA ACAAACTCCG	60
AATGCCAATT AATTAACTT GGGAAAGTAG ACACATGGGT GATAAGGTCC GTATTCGAAA	120
nGGAAACAGC CCAGACCACC AGCTAAGGTC CCAAAATATA TGT	163

(2) INFORMATION FOR SEQ ID NO: 4706:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 203 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4706:

TAAGGTTGGG ATTGTTGTG GGCTCGTTGC CACCCATTGT ACggcactca TCAnTTCAAG	60
CCACCAGCTA CAGTATATCT CCTTGACCAAG CCATAATTG ATTGGCTGA GTCGCGATGG	120
TTTGTAAATCC TGATGAGCAG TAGCGATTCA TGTTGACCh GTACCCGTCA GATATCCGCA	180
GCAATGCAAT GTTGTGCAAG TTT	203

(2) INFORMATION FOR SEQ ID NO: 4707:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4707:

CGGGTGAGAA TCCGTCCACC GATTGACTAA GGTTTCCAGA GGAGGCTCGT CCGCTCTGGG 60
TTAGTCGGGT CCTAACGCTGA GGCGCAGnGT AGGCGATGGA ATAACAGGTT GATATTCCGT 120
TACCACTAT AATCGTTTA ATCGATGGGG GGC 153

(2) INFORMATION FOR SEQ ID NO: 4708:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4708:

nCTATAATGA ATAAATAATT TAGAAATATG CTTCCGATTG TTGATGCTT TAATTCAAGTT 60
AGAACATCA TAGAATGCAT GATTACTGTT GTAAAGATAC GTAATGTTT GTATTGACTG 120
TATGTCTTG GATAGAGTTA CAAACTTATT 150

(2) INFORMATION FOR SEQ ID NO: 4709:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4709:

)
AAAATTGGG TTCTCAAATC ATCGAACAT AACAAACAA CCTAACGAAAC ATGTAGGCCG 60
TTGTCACTTA ACTTCTTGTT TTTCCGATGA CAGCTTCTA TnAGAGAATG TCATGATTAT 120
TTTATATTCA CTTCAATGTT ATCAGTATTA GTGCCA 156

(2) INFORMATION FOR SEQ ID NO: 4710:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4710:

GTTGATATTCTGTACCACTATAATCGTT TAATCGATGG GGGGGACGCA TAGGATAGGC 60
GAAAnGTGCGA TTGGATTGCA CGTCTAACGCA GTAAGGCTGA GTATTAGGCA AATCCGGTA 120
TCGTTAAGGC TGAGCTGTGA TGGGGAGAA 149

(2) INFORMATION FOR SEQ ID NO: 4711:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 160 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4711:

TTGACTTCAA TACCATGGGC CAGGTACnCT TTAAATGTTG TTGTCTCAGT TAATATTAAT	60
TGGCTTTCT TTTGCATAAT TGACAATGGC TTCTGCCAAT GGGTGTTCAG AATCTTTTC	120
AGCAGTAGCA AGTAGTTGGT AGCGTTTGAT TGGTCACCAG	160

(2) INFORMATION FOR SEQ ID NO: 4712:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4712:

ATAGTGAACC AGTACCGTGA GGACnAGGTG AAAAGCACCC CGGAACGACG TGAAATAGAA	60
CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC GTGCCTTTG	120
TAGAATGAAC CGGCGAGTTA CGATTTGATG C	151

(2) INFORMATION FOR SEQ ID NO: 4713:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 145 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4713:

ACCAAGTTGAT CTACCCTTGG TCAGGTTGAA GTTCAGGTAA CACTGAATGG AGGACCGAAC	60
CGACTTACGT TGGAAAAGTG AGCGGGATGA ACTGnGGGTA GC GGAGAAAT TCCAATCGAA	120
CCTGGGAGAT AGCTGGTTCT CTCCG	145

(2) INFORMATION FOR SEQ ID NO: 4714:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4714:

TGTnACGCAG AGATCGCGGG TTCGATTCCC GTCGAGACCG CCATTTAATT TTATAATTAA	60
TAGCGATGTA CCTATAATAA TGGAGGAATA CCCAAGTCCG GCTGAAGGGA TCGGTCTTGA	120
AAACCGACAG GCCTTAACGG GCCGCGGGGG T	151

(2) INFORMATION FOR SEQ ID NO: 4715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4715:

TCGTATTGAA TGGCTTCGTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT	60
GCTCCCTCAG GAGTCTGCC ATTAACTA CGTATTAACG TGTAATTAA CTTTGnAATA	120
CTTTAAAAAA ATAAGACACT TTGCCAACCTT G	151

(2) INFORMATION FOR SEQ ID NO: 4716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4716:

GCTGTCATCG GAAAACAAG AAGTTAAGTG ACAAGGGTT ACATGTTGCT TAGCTTCTT	60
TATTATGCGT AATGATGTAA AAAGACGAAT ATTCATTTGT TTGTAAAAGT GGCATTTCTA	120
TGTCTTAAAA GTGACGAAAC TTCACnCTGT GC	152

(2) INFORMATION FOR SEQ ID NO: 4717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4717:

GGATACTAGT AAAACCATAAT TTAGTAAATA CAGATEGAnT AAATCTTTA AGGCTTATAAA	60
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ACGCTCATCT GACATTGTAG AATTCATGCT TTCAAAAGAC GATATACTAC GACACTCCTA 120
CGAACTTGTC CAAGGATTAC GAAA 144

(2) INFORMATION FOR SEQ ID NO: 4718:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4718:

ATCATAAGGG GCATGATGAT TTACGTCATC CCCACCTTCC TCCGGTTGT CACCGAGTC 60
AACTTAGAGT GCCCAACTnA ATGATGGCAA CTAAGCTTAA GGTTGCGCT CGTTGCCGGGA 120
CTTAACCCAA CATCTCACGA CACGA 145

(2) INFORMATION FOR SEQ ID NO: 4719:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4719:

AAATACCTT CCACGATCTT CAGCTGGCG CCTCTGCACT CGCAAACGCA CTTGATGCAT 60
CAACAACACC ACCAAATAGT CCCTGCAATA ACCTCACAGT ACAAACTGTA ATGGTGTGCGT 120
ACACnATGCC ATTTAAAAAT AGCATACCGG CAAAGC 156

(2) INFORMATION FOR SEQ ID NO: 4720:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4720:

TTAAATCGAG TCTCTTTAC AGGTCCATAT TTTGTTACGT ATCGACCGGT GGCTAACTAC 60
GTCTCCTGTT TCTGGATTCT TAATTGGGT TTACTGGAAC TTCTTCTTTC TCTCnGTTGG 120
TAACTCGGAT CAAATTCGTC TCGATGACCT GG 152

(2) INFORMATION FOR SEQ ID NO: 4721:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4721:

CACTAGTTCA AGTTCAAGTG GCGACGATTG GTATTTACA AGAATTTCAT CAACAAGGAT	60
TTAATTAGCT TAAACGCnGC AATCCCTGTG TTACTAGGGC GGATA A ATT GGTACCACGG	120
TTACAGCTAT CTTAGCTAGT TTAGCC	146

(2) INFORMATION FOR SEQ ID NO: 4722:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4722:

CCACACCAAT ATTTTGCCT AAGTA n ATCG CATTAAACGT TTGTCTTCCG CCATTTGAGC	60
CACACTGCTC CAGCTCATAG CGCTATATCG CAGGAAATAA TCATTCCGCC ACCACAACCC	20
TAACATTACC CAGCCATACA GCCATACCAAG GGCCAC	156

(2) INFORMATION FOR SEQ ID NO: 4723:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 161 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4723:

ACGGTCTTGC TGTCACCTAT AGATGGATCC GCGCTGCATT AGCTAGTTGG TAAGGTAACn	60
GCTTACCAAG GCAACGATGG CATGAGCCGA CCTGGAGAGG GTGGATCGGG CCACACTGGG	120
AACTGAGACA CGGTCCAGAC TCCTACGGGG AGGCAGCAGT A	161

(2) INFORMATION FOR SEQ ID NO: 4724:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4724:

CAGAAAGCTC ACGGGGCTTT CGTCTGTCGC GGGTAACCTG CATCTTCACA GGTACTATGA	60
TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGnCTTCGT GCGGGTCGGA	120
ACTTACCCGA CAAGTAATT CGCTACCTTA GGACCGTAT AGTTA	165

(2) INFORMATION FOR SEQ ID NO: 4725:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 149 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4725:

GGACGTTATA AGTGCTGAAA CATCTAAGCA TGAAGCCCCC CTCAAGATGA nATTTCCTCAA	60
CTTCGGTTAT AAGATCCCTC AAAGATGATT AGGTTAATAG GTTCGAGGTG GAAGCATGGT	120
GACATGTGGA GCTGGACGAA TACTAATCG	149

(2) INFORMATION FOR SEQ ID NO: 4726:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 4726:

TTGAATTTTT GAAAAAAA TGCCGAAATA AAAGATGCCA AGATATCCGC CGGGTAAAAA	60
ATTAAGTTTC CGAAAAACCA GGTGTTGGTA CCCATTGCAT CTGGGGTGGC AAAAGCATTT	120
GCAGATAAAA TTGTCATCAG TGGTTACGAT GGTGGTACAG GGCTTCACCC AAACGAGTAT	180
CAGCATGCCG GTGTTCTGG GAGATGGTTA GCAGAACACA TCAACATAAA CTAATGCTAA	240
GAncGGTAAA GTAGACAnCG GTAGTATACT GAAAT	275

(2) INFORMATION FOR SEQ ID NO: 4727:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 149 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4727:

ATCAATGAAC AACACATACA GATGGTACTG CGACGCCTAG AGTAACAAAA TAAGTTTGT	60
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AACTCTATCC AAAGACATAC AGTCAAT~~CA~~ AAACATTACG TATCTTACA ACAGTAATCA 120
TGCATTCTAT GATGCTTCTA ACTGAATnA 149

(2) INFORMATION FOR SEQ ID NO: 4728:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4728:

GCACGTTATT CCATTATCTT AATGGTTATC TTATCCTCAA CTAAATTGGA GGAATCACTA 60
TGACAATTAA TAAAGAACCG TTCTTGGCGC AGCACAATGG GCGCTCA~~TG~~ GCAGACTTT 120
GTGATGCTGA CTTAAAGTAA ACTATTAGAT ATTGnGTG 158

(2) INFORMATION FOR SEQ ID NO: 4729:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4729:

TCATTGACAT CGCTGGAATA GGTGTAAATC CTGCGATTG ATCTGGACCA TATTTTTTA 60
TTGTATACAG TAATTGTGCT GCGATTATCT CTGTAACGTC TTTCCAATTG GAnCGCACGT 120
GCCCTCCCAC ACCTCGGG 138

(2) INFORMATION FOR SEQ ID NO: 4730:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4730:

TAAAGACTAT ACCATTCTAT CCAATAATAA TTGGATTGG ATTTGTCTGA ATTGTAACC 60
GAGAGGCCCC TCGTCCAAAC AGTGCTCTAn CTCCAATAAT CATCACTTGA GGCTAGCCCT 120
AAAGTATTTG GGAGAGAACC AGCTATTTCC AGTCGATTG GAATTCTCC GCTACCCTCA 180
GTTCATC 187

(2) INFORMATION FOR SEQ ID NO: 4731:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4731:

CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT TCGCCATTAA AGCGGTACGA	60
AGCTGGGTTTC AGAACGTCGT GAGACAGTTC GGTTCCTA CCGTCGTGGG CGTAGGAAAT	120
TTnAGAGGAG CTGTCCT	137

(2) INFORMATION FOR SEQ ID NO: 4732:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4732:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA	60
TCTATTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTT	120
TCTTCAACTA AGTCACG	137

(2) INFORMATION FOR SEQ ID NO: 4733:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4733:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA	60
TCTATTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTT	120
TCTTCAACTA AGTCACG	137

(2) INFORMATION FOR SEQ ID NO: 4734:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4734:

AAAACATAAA TACAAAAATA TAGCTATTAC TATAAAAAAC AGCAGTAAGC ATATTTCAA	60
ATTGCAAATT ATCCTACTGC TGTTCTTTT GGGCAGTGGG nACAGCAAAT GATATTTCG	120
ACAAAAATTAA TTTCGTCGTC CCACCCCCAAC TTG	153

(2) INFORMATION FOR SEQ ID NO: 4735:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 142 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4735:

TAGAAATTAC GGACCCAATT TCTCTATGTT GGGGCCATC CCCAACTTGC ACATnATTGC	60
AAGCTGACTT TTCGTCACTT GCTTTGTTGG GGCCCCGCCA ATAAGCGTTG TAGTGCCTAG	120
TACTTGATT GATGTCCAAG TT	142

(2) INFORMATION FOR SEQ ID NO: 4736:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4736:

ATGTTATTCA AAGTAAATTG CTTTGCCTGA TTTTGCAGAC TGATAAAATCG CTTCAAGAAT	60
TTTTGTAACT ACCATTGCTT GTTCCGGTTT CACAAC TGTTGTCAGTATCAT TTACAAACnGC	120
ATCAATCCAA GCTTTG	137

(2) INFORMATION FOR SEQ ID NO: 4737:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4737:

GGTCGTTTAG TATTTGGTCG TACACCGCAA ACCAGGTGCA TCTACCCTTG GTCAGGTTGA	60
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AGTCAGGTA ACACGTAAAT GGAGGACCGA ACCGACTTAC GTTGAAAAnT GAGCGGATGA 120
ACTGAGGGTA CGGGAGAAAT TCCA 144

(2) INFORMATION FOR SEQ ID NO: 4738:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4738:

GGGTAGCTAT GTGTGACGG GATAAGTGCT GAAACATCTA AGCATGAACC CCCCTCAAGA 60
TGAGATTCC CACTTCGGTT ATAAGATCCT CAAAGATGAT GAGGTTAATA GGTCGAGGTG 120
GAACATGGTG ACATGTnATC TGCTTTCTA ATCATAAC 157

(2) INFORMATION FOR SEQ ID NO: 4739:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4739:

GCTTTATGTC TAAAACGTCA AAATAAAAAG CAAA@CAAA GAAAAATGGC TTGGCGAAGT 60
GAAAACGGTT GAATCTGACG AAACGAGAAA AGAACGCAAC GAGTTTAGTA GAGCTAnATG 120
AGTAAGTGAG AGCCGAAGAG AGGGA 145

(2) INFORMATION FOR SEQ ID NO: 4740:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4740:

TAGTAGCACC ACCCTTAGAC CTTCTTGATT TGACATCGTT GTTCTTCCTT CCTTGGTCT 60
CGTTACTCAT TTAGCTCTAC TAAACTCGTT GCGCTTTTC TCGTTTCGTC AGATCAAACG 120
TTTCACCTCG CCAAGCCATT TTTCTTGTGT TTATTTTATT TGACGTTTAG ACATAAAAAA 180
GAGACCCACG TTCAACTTGC CnGCACGTTC TACTCTGCGG AnTAGTGGCT ACCA 234

(2) INFORMATION FOR SEQ ID NO: 4741:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4741:

GCAAGTCTTT TTAAAGGTAA CACTATCATT TATGCAATAAC GGCGCATTAC CAGAGTTGCA	60
TGGTCAAAAT ATATTGTTGT CATTGAAAGA TGGACGTGTA CAAAAATGCG TGTTACGTGA	120
TCATGATACT GTCAn	135

(2) INFORMATION FOR SEQ ID NO: 4742:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 145 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4742:

ACCCTGGTAC AGTTGAATTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA	60
AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGA GAnACCTGGT	120
TCTCTCCGAA ATAGCTTTAG GGCTA	145

(2) INFORMATION FOR SEQ ID NO: 4743:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4743:

TGTCATTCAA GTAGCGAAAG AATTTGCGCA AAACGCTATC GATAC B AAG GGGCGTTCAA	60
TGATTATCAT GGGTGCGGGT ATTAACCATT GGTTAACTC AGATACGATT TATnGTGCAA	120
TCTTAAACTT AGTTATGGTA TGTGGCGTCA A	151

(2) INFORMATION FOR SEQ ID NO: 4744:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4744:

TAAAGCTAAA AACACAGCTC ATAATATCAA AAAAGGTGCA GAAGAAATGG TTGAAGCGGC	60
AGGCGATAAA ATCAnAGATG GTGCATCTTGT TAGGCGAT AAAATCGGCG ATGTGTGGGA	120
TTATGTACAA CA	132

(2) INFORMATION FOR SEQ ID NO: 4745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4745:

CGTGCCTCT AACCAAGCTGA GCTATAGGCC CATTAATTG AATGAACAAA CATTCAAAAC	60
TGAATACAAT ATGTCAGTT ATTCCGCATC TTCTGAAGAA GATGTTCCGn ATATATCCTT	120
AGAAAGGAGG TG	132

(2) INFORMATION FOR SEQ ID NO: 4746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4746:

GTGATCCGAC TCAGATAGCG ATCCGACTCA GATAGCGACT CAGATTAGA CAGCGATTCA	60
GATTCAAGACA CGGATTAGA TTCAGATAGC GATTCAATT CCGACAGTGA CTCAGATTCC	120
GACAnTGACT CGGATTCA	138

(2) INFORMATION FOR SEQ ID NO: 4747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4747:

CATTATTGTA AACTGAACCTT TTCTGTCACCTT GCTGGTGnTT GGGGACCCCA CCAACTTGGC	60
ACATTATTGG TAAGCTGACT TTTCGTCACCT TACTGTGTTG GGGCCCCGCC AACTTGATT	120

GTCTGTAGAA ATTGGGAATC CAATTCTCT ATGTTGGGGC CCACACCCCA ACTCGACATT	180
GCCTG	185

(2) INFORMATION FOR SEQ ID NO: 4748:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 173 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4748:

ACCGAATCCC TTCAGACCGG TACTTGGTA TTCTCCAAA ATTATATGGA CCTTGACAGT	60
ACTCGAACCT GACGTACCGA AACGGTTATG AAGACCGTTA nCTCTAACCA ACTGAGCTAA	120
AGGATCCTAA ATATAATTAA ACAACTAATA AATAGTGGAC GGTGGAGGGA TCG	173

(2) INFORMATION FOR SEQ ID NO: 4749:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4749:

ACACAAGGAT AAGGCATTGT TGGATGTGGG ATGCTTAAC TGGGCAAGCG ATTGGTCGTC	60
CTAAAACAGG TACATATGCC GGCTATCTA CCTAGTCGGT TTAGATATTG CAGTGTCTGT	120
AATTAAAGGG CATGCAACCA AGTAnCTGAG GAAACAACCTT ATTTCATGG TGTCAAAAT	180
TGnTAAATAC GGTGTTGAC AATTGCGCAC CT	212

(2) INFORMATION FOR SEQ ID NO: 4750:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 140 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4750:

AATCTCAGGT TTTACCAAGC AAAACCGATG AATAAAGAGT TTTAAATAG CTTGAATTCA	60
TAAGAAATAA TCGCTAGTGT TCGAAAGACn GCAGCAAGAT TAATAACGCG TTTAAATCTT	120
TTTATAAAAG AAAACGTTA	140

(2) INFORMATION FOR SEQ ID NO: 4751:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 184 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4751:

ATTCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT CATCATCTT	60
GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGTTCAT GCTAGATGCT	120
TCAGACTATC CCGTCCACAC ATGTAACCAG nATGCGTGGA CGCATGGAAC AGGGATGTCA	180
TCCG	184

(2) INFORMATION FOR SEQ ID NO: 4752:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4752:

GGGATCTTCC GCAATGGGCG AAACTGTACG GAGCAACGCC GCGTGAGTGA TGAAGGTCTT	60
CGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACGTG CACATCTTnA	120
CGGTACCTAA TCA	133

(2) INFORMATION FOR SEQ ID NO: 4753:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4753:

GTATGCTGTG TGGCTTGTCA TGTTGGGTT TGGTGGCGA CCTGATTATT CCTGCGnTAT	60
ACGCTATGGC TGGAGCAGTG TGGCCAAATG GCGGAAGACA AACGTTAAT GCGATCTACT	120
TGGCGCAAAA TATTGGTGTG GCTGTCGGTG CTGCAATGGG CG	162

(2) INFORMATION FOR SEQ ID NO: 4754:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 134 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4754:

AATTCGATT C	CCTTAGTAGC	GGCGACGAAA	ACGGGAAnGA	GCCCAAACCA	ACAAGCTTG	60
TTTGGGGGTT	TGTAGGACAC	TCTATACGGG	GTAAACAAAG	GACGACATTA	GACGAATCAT	120
CTTGGGAAAG	ATGA					134

(2) INFORMATION FOR SEQ ID NO: 4755:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4755:

AGAGTGCCTA	ATAGCTCACT	AGTCGAGTGA	CACTGCGCCG	AAAATGTACC	GGGGCTAAAC	60
ATATTACCGC	AAGCTGTGGA	TTGTCCTTG	GACATGGCTA	GGAGAGCGTT	CTAAGGGCGT	120
TGAAGCCTGn	ATCGTAAGG					139

(2) INFORMATION FOR SEQ ID NO: 4756:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 163 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4756:

GGTCATTGGA	AACTGGAAAA	CTTGATTGCA	GAAGAnGAAA	TTGGAATTCC	ATGTGGTACC	60
CGTGAAATGC	GCAGAGATAT	GGAGGAACAC	CAGTGGCCGA	AAGCCACTTT	CTGGTCTGTA	120
ACTGGACGCT	GGATGTGCCA	AACCTGGGGG	ATCAAACAGG	TTA		163

(2) INFORMATION FOR SEQ ID NO: 4757:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4757:

CATGAAACTA GATAAGTAGT AAATATAGAT TTTACCAAGC AAAACCGACT GAATAAAGAG 60
TTTTAAATAA GCTTGAATTc ATAAGAAATA ATCGCTAGTG TTCGAAAGACATCACAnGAT 120
TAATACCGCG TTTAATCTTT TATAAAGGAC CGTAACCTCA 160

(2) INFORMATION FOR SEQ ID NO: 4758:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4758:

TACATGGGTT TATTGTTGAA GATGACGAAA TTGTAGAAAT TTAATATTCT AAAAAGGTTG 60
GGGACATAAA TCCCCCTAAA AAAACCAGCA GTAAGATAAT TTTCAATTAG AAAATATCTT 120
ACTGCTGTTc TCTATTTATA CCAnATTACT TTCGTAATTG TTAAAATTAA AAAAGGA 177

(2) INFORMATION FOR SEQ ID NO: 4759:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4759:

CGGTGTGTAC AAGACCCGGG AACGTATTCA CCGTAGCATG CTGATCTACG ATTACTAGCG 60
ATTCCAGCTT CATGTAGTCG AGTTACAGAC TACAATCCGA ACTGAGAACAC ACnTTATGGG 120
ATTTGCT 127

(2) INFORMATION FOR SEQ ID NO: 4760:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4760:

GGGCCCTCG TCGGGTTACC GAATTCAAGAC AAACCTCCGnA ATGCCAATTA ATTTAACTTG 60
GGAGTCAGAA CATGGGTGAT AAGTCCGTGT TCGAAAGGAA ACAGCCCAGA CCACCAGCTA 120
AGTCCCAAAT ATATGTTAAT GAAAG 145

(2) INFORMATION FOR SEQ ID NO: 4761:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4761:

TAAACAAGGC GCGTTGGGCC TATTCACTGC GGCTCTTCTG GGCGTTAAC	CTAAAGAGCA	60
CCCCTTCTCC CGAAGTTACG GGGTCATTTC GCCGAGTTCC TTAACGAGAT	TGCTCGCTCA	120
CCTTAGAATT CCATCTGACT ACGGTCGTTG CGTACGGCAC TATTCTTCA AGCTTCCGCA		180
TTAACACACC AAAACAGCTC CCACCACCA C TAnATCGAnC AACACTAG		228

(2) INFORMATION FOR SEQ ID NO: 4762:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4762:

TnGCCAAATC TTAGTAGTCG CTTGGTTCGG TTGTGGTGCG ACAGCTGTGA AATCATCA	60
ACGTTGCTCA TCACTCACTG TCTCTCCGCT TCCTTGCCTT GCAACAGCTT GAATTGTATC	120
AGCAGGGTTG	130

(2) INFORMATION FOR SEQ ID NO: 4763:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4763:

CAAATCGTAG TCAGGGTCGA AAGACGGGAC TTAGTGATCC GGTGGTCCG TCATGGGTAG	60
GGCCATCGTC TCAACGGTAT AAAAGCTACC CCGGGGATAA CAGGCTTATC TnCCCCAAGA	120
GTTCACATCG ACGGGGAGGT TTGGCACCTC G	151

(2) INFORMATION FOR SEQ ID NO: 4764:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4764:

ACCCCAACTT GCATTGnCTG TAGAAATTGG GAATCCAATT TCTCTTGTT GGGGCCCGC	60
CGGCAAGGTT GACTAGAATT GACCAAAAGC TTGTTACAAG CGCATTTCG TTCAGTCAAC	120
TACTGCCA	128

(2) INFORMATION FOR SEQ ID NO: 4765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4765:

AATACAGCCC CAGAGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT CGATGTGAAC	60
TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTT ATCCGTTGAG CGGATGGCCC	120
TTTCCATGTG GnAAC	135

(2) INFORMATION FOR SEQ ID NO: 4766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

GATTCTCACCC CGTCTTCGC TACTCACACC GGCATTCTCA CTTCTAACGCG CTCCACATGT	60
CCTTACGATC ATGCTTCAAC GCCCTTAGAA CnCTCTCCTA CCATTGTCCA AAGGACAATC	120
CACAGC	126

(2) INFORMATION FOR SEQ ID NO: 4767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4767:

TTAATAGTTT TATAAGAGAG GTGTTGATC TTGAGCTAAC CACnTCATTC GAGTACTGTC	60
--	----

ATGAAGTAAT TTCTCTATTAC TACGACCAGA AAATACAGAT GGGGTATATG CATATAAGAT 120
GATTTTTAAC 130

(2) INFORMATION FOR SEQ ID NO: 4768:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4768:

GTTAACCTA AAGAGCACCC CTTATACCGA AGTTACGGG TCATTTGCC GAGTCCTTA 60
AnGCGCGTTC GATCGCTCAC CTTAGGAATT CTCATCTTGA CTACCTGTGT CGGTTTGCGG 120
TAGGGCACCT ATTTTCCTAT CT 142

(2) INFORMATION FOR SEQ ID NO: 4769:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4769:

CCTTGGGACC GACTACAGCC CCAGGATGCG ATGAGCCGAC ATCGAGGTGC CAAACOTCC 60
CGTCGATGTG AACTCTTGnG TGGAGATAAG CCTGTTATCC CCGGGGTGAG CTTTGTATCC 120
GTTGAGCGAT GGCCCT 136

(2) INFORMATION FOR SEQ ID NO: 4770:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4770:

CTAAAAGTTG TATTTAAAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA 60
ACCGTTAAC AATGCATAGT TTGCTTAAC TCCAATATTG ACTCATCATT ACAATTGACA 120
TAGAGCTATT AAGCGTnGCC ATGAG 145

(2) INFORMATION FOR SEQ ID NO: 4771:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4771:

TCGAGTGACA CTGTCGCCGA AAATGTACCG GGGCTAAACA TATTACCGAA GCTGTGGATT	60
GTGCCTTGAG AAATGGTGAG GnGAGCGTC TAAGGGCGTT GGAAGCATGA TCGTAAGGAC	120
ATGTGGGA	128

(2) INFORMATION FOR SEQ ID NO: 4772:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4772:

GGGCAGATGT TCCTGCAGTC ATAGTGCCGT CAACTTTAAA TACTGTACGT AATTTGGCTA	60
ATGCCTCCAT CGTGGnTGTC AGGGCGTATA AATTCACTT GGGTCAA AA TATTTGGTGT	120
GTACTT	126

(2) INFORMATION FOR SEQ ID NO: 4773:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4773:

GTCTTTCTC GTTTCGTTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTGT	60
GTTTACTTTT TATTTGACG TTTTAGGATA AAAAAGAn ACCTTGC GG CTCAATGCGG	120
CTCATC	126

(2) INFORMATION FOR SEQ ID NO: 4774:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4774:

ATTCATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCGGGTAACC	60
TGCATCTnA CAGGTACTAT GATTCACCCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT	120
TACG	124

(2) INFORMATION FOR SEQ ID NO: 4775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4775:

ACCAAGTGAG CCGGAAACAC CAACGCCACC AACACCAGAA GTACCAAGTG AGCCGGAAAC	60
ACCAACACCA CCGACACCCAG AAGTGCCGAG TGAnCCAGAA ACTCCAACAC CGCCAACACC	120
AGAG	124

(2) INFORMATION FOR SEQ ID NO: 4776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4776:

CCCGCTAGTC TCCACCATT ATTTCCTACA CGATGAACAT TGAAAACnA ATACAATATG	60
CAACGTTAAT TCCAAAAAAC GTAACTATAA GTTACAAACA TTATTTAGTA TTTATGAGCT	120
AATCAAACAT CATAA	135

(2) INFORMATION FOR SEQ ID NO: 4777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4777:

AGTGCAGAAG AGGAAAGTGG AATAnCCCCA ACATAGCGGT GAAATGCGCA GAGATATGGA	60
GGAACACCCAG TGGCGAAGGC GACTTTCTGG TCTGTAACTG GACGCTGGAT GTGCGAAACG	120

TTGGGGTTC AAACAGGATT TAGA

144

(2) INFORMATION FOR SEQ ID NO: 4778:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4778:

AATTTTGAT GACGGGTCCC TTCTAGGGT GCCGTCTCAG CCACCCCAAC CGGCACATTG	60
TTGTAAGCTG ACTATATGTC nTTCATGTGT TGGGGCCCT GTCTCGACT GGCACTGCTC	120
CCT	123

(2) INFORMATION FOR SEQ ID NO: 4779:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4779:

GCGCATTAAC TATCGCGATA TTAATCGCTA TTCTATATCG TCACTTAGA GGATATCCTG	60
AACAATATAG CTCAGGTATT ACGTTTCAT CTAAATATTT ATTAAGATTT GCAATCATCC	120
TAnATGG	127

(2) INFORMATION FOR SEQ ID NO: 4780:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4780:

GGTAATATGT TTAGCCCCGG TACATTTCG GCGCAnTGTC CTC A CTAGT GAGCTATTAC	60
GCACCTTTA AATGATGGCT GCTTCTAACGC CAACATCCTA GTTGTCTGGG CAACGTCACA	120
TCCTTT	127

(2) INFORMATION FOR SEQ ID NO: 4781:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4781:

ACACnGGGTG AGAATTGTC GCTATTTGTA AATTGTATCC TGGCTTAAGT TGGCCAAAGT	60
GTCTTATTGTT TTTAAAGTAT TTAAAAGTAA ATTACATGT TAATACGTAG TATTAAATGG	120
CGAGACTCC	129

(2) INFORMATION FOR SEQ ID NO: 4782:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4782:

CTCATTCCCC TTGCATTTA TCTTCTGCAA CAACAAACATT TCGTCTTTAT CGTCTTCCAT	60
AGTAGTAGGA TTTTCTACTA CTTGACCATT CATAATCTGT TGCATTTCAT GTTTGnTTG	120
GTCAGATTAA GGACCA	136

(2) INFORMATION FOR SEQ ID NO: 4783:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4783:

CATCAACATC GGCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC	60
AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGGATT ATTGnGACGG TATTGTTGG	119

(2) INFORMATION FOR SEQ ID NO: 4784:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4784:

ATCACTAACATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC ATACGTGTTT TAACCTGCGT	60
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nATCCCATTG CATCCCATAA TTGTGAATGG ACCAAGTTTC CAGTTGAACC CCCAGACAAG 120
CGCACGG 127

(2) INFORMATION FOR SEQ ID NO: 4785:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4785:

ACACCGGCAT GCTGAATACT CGTTTGGGT GAAGCCCCTG nACCACCATC GTAACCAC TG
ATGACAATT TATCTGAAA TGCTTTGCC ACCCCAGATG CAATGGTACC AACACCTGT 119

(2) INFORMATION FOR SEQ ID NO: 4786:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4786:

CTTTCTAAC CCGnCACCAC TTTATCGTGG TGGGGAGACA GTGTTCAGGC GGGCCAGTT 60
GACTGGGCC GGTCGCTCCT AAAAGTAACG AGGCGCTCAA AGTTCCCTCA GAATGTTGGA 120
AATCATTCTAT AGAGTGT 137

(2) INFORMATION FOR SEQ ID NO: 4787:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4787:

GTTTTAAC A CTGTTACCGT TTTCATCTT TAATGTTACC GTTACGCCAG AnATACCTTT 60
TTCATCTTGG TCTTGATAC CATTCTTATT TGTATCTTCC CAGACATAGT CACCTAAGT 119

(2) INFORMATION FOR SEQ ID NO: 4788:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4788:

CATGCTTCCA CCTCGAACCT ATTAACCTnC ATCATCTTG AGGGATCTTA TAACCGCAGT	60
TGGGAAATCT CATCTTGTAG GGGGGCTTCA TGCTTCAGAT GCTTTGCAGC ACTTAGCCCG	120
GCCACACATA GCTACCCAGC T	141

(2) INFORMATION FOR SEQ ID NO: 4789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4789:

CTGGGTTCAAG AACGTCTAAG CAGTTCGGTC CCTATCCGTC GTGGCGTAA GAAATTTGAG	60
AGGAGCTGTC CTTAGTACGA GAAGACCGGG ATGGACTACC TCTnGTGTAC CAATTGTCGT	120
GCCAACGCAT AGCTGGTA	139

(2) INFORMATION FOR SEQ ID NO: 4790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4790:

CATTATTTAG TATTTATGAG CTAATCAAAC AnCATAATT TTATGGAGAG TTTGATCCTG	60
GCTCAGGATG AGCGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGACGAGATG	120
CTTGCTTCG	129

(2) INFORMATION FOR SEQ ID NO: 4791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4791:

GGGTGCTCTT TAGGGTTAAC GCCCAGAAGA GCCGCAGTGC AATAGGCCCA AGCGACTGTT	60
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TATCAAAAnC ACAGGTCTCT GCTAAACCGT AAGGTGATGT ATAGGGGCTG ACGGCTTCCC 120

(2) INFORMATION FOR SEQ ID NO: 4792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4792:

CAAATTCTTT CGCTACTTGA ATGACAACAC TTTGTTTAC GCCTGAAATG GCTTCTTGCC 60

AAGCAGGTGT ATATTTGAT TCTGCATCGT CGTATCCTTT TGATCTAATT ATGATCAAAC 120

CGn 123

(2) INFORMATION FOR SEQ ID NO: 4793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4793:

TTCTAAGATA TATTGGAAC ATCTTCTTCA GAAATCGGAA TAACGTGACA TATTGTATTC 60

AGTTTTGAAT GTTTGTTCAT TCAAATTAAT GGGCTATAG CTCAGGGT TAGAGCGCAC 120

nCCTGATAAC 130

(2) INFORMATION FOR SEQ ID NO: 4794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4794:

CACAGCCACA AGTGATTAAA GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT 60

TAACTCATT TTCAATAGAT CAGGAAGACT ACCAAGCTTA TGTnGAAGGA CATCT 115

(2) INFORMATION FOR SEQ ID NO: 4795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4795:

nTTAAAAAAA ATTCCAATT TTTTTGGGG GGTGGGAAT TTAAAAATT GGTTTTAAC	60
CCAAAGGCC CTTTCCAAA AATTAAATT CCCTAAAAA TTTAAAATT GGGATT	120
TTTnGGCCC AAAATTTT CCCTTTTT AAAGGCCCCA ATTTTAATT TAACCCTAA	180
AACCCCCAAA CCTTTTCC TTTTTAAA TTTTTAAA TGGA	224

(2) INFORMATION FOR SEQ ID NO: 4796:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4796:

TCGCGTACCG CTTAATGGG CGAACAGCAA GACCTGGGC ACCGACTACA GCCCCAnGAT	60
GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCGTCGAT GTGAACCTTT GGGGGCAGAT	120

(2) INFORMATION FOR SEQ ID NO: 4797:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 125 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4797:

AATTCGATT CCTTAGTAGC GGCGAGCGAA AGTGAAGAG CCCCAAnACCA ACAAGCTTGG	60
CTGTTGTGGT TGTAGGACAC TCTATAACGG GAGTTACAAA GGACCGACAT TAGACGAATC	120
ATCTG	125

(2) INFORMATION FOR SEQ ID NO: 4798:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4798:

CAAAATAATG ACTCCTACGG GnCTCGAACCG CGTGTACCG CCGTGAAAGG GGGTGTCTT	60
--	----

AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACC

113

(2) INFORMATION FOR SEQ ID NO: 4799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4799:

CCGGTGGGAG GTAACCTTT AGGAGCTAGC CGTCGnAGGT GGGACAAATG ATTGGGGTGA 60

AGTCGTAACA AGGTAGCCGT ATCGGAAGGT GCGGCTGGAT CACCTCCTTT CTAAGG 116

(2) INFORMATION FOR SEQ ID NO: 4800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

AGGACTTAAA AGCAGAATT AATTGACCAAG TCGGTTACTT CATTGAGCCA GAAGATTTAT 60

TCAGTGCGAT GATTCTGAA ATTGAAACGC AAGATTCGA TATCGAnCAC CT 112

(2) INFORMATION FOR SEQ ID NO: 4801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4801:

ATAGGATAGG CGACGTGCGA TTGGATTGCA CGTCTAAGCA nTAAGGCTGA GTATTAGGAA 60

ATCCGGTACT CGTTAAGGCT GACTGTGATG GGGAGAAACA TTGTGTCTTC 110

(2) INFORMATION FOR SEQ ID NO: 4802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4802:

GAACCAAGTT GTTATTGAAA AnTCGTTCGT AAAGTTACGG TACGCCACC GTGAGTGCTT 60
TTACTTCTAT ATCAGCACCT ACTGTATCTT TCATTAATT AACGTCTTCT GCAGTCGCAC 120
CGCCACCTGC AAAACCTGTT GAATTTACG AGTCCGACC GCGCTTGTA ATCATnCTTA 180
CATTCTCTGT CACAACGCCA TACCTTCGGG ACTGACTCAC AGTCAGCGG AACACAA 237

(2) INFORMATION FOR SEQ ID NO: 4803:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4803:

CTTGAACCCC CAACCTACTG ATTACAAGTC AGTGCTCTA CCAATTGAGC TAAGCCGGGC 60
AATATGTAAG AATAAATGGT GGAGAATTGA CGGGTTCGAA CCGCCGAnCC TCTG 114

(2) INFORMATION FOR SEQ ID NO: 4804:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 4804:

GGATCAAACA GGATTAGATA CCCTGGnTAG TCCACGCCGT TAAACGCATG AGTGCTAAGT 60
GTTAGGGGTT TCCGCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCT 113

(2) INFORMATION FOR SEQ ID NO: 4805:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4805:

TACCAGGGTA TCTAACCTG TTTGATCCCC ACGCTTCGC GCATCAGCGT CnGTTACAGA 60
CCAGGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT CTGCGCAT 108

(2) INFORMATION FOR SEQ ID NO: 4806:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4806:

TTTCAGCACT TATCCCGTCC ACACATAGTC TACCCAGGCT ATGCCGTTGG CACGACAAC⁶⁰
GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGAnAGCTC CTCTC¹¹⁵

(2) INFORMATION FOR SEQ ID NO: 4807:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4807:

CAGCCACATA ACATAACTAA GTTTAAGATT GAACGATAAA TCGTATCTGA GTTAAACCAA⁶⁰
TGGTTAACAC CCGCACCCAT GATAATCATT GAACGCCTTC AGTATCGTAG GTTTGGAATT¹²⁰
TTCGTCTTAT GCACATTnTT CGCTGATGTC TGCAAGAGTTT TTGTTGA¹⁶⁷

(2) INFORMATION FOR SEQ ID NO: 4808:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4808:

TGCTTACATC ATTAGCTAAT TGAGCACATG TTGCCATGC TTGCAGCTAA ATTACCTTGC⁶⁰
ATCATTGCTA GCTTTCTTG TATTAACTGA TAnTTACTAA TTGGTTGCC GAATTGCT¹¹⁸

(2) INFORMATION FOR SEQ ID NO: 4809:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:

TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCGA TTGGAATTTC⁶⁰
TCCnATACCT CAGTCATCC GCTCACTTTC AACGTAAGTC GGTCGGTCC TCATCATGG¹²⁰

TACCTGACTT CAACTGACCA GGGTAGACAC

150

(2) INFORMATION FOR SEQ ID NO: 4810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:

AAGAAGGCAG CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCA

60

AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA

107

(2) INFORMATION FOR SEQ ID NO: 4811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4811:

AGAGTGTnATT AGGTTATGAA GGTGGGCAAA ATAGGGTAAC CAGTCATTG AGGAAGACAC

60

AGAAGAAGAC AAACCTAAAT ATGAACCAAG GTGGCATATC GTAGATATCG ATTTCCA

117

(2) INFORMATION FOR SEQ ID NO: 4812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4812:

CTTTTATCCG TTGAACGATG GCCCTTCCAT GCGGAACCAC CCGATnACTA AATCCGTCTT

60

TCGACCCTGC TCGACTTGTA AGCTCGCAA TCAAGTCCCT TATGCCTTTA CACTCTATGA

120

ATG

123

(2) INFORMATION FOR SEQ ID NO: 4813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4813:

TAACCCGAGA GGGTCCCCTn GTCCAAACAG TGCTCTACCT CCAATATCAT CACTTGAGGC 60
TAGCCCTAAA GCTATTCGG AGAGAACCGAG CTATCTCCAG GTCGA 106

(2) INFORMATION FOR SEQ ID NO: 4814:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4814:

CTATTGCTTT AGATGCATAT GAATCATTGA nTGACGCGAT GCCGATGATT TCTGAACACG 60
GAATCGCGAA CGTTGGCCAA CTGCCAACGA TTGGCGTGGG AATCATCCAG TG 112

(2) INFORMATION FOR SEQ ID NO: 4815:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 125 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4815:

ACGTGGAGAG CATGTCCGTT CAAGCAGAGG GGCGGCGGTT GAACCCGTCA TTCTGOACA 60
TTTATTCTTA CATATTGCCG GnCTAGCTCA ATTGGTAGAG CAACTGACCT TGTAATCAGT 120
AGGTT 125

(2) INFORMATION FOR SEQ ID NO: 4816:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4816:

GTGCTGGCGC AGTTGCGATG GTTATTGCAC ATAATCCAAG CATGGCATTAA AATGAAGATG 60
CTGTTGCTTA CACTGAAGAC GTTTATGnTT TCTGGCGTCC AACT 104

(2) INFORMATION FOR SEQ ID NO: 4817:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4817:

GTCGGGTAAG TTCCGGCCCCG CACGAAAGGC GTAACGATTT GGGCACTGTC TCAACGnGAG	60
ACTCGGTGAA ATCATAGTAC CTGTGAAGAT GCAGGTTACC CGCGGCAGGG CGGAAAG	117

(2) INFORMATION FOR SEQ ID NO: 4818:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4818:

CTAAGGAACC TTGTCTTGGA CTGTGCACA ATCGCTTTCT TCTTCCTCT CCTTCGGCTC	60
TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGACGCTCT TTTCTCGnTT CGTCAGATT	120
A	121

(2) INFORMATION FOR SEQ ID NO: 4819:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4819:

TCAGTTCGGT ATTGTGAGTC TGCAACTCGA CTGACATGAA G T GGAATCG CTAGTAATCG	60
TAGATCAGCA TGCTACGGTG AATACGTTCC CGGGTCTTGT ACACAACGCC CGTnAAGA	118

(2) INFORMATION FOR SEQ ID NO: 4820:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4820:

CAAACAGTGC TCTACCTACA ATAATCATCA CTTGAGGCTA GCCCTAAAGC TATTCGGAG	60
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AGAACCCAGCT ATCTnCAGGT TCGATTGGAA TTTCTCCGCT ACCC

104

(2) INFORMATION FOR SEQ ID NO: 4821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4821:

TCGTAGTGGT TTCCAACCAA GTTTTATAA GTCAAACGCT CACATACGGC TTCGTTTCA 60
TTATTTAAA TGCTCATTAA CATAGTnAAC TCGCTTAAA ATAATTAAAC TCATGTCGCT 120
AACGTTTCT TTTATAAAAG TTTAACGGTT TTATCTGTGG TGTCT 165

(2) INFORMATION FOR SEQ ID NO: 4822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4822:

GAGTTTGATC CGGGCTCAGG ATGAACGCTG GCGGCCTGCC TAATACATGG CAATCGAGCG 60
AACGGACGAG AAGCTTGCTT CnCTGAGGTA GCGGCCTGACG GGTGAGTAAC ACG 113

(2) INFORMATION FOR SEQ ID NO: 4823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4823:

CCGGCAACGT TCTACTCTAG CGGAACGTAAC GTTGGCTACC ATCGACGCTA AGAACCTTTC 60
TTTGAAnTTGT GACAATCGCT TGCTTCTTC CTCTTCTTC GCTCTC 106

(2) INFORMATION FOR SEQ ID NO: 4824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4824:

TAAACGGCGG CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCCTGTC GGGTAAGTTC 60
CGACCCGCAC GAAAGGCCTA ACGATTGGG CACTGTCTCA ACTAGAGn 108

(2) INFORMATION FOR SEQ ID NO: 4825:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4825:

TCTAGTGACC GATA GTGAAC CAGTACCGTG AGGATAAGGT GAAAGCACC CCGGAAGTAG 60
nTGTAAATAG AACCTGAAAC CGTGTGCTTA CAAGTAGTCA GAGCCCGGT A TGGGT 116

(2) INFORMATION FOR SEQ ID NO: 4826:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4826:

ATAATATTGT AAATTAATCC ATTGATGCCA CAAGTGCCGG ACCAGAAATG ATGGTATTAA 60
ATAATGTGCC ATCTTATCT TTACGCCAAT CATAATTGGT AAAAATTCCC CCTTCTAATA 120
ATCCTTGTAT TGC GTGT CAT AnAGTCTTG CTCCTTGCAC 160

(2) INFORMATION FOR SEQ ID NO: 4827:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4827:

CGCATTGAGA CCGCAAGCTC TTTTTTTAT GTCTAAAACG TCAAAATAAA AAGTAAACAC 60
AAAGAAAATG GTTGGCCnAG TGAAAACGTT TGAATCTGAC GAAACGAGAA AGAGC 115

(2) INFORMATION FOR SEQ ID NO: 4828:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4828:

CCAAAATAGC CTTCATATAATC CAAAAAACAGG CTCCTTGAC TATAGATTTC CGTTTCTGGT 60
TCAGAAAGCT TTTGATTAAC TTTAAAGTAT nCCCAATTAT AAT 103

(2) INFORMATION FOR SEQ ID NO: 4829:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4829:

GGACCGAACT GTCTCACGAC GTTCTnAACC CATCTCGCGT ACCGCTTTAA TGGGCGAAC 60
GCCAACCCCTT GGGACCGACT ACAGCCCCAT GATGCGATGA GCCGACATCG A 111

(2) INFORMATION FOR SEQ ID NO: 4830:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4830:

GTTGTTGGGG CCCCGCCGGC AAGGTTGACT AGAATTGAGA AAAGCTTGTT ACAACGCTAT 60
TTTCGTTTCAG TCAACnACTG CCAATATAAC TTTGTAGAGC ATTGA 105

(2) INFORMATION FOR SEQ ID NO: 4831:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4831:

ACATTGAGTC TTCGAGTCGT TGCATTTCAC ACTGCCnGA AAGCCTCTA GATAGAAAAT 60
AGGTGCCCGT ACCGCAAACC GACACAGGTA GTCAAGATGA GA 102

(2) INFORMATION FOR SEQ ID NO: 4832:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4832:

TTnTAGAATG AACCGGCGAG TTACGATTG ATGCAAGGTT AAGCAGTAAA TGTGGAGCCG 60
TAGCGATAAG GAGGTCTGAA TAGGGCGTTT AGTATTTGGT CGTAGCC 107

(2) INFORMATION FOR SEQ ID NO: 4833:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4833:

TGCAACTAAT GAAAAGTAGA GTTCCGGGGA GTTAAAACCA GTGACTGTTG ACCTTGTTGT 60
CTCCATTGGA ATGTACTACC TGATGCAAGA TAATTATCAT CACTTGTTG ACGTGCTTnA 120
TTTCAGCAT CAATTGATC AATC 144

(2) INFORMATION FOR SEQ ID NO: 4834:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4834:

GGCTCAGATG nACGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGCACCAGAA 60
GCTTGCTTCT CTGGATGTTA GCGGCGGACG GGTGTAGTAA CACGTGGG 108

(2) INFORMATION FOR SEQ ID NO: 4835:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4835:

GACAATGGTA GGnGAGCGTT CTAAGGGCGT TGAAGCATGA TCGTAAGGAC ATGTGGAGCG 60

CTTAGAAGTG AGAATGCCGG TGTGAGT~~AC~~ GAAAGACGCA GT 102

(2) INFORMATION FOR SEQ ID NO: 4836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4836:

TTGCAGACTA CAATCCGGAA CTGGAGTAAC AACCTTATGG GATTGnCTT GACCTCGCGG 60

TTTCGCTGGC CCTTTGGTAT TGTCCATTGT AGCACGTGTG TAGCCAAA 109

(2) INFORMATION FOR SEQ ID NO: 4837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4837:

CTCCACGTAA GCTAGCGCTC ACGTTCAAA GGCTCCTACC T~~A~~CCTGGTA CAAGCTGTGC 60

CGGAATTCA ATTTGCAnGC TACAGTAAAG CTCCACGGGG GTC 103

(2) INFORMATION FOR SEQ ID NO: 4838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4838:

TCAAACACTC nCATACTGCT TTATTTCAT AAACAATATC ACTTTAACCA AAAAATATTT 60

GAATGTTAAA TAAACATTCA AAACTGAATA CAATATGTCA CGTTATTCCA CATCTTCTGG 120

A 121

(2) INFORMATION FOR SEQ ID NO: 4839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: ~~o~~uble
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4839:

AAACCATGAA TTAAGAATCC AGAAACAGGA GATGTAGTTA GACCACCGGT CGATTAGCGT 60
ACCAAAATAT GGACCTGTAA AAGGAGACTC GATTGTAGAn AAAG 104

(2) INFORMATION FOR SEQ ID NO: 4840:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4840:

CCGTGGAGTT TATGTAGCCT GATATTGAAT TCGGCACAGT TGTACAGGTA GGTAGGAGCC 60
TTGAAACGTG AGCGCTATTA GTGnAGGC GTGTTGGTACT ACCCTAGCTG TGTTGGCTTT 120
CTAACCC 127

(2) INFORMATION FOR SEQ ID NO: 4841:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4841:

CATCCCACCC CGGGCAAGGT TGACTAGAT TGGAAAAAAA CTTGGTTACA ACGTTATTT 60
CATTCAGTCA ACTACTGCCA ATATAATATT GnAAACTATA GGACATTAT TAGTGTTCA 120
GTTCT 125

(2) INFORMATION FOR SEQ ID NO: 4842:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4842:

TGGTACGGCA TCTCACCCGT CTTTCGCTAC TCACACCGGC ATTCTCACT CTAnGCGCTC 60
CACATGATCC TTACGATCAT GACTTCAACG CCCTTAGAAC GCTCGTCC 108

(2) INFORMATION FOR SEQ ID NO: 4843:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4843:

TAATGAAGGT CTTGGATCG TAAAACCTCTG TTATTAAGnA GGAACATGTG TGTAAGTAGC	60
TGTGCACATC TTGACGGTAC CTAATCAGAA AGCCACGGCT AACTACGT	108

(2) INFORMATION FOR SEQ ID NO: 4844:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4844:

CGGTCTCAAT GCGGCTCATC GCATCCATT TTTGACCTGG GCAACGTTCT ACTCTAGCGG	60
AACCTAAGTT GGGCTACCAT CGACGnCTAA GAACCTTTCT TGACTTGTGT ACAATCG	117

(2) INFORMATION FOR SEQ ID NO: 4845:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4845:

GACTGTTTAT CAAAAACACA GGTCTCTGCT AAACCGTAAG TGATGTATAG GGGGCTGACG	60
CCTGnCCGGG TTCTGGTAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAA	108

(2) INFORMATION FOR SEQ ID NO: 4846:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 118 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4846:

CAATATTTGA AGCGATTGGC TTGTCTCATG ATGTGATTGA TCGTTATTTC ACTGGGACAC	60
---	----

AGTCTAAGTT ATCTGGTATT TCGATTGATC AAATTnTGCC TGAAAAAGAC GCACAAGT

118

(2) INFORMATION FOR SEQ ID NO: 4847:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4847:

GATCCCCGGA CGGAGTGCTT AATGCGTTAC TGACAGCACT AAGGGGCGGA AACCCCCTAA

60

CACnTAGCAC TCATCGTTA CGGC GTGGAC TACCAGGGTA TCTA

104

(2) INFORMATION FOR SEQ ID NO: 4848:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4848:

CTGGCGATT A TGCTCTGTAA CGTGCTTC C AATTGGAAC GCACGTGnCC CTGCCCATAC

60

CTACGGGACT TGACTTATAT TGTGCTTGC TTGTACGT CAT TTCAACAAA GACGCCATG

120

CCAGCAACGC GATTACC

137

(2) INFORMATION FOR SEQ ID NO: 4849:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 116 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4849:

GTTTAGGCTC ATCTTAAGAT GTTAGGTCCA CTCGGTTAC ACCATATT TTACTTACCG

60

TTTTGGCAGA CGGC ACTTGG TGGTACTTTA GAAGTCAAAG ACAnGGGGGG GGGGGG

116

(2) INFORMATION FOR SEQ ID NO: 4850:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 125 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4850:

TCCCTTCGTG ACGGGCTCGG TAACTTACCC GACAAGGTAA TTTCGCTACC TTAGGnACCG 60
TTATAGTTAC GGTCCGCCGT TTACTGGGGC TTCAATTGCGT ATCTTCGCAG CTATATCTCA 120
CTCCT 125

(2) INFORMATION FOR SEQ ID NO: 4851:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4851:

AAGTTGTATT TTAAAAATAG TTCTTTAAAT TATATACCCA CCACATTGG TGGGAGAACCC 60
TAAAAAAAAG CACTTCCCC AAAAATGGGA AAGTGC 96

(2) INFORMATION FOR SEQ ID NO: 4852:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4852:

ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGnAT 60
GAACCGGCAGA GTTCACGATT TAGATGCAAG GTT@AGCAG 100

(2) INFORMATION FOR SEQ ID NO: 4853:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4853:

CCGACAGCGT AGnCGATGGA TAACAGGTTG ATATTCTGG TACCACCTAT AATCGTTTA 60
ATCGATGGGG GACCCATAGG ATAGCGAACCC TGCGATTGGA T 101

(2) INFORMATION FOR SEQ ID NO: 4854:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4854:

GGACATCTCC TAAGGCTAAA TACTCTCTAG TGACCGTAGT GAACCAGAC GTGAGGAAAG 60
GTGAAAnACC CCGGAGGGGA GTGAATAGAC CTGAAACCGT GT 102

(2) INFORMATION FOR SEQ ID NO: 4855:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4855:

ATAACCGCAA TTGGCGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA 60
CTTATCCCGT CCACACATAn CTACCCAGCT ATGCCGTTGG CACG 104

(2) INFORMATION FOR SEQ ID NO: 4856:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4856:

CTACTGTCTT CATTCTTCA GTTCTTTTT ACGGGTCTGT TTTCTAATTT GAGCACATCT 60
TCGATTCTTT ATCAAATGAC TACCAATTAA ATCTATTCTT CTnTGGTAAA TCGCTAACTC 120
CATCTCCTTA ACCCGGTA 138

(2) INFORMATION FOR SEQ ID NO: 4857:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4857:

TCAAACGnTT GTCATCTATT AAAGAAGTAG GTCTAGATAT ATCACGTACG TAATGTGTAA 60

TGGATGGCGC TATTGCTTTA GGTCATCCAT TAGGTGCTAC

100

(2) INFORMATION FOR SEQ ID NO: 4858:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4858:

CTTAACCTTG CAGCACCGTG CAGGCGTCAC CCTATACATC AnCTTACGGT TTAGCAGAGA 60

CCTGTGTGTT TGATAAACAG TCGGTTGGGC CTATCACTG CGGCTT 106

(2) INFORMATION FOR SEQ ID NO: 4859:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4859:

GTAACTCGCC GGTCATTCT ACAAAAGGGC ACGCCAATCA CCCATTAACG GGCTCCTGAA 60

CTACTTGTAA AGCAACACGG TTTCCAGGGT TCTATTTCCA CTTCCCCTTT CCGGGGTnGC 120

TTTTCAACC TTTTCCCCC TCCACGGTTA CT 152

(2) INFORMATION FOR SEQ ID NO: 4860:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4860:

GCCC GTACCG CAAACCGACA CAGGTAGTCA AGATGAAnGAA TTCTAAGGTG AGCGAGCGAA 60

CTCTCGTTAA GGAACCTCGGC AAACTGACCC CGTCACTTCG 100

(2) INFORMATION FOR SEQ ID NO: 4861:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4861:

CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTAA AAAGTAAGCG GATGAACTAA 60
AGGTAGCnGA GAAATTCCAA TCGAACCTGG AGATAGCTGG TTCT 104

(2) INFORMATION FOR SEQ ID NO: 4862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4862:

TTACTTATCT AGTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60
CCTCCTGCGT GCAAAGCAGG CGCTCTG 87

(2) INFORMATION FOR SEQ ID NO: 4863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4863:

ACCGTTTGAT TTCTTATCTA ATTCAAGCTT ATTTAAAAT CTTTATTCAC TCGGTTTG 60
CTTGGTAAAA TCTATATTCT ACTTACTTAT CTAnTTTCA ATGTA 105

(2) INFORMATION FOR SEQ ID NO: 4864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4864:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60
TGCCTTGCTG GATGATGCTA TGATATTGCA CATATGAAT CAACAGTGGT GCATGAACCT 120
GCAnTGGCT 129

(2) INFORMATION FOR SEQ ID NO: 4865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4865:

AAACCGCAAG GTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC 60
TCGACTACnT GAAGCTGGAA ATCGCTATAA ATCGTAGATC 100

(2) INFORMATION FOR SEQ ID NO: 4866:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4866:

TGAGATAAGAT TAGCAGAAAA TGGATGGTGT TAAGAGAGTT AATTGGTTTG GnGGTATGCT 60
TATTTTAAT GGCATTGTGT ACGAGAGCAT TAGAGTTGT ACTTGTGAGG TTATT 115

(2) INFORMATION FOR SEQ ID NO: 4867:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4867:

ACACCACTCC TCATTAACCT TCCAGCACCG CAGCAGGCGT CACCCCTATA CATCACCTTA 60
CGGTTTAGCA GAGACCTGTG TTTTGATAA 90

(2) INFORMATION FOR SEQ ID NO: 4868:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4868:

CACGAACGAT TGTCTGCGT GCGGGGATTA TCTGACACGG TACCGGTCAA ACAGTGAATC 60
GCTACTGCTC ATCAGGGATT ACAAAACC 87

(2) INFORMATION FOR SEQ ID NO: 4869:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4869:

GAGCACCCCT TCTCCCGAAG TTACGGGTC ATTTGCCGA GTTCCTTAAC GAGAGTCGCT	60
CGCTCACCTT AGAACATATT TACACTGGTG TTGGTAGGCA CTTTTTCAA GCTTCCGATT	120
AACACATGAA AAGCTTCAA AGTACTAGGA CGTTCAATAC ATGTA	165

(2) INFORMATION FOR SEQ ID NO: 4870:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4870:

AATATCATT ATAACATTAA GTAATAACTT TTTTATTT GTCCATTTA TTTTTnAACC	60
AAAATTTGAT TAAAAAACTG CCTGGCAACG TTCTACTCTA GCAGGAACCTAA G	111

(2) INFORMATION FOR SEQ ID NO: 4871:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4871:

TAGCAGAGAC CTGTGTTTT TGATAAACAG TCGCTGGGC CTATTCAGT CGGCTCTTCT	60
GGGCCTTAAC CCTAAAGAGC ACCC	84

(2) INFORMATION FOR SEQ ID NO: 4872:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4872:

ACAGTAAAGC TCCACGGGTC TTTCCGTCCCT GTCGCAGGTA ACTGCATCTT CACAGGTACT 60

ATGATTCAC CGATCTCTCn ATGAACAGTG CCAAATCGTA C 101

(2) INFORMATION FOR SEQ ID NO: 4873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4873:

GACAGGCGTA GGCGATGGAT AACAGGTTGT ATTCCGTAC CACCTATGAT CGTTTAATC 60

GATGGGGGGGA AGCATAGGAT AGGCGAA 87

(2) INFORMATION FOR SEQ ID NO: 4874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4874:

GGGAGAGCGC CTGCTTGCA CGCAGGAGGT CAGCGGTTCG ATCCCCTAG TCTCCACCAT 60

TATTTGTACA TTGAAAAACTA G 81

(2) INFORMATION FOR SEQ ID NO: 4875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4875:

TATGTTTCGA AATATCTTA TCACCTCTAAA ATGATATACA AGAAATCCAA GAAAAATAAG 60

CGAACTGAAT AAATAAAGAT T 81

(2) INFORMATION FOR SEQ ID NO: 4876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4876:

AACGCGTTAA ATCTTTTAT AAAAGACGTA ACTTCATGTT AACGTTGCTT ATAAAAATGG	60
TGGAACATAG ATTAAGTTAT TAAGGGC	87

(2) INFORMATION FOR SEQ ID NO: 4877:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4877:

ACAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG TTCACATCGA	60
CGGGGAGGTT TGnCCTCAAT GTGGCTCATC GGATCTTGGG G	101

(2) INFORMATION FOR SEQ ID NO: 4878:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 79 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4878:

ATTTATTAGG TGTACAAATG ACCACCGCAT CAACAAGTTT AAACAGCTCG CTAGGTECT	60
CAACTGCATG AGGTATATT	79

(2) INFORMATION FOR SEQ ID NO: 4879:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 83 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4879:

ACATCGTTTC AATGGGTCGC TAACGCTGCT AGGACATTAT AACAGACGTG TACAAAAGA	60
AAATTGGTAT GGTAATTGTG GCA	83

(2) INFORMATION FOR SEQ ID NO: 4880:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4880:

CTTCATCCTG ATCCAGATCA AACTCTCCAT AAAAATTATG ATGTTGATT AGCTCATAAA	60
TACTAAATAA TTTTGTAACT AATA	84

(2) INFORMATION FOR SEQ ID NO: 4881:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4881:

TTGTGCAGTT GCATGCCAT TGATCAATAA CACGTTGAGC TGCAGTTATT TCAGTTCTG	60
CTTCACGCTT CTTCGCATTA	80

(2) INFORMATION FOR SEQ ID NO: 4882:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 86 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4882:

TCTGATGTGA AAGCCCACGG CTCAACCGTG GAGGGTCATT GGAAACTGGA AAAACTTGAGT	60
GCAGAAAGAGG AAAGTGGGTT CCATGT	86

(2) INFORMATION FOR SEQ ID NO: 4883:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 127 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4883:

TGATCGCATA TCTACGCAAC ATCGGCATAA GTnTGATGACAACAGCTT CCATGACAAA	60
AGTAATGGAC GAATATCGCA TTTGGGGAAA GTCCTCTAAA AATGCCTTT GAAGGAACGT	120
CGGTTAA	127

(2) INFORMATION FOR SEQ ID NO: 4884:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4884:

AGTAGGAATC GAACCCACAC CAAAGTTTG GAGACCTCTA TTCTACCTTG AACTATGCC	60
CTATTAAAAA TAATAAAT	78

(2) INFORMATION FOR SEQ ID NO: 4885:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4885:

CTCACTATTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT	60
GTGGATTGTC CTTTGGAAAT GGGT	84

(2) INFORMATION FOR SEQ ID NO: 4886:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4886:

GGTATCTGTT CACTCTTCG GTGGTGCAGT TGCGACCAAC AATGGGTTGG AGATTGGATT	60
TCATCCTTCT CAATTAATCG TTGCCGTACT TTTCAAAnTGG TACCCCATCC AAAAGGG	117

(2) INFORMATION FOR SEQ ID NO: 4887:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4887:

CGGATCTGGG AGGAAATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCAGT	60
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ACCGTGAGGA AAGGTGAAAA

80

(2) INFORMATION FOR SEQ ID NO: 4888:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4888:

AATATGCAAG CACATGGTGA ATATGACGAG GTTGCAACTT CAACGGCGAA GATGATGGAA 60
GGCCTTACGT TTGCGTG 77

(2) INFORMATION FOR SEQ ID NO: 4889:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4889:

TCTTCTGGGC GTTAACCCTA AAGAGCACCC CTTCTCCCGA GTTAGGGGT CTTTGCCGA 60
GTTCCCTTAAC GAGAGT 76

(2) INFORMATION FOR SEQ ID NO: 4890:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4890:

GTGGGGGCC CAACATAGGA GCTGATTTTC TGTCAGCTTA CCATnATGTG GCAAGTTGGC 60
GGGGGGCCCCC AAACCAAGGA GCTGGCTTTC TGTCACTTTA CCATTAATGT GGCAAGT 117

(2) INFORMATION FOR SEQ ID NO: 4891:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ IDNO: 4891:

TTAATCCnCC TGCATATGAT GACTTTGTTG AACCGTCATT GCATACTTTC AACATGAATA 60

CGCTGAACAC CTTCACTTAC TGCATATCTT AGTCCTCGG TCTGTCTTA 109

(2) INFORMATION FOR SEQ ID NO: 4892:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 88 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4892:

CTCTAACCT TGCAGCACCG GGCAGGGCGTC AGCCCGTATA CATCACCTTA CGGTTTGCAG 60

AGACCGTGTG TTTTGAGAA ACAGGTGC 88

(2) INFORMATION FOR SEQ ID NO: 4893:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4893:

TAGCGAATGA GATAAACGCG GCGGACTGTA AATCCGCTCC TTCGGGTTCG GCAGTTCGAA 60

TCTGCCCCCCC TCCATTATT ATTGTTnAAAA AAAGCATAGT TC 102

(2) INFORMATION FOR SEQ ID NO: 4894:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4894:

CGAGCGATTC CGACTCAGAC AATGACTGG AATTAGATA ACGAATCTGA CTCAGACAGT 60

GACTCAGATT CCGACAGT 78

(2) INFORMATION FOR SEQ ID NO: 4895:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 141 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4895:

ACTAGATAGT AAGTAAAAGT GATTTGCTT CCGAACATT TATTTGATTA GTCTTCGTG	60
TTAGTATTAG CACTCACATG TCACATGCTT CACTCGACCT ATTACCCAC ACTTGGGGAC	120
TTATACCGAG TnGGAATCTC A	141

(2) INFORMATION FOR SEQ ID NO: 4896:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4896:

GTTCGGATT AATTTGATTC ATTTGTTGCG TAATTCAGA AGCCATTTA TGAAAAGAGT	60
GATTTAATTC ATAAATTCT	80

(2) INFORMATION FOR SEQ ID NO: 4897:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4897:

GGTATGGCTG GCGCTTACG TGCCACATTA GATTATGTCA CTGAGCGTAA GAAGTTCGGC	60
AAACCAATTAA GTA	73

(2) INFORMATION FOR SEQ ID NO: 4898:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4898:

GTGCCGAGGA CCGGAATCGA ACCGGTACGG TGATCACTCA CCGCAGGATT TTAAGTCCTG	60
TGCGTCTGCC A	71

(2) INFORMATION FOR SEQ ID NO: 4899:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4899:

AGCCGCTGGA TTCCACGGTG TAAGCAGTAA GGCTGAGTAT TAGGCAAATC CGGTACTCGT	60
TAAGGCTGGA GCTGThGATG GGGAGAACAC ATGTGTGCTT ACGTAGTGCG TGGTTT	116

(2) INFORMATION FOR SEQ ID NO: 4900:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4900:

TTCCGGCCCC TGGCGGTnTC CTAGGAGTTC CACGGAACCC CAGGATTTC TAGGACCCCC	60
CGGGCAGAGT CCCCTTCGAC TAAGAAAATC TCACATTCTT CAGGGACTTT TAC	113

(2) INFORMATION FOR SEQ ID NO: 4901:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4901:

ACTTAATGGA TTGATTAAGT AGTGGGTTCT TAACATTAGG CCTCAGCTAA TGTGGTACTT	60
AAAAATAGGG AATACATG	78

(2) INFORMATION FOR SEQ ID NO: 4902:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4902:

ATGGGACATG GTGTGCCTCC TTGCTATAGT CACCAGACAT ATGAATGTAA TTTATACATT	60
CAAAACTAGA TAGTAAGTAA AAGT	84

(2) INFORMATION FOR SEQ ID NO: 4903:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4903:

TTGTCGGGTA AGTTCCGACC CGCACGAAAG GCGTAACGAT TTTGGCACTG TCTAACGAG 05
AGACTCGGTG 70

(2) INFORMATION FOR SEQ ID NO: 4904:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4904:

TAAGTTGGCT ACCATCGACG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60
TCCTCTTCTT GGCTCTGCTT CTATTTGCCT CTAATGTGGC TTTTTGTTGT AATAAGTTAT 120
GCGCTTCGGT GTTATnGTGA AAAAGCGGTC A 151

(2) INFORMATION FOR SEQ ID NO: 4905:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4905:

TGACTTGTAG GCGCTGGTGG GATACTACCC TAGCTGTGTT GGCTTCTAA CCCGCACCAC 60
TTATCGTGGT GGGGA 75

(2) INFORMATION FOR SEQ ID NO: 4906:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4906:

CGATTGGAC TCAAGATAGC GGATTAGGA TC~~A~~CAGGC GAATCCAGAT CAGACCAGCG 60
ACTCAGACAG TGACTCAGAT CAGATAGTGN CTGGATTCA GCGATTATTC AG 112

(2) INFORMATION FOR SEQ ID NO: 4907:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4907:

GTAAAAACAC CCCAGCCAGG TCACCTTACG CCTACGCATC GCTTGTACAC GTGCTACTAA 60
AGGTTTACCA 70

(2) INFORMATION FOR SEQ ID NO: 4908:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4908:

AGAAGATACA AATAAAGnTA AACCCAAATT ATTCAATTTC GGTGGGACAC AATAGTGGTG 60
ACTTTGAAGA AGATACACTT TCCCACCAAG TTAAGTGGGT CCATAATTGA AGGGTCCAAC 120
C 121

(2) INFORMATION FOR SEQ ID NO: 4909:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4909:

GGGAACAAAG TGGACAGGTG GTGCATGGTT GTCGTCAACT CGTGTGTTGGGG 60
TTAAGTCCCCG 70

(2) INFORMATION FOR SEQ ID NO: 4910:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4910:

GGACACCCGG AGAACTGAAA CATTAGTAC CCGGAGAAGA GAAGAAATTC GTTCCCTTAG	60
TAGCGGGACG AACGGGAGAG CCCAAACCAC AGCTTGTGnG	100

(2) INFORMATION FOR SEQ ID NO: 4911:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4911:

nTCTGTGTTG GGCATGGAA CAGGTGTGAC CTCCTTGCTA TAGTCACCAG ACAAAATAAC	60
TTACTTATTC ATGATAACAG CTAAATTAAT AAGGTGCAAT AGTTAATTT ACACTTGAT	120
GTAAACTTG GCACATCAGC TTTAGTGTG TTTCG	155

(2) INFORMATION FOR SEQ ID NO: 4912:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4912:

CCCGTCACAC CACGAGATTG GTAACACCCG AAAGCCGGTG GAGTGAACCT TTTAGGAGCT	60
AGCCGTCGA	69

(2) INFORMATION FOR SEQ ID NO: 4913:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4913:

TATGCTCTCC CAGCTGAGCT AATTCTCCGA TTTAAAATG CCTGGCAACG TTCTACCTA	60
GCGAACGT	69

(2) INFORMATION FOR SEQ ID NO: 4914:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4914:

CAAATGCTTC TGTCAATTAG ATCAAATCAA TGTCTTCAAC AGATAGATTG CTGAGTGACA	60
ATACTTCAT	69

(2) INFORMATION FOR SEQ ID NO: 4915:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4915:

TATTCGGAG AGAACCGAGCT ATTTCCAGGC TCGATTGGAA TTTCTCCGGT ACCCTCAGTT	60
CATCCGCTCA	70

(2) INFORMATION FOR SEQ ID NO: 4916:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 67 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4916:

TCACCCATTA ACGGGCTCTA ACTACTTGTA AGCACACGGT TTCAGGTTCT ATTTCACTCC	60
CCTTCCG	67

(2) INFORMATION FOR SEQ ID NO: 4917:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 161 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4917:

TACTAAGACT GTGGACGCTA GAATGAGATG CCGTGTGATA GCGAAAACGG TGAGAATCCC	60
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TCCACCGTTG ACTAAGGTTC CAGAGAGGCT CGTCCCTCTG GGTAGTCGGG CCTAAGCTGA 120

GGCGCACGTA GGCGATGATA CAGGTTATAT CCTnACACCT A 161

(2) INFORMATION FOR SEQ ID NO: 4918:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4918:

GCACGTAGTT AGCCGTTGGC TTTCTGATTA GGTACCGGCA AGATGTGCAC AGTTACTTAC 60

ACATATGT 68

(2) INFORMATION FOR SEQ ID NO: 4919:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4919:

GAAAGCAAAT GTCTTCGTTG CAATTGATC AAATCAATGT CTTAACAGA TAGATTGCTG 60

AGTGACAATA CTTCAGGG 78

(2) INFORMATION FOR SEQ ID NO: 4920:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4920:

AATTCGCTA CCTTAGGGAC CGTTATAGTT ACGGCCGACG TTTACTGGGG CTTCGATTG 60

TACTTCGC 68

(2) INFORMATION FOR SEQ ID NO: 4921:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 67 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4921:

AATCATAGTA CCTGTAAAGA TGCAGGTTAC CCGCAACAAG ACGGAAAGAC CCCGTGGAGC	60
TTTACTG	67

(2) INFORMATION FOR SEQ ID NO: 4922:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4922:

GGGAGCTGTA ATAAGCTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT	60
GTCATG	66

(2) INFORMATION FOR SEQ ID NO: 4923:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4923:

GTGGAGGCGC TGGTGGGATA CTACCCTAGC TGTGTTGGCT TTCTAACCCG CAACCACTTA	60
TCGTGGGTGG GAG	73

(2) INFORMATION FOR SEQ ID NO: 4924:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4924:

GAGGTCAGCG GTTCGATCCC GCTAGTCTCA CCATTATTT TTTACAGAT GACATGAAAC	60
TGATGACATA TGCACCGTAA TTCCAAAAA	89

(2) INFORMATION FOR SEQ ID NO: 4925:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4925:

AATGGCATCG GAGTTGTCTG AATTGGTAA CCCGAGAGGC CCCTCGTCCA AACAGGCTCT	60
ACCTCCAA	85

(2) INFORMATION FOR SEQ ID NO: 4926:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4926:

ACGAAAGGCG TAACGATTTG GGCACTGATC TCGACGAGAG ACTCGTGAAA ATCATAGATA	60
CCTGTGAAGA TGC	73

(2) INFORMATION FOR SEQ ID NO: 4927:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4927:

ATTCTCTATTAA ATTATTTGCA TAGAAATCAG CTTTTTGAT ATGTATTTA TAATGTACAG	60
CTCGTTGAG	69

(2) INFORMATION FOR SEQ ID NO: 4928:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4928:

AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACATCTC CTCTCAAATT TCCTACGCC	60
ACGACGTATA	70

(2) INFORMATION FOR SEQ ID NO: 4929:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4929:

GGCGGGGCC	CAACACAGAG	GCTGGCGGAA	AGTGCAGCTT	ACAATAGTGT	GCAAGTTGGG	60
GTGGGTCCCG	ACACAGAGAA	ATT				83

(2) INFORMATION FOR SEQ ID NO: 4930:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4930:

CTTGGTAGAG	CACTGGTTT	GGGACCAAGG	GGTCGCAGTT	CGAATCCTGT	CTTCCCGATT	60
ACTCTA						66

(2) INFORMATION FOR SEQ ID NO: 4931:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4931:

AAGAACCTTG	TTATGCTGCA	ACACCAGCAA	TTCAAGTAGC	TAAAGATTAT	TTAGCAACTA	60
GACCG						65

(2) INFORMATION FOR SEQ ID NO: 4932:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4932:

TGCAGAACAG	GAAAGTGGAA	TTCCATGTGT	AGGGTGAAAT	GCGCATAGAT	ATGGCAGGAA	60
CACCAGTGGG	CGA					73

(2) INFORMATION FOR SEQ ID NO: 4933:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4933:

TCGCTATCCG AGTCTGGTC GCTATCTGAG TCTGAGTCGC TATCTGAGTC TGAAATCGCT	60
GTCTG	65

(2) INFORMATION FOR SEQ ID NO: 4934:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4934:

GAGCATGTGG GTTTAATTG AAGCAACGCA GAGAACCTTG ACCAAATCTT GGACATCCnT	60
TGACAACTCT GAGAGATTAG AGCCTTGCCC CTTGCGGGGT AACAAATGTA CAGGTTGGTG	120

(2) INFORMATION FOR SEQ ID NO: 4935:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4935:

GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA GGCGAGCAG GTACGGCGAT	60
GGATAACGGT TG	72

(2) INFORMATION FOR SEQ ID NO: 4936:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4936:

CACATCAGCG TCAGTTACAT ACCAGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT	60
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CTGC

64

(2) INFORMATION FOR SEQ ID NO: 4937:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4937:

ATCACCTGGT GTAAACCAAT TAGTACGTGT ATATATCGTT CAAAACCGTA **AATT**CATGT 60
TGGT 64

(2) INFORMATION FOR SEQ ID NO: 4938:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4938:

CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAACATC TAAGCATGAA GCCCCCTCAA 60
GAT 63

(2) INFORMATION FOR SEQ ID NO: 4939:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4939:

TAGAAATCAG CTTTTTGCA TATGTATTT ATAATGTACA GCTCGTTGAG CTGCTATTT 60
CCT 63

(2) INFORMATION FOR SEQ ID NO: 4940:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4940:

GGTAGTCGAA CTTACGTTCC GCTAGAGTAG AACTTGCCAG CAAATGACAA ATCGGAGAAT 60
TAGCTCAG 68

(2) INFORMATION FOR SEQ ID NO: 4941:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4941:

CTGAAACATC TTAGTACCCG GAGAAGAGAA AGAAAATTAG ATTCCCTTAG TAGCGGCGAG 60
CG 62

(2) INFORMATION FOR SEQ ID NO: 4942:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4942:

TTACAACAAT GCAATTGGCG GGGCCCAACA TAGAACGGC AATAGTTACT TTCAATAATG 60
TGCAAGTTGG GGTAGGGCCC AACACAGAA 89

(2) INFORMATION FOR SEQ ID NO: 4943:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4943:

AATGGACAAT ATGTCAACGT TAATTCCAAA AAACGGTAAC TATAATTAC AAACATTATT 60
TAGTATTGA 69

(2) INFORMATION FOR SEQ ID NO: 4944:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4944:

CCCGTGAAAG ATGATGAGGT TAATAGGTTT GAGGTGGAAG CATGGTGACA TGTGGAGCGT 60
GACGAATACG TAATTGA 77

(2) INFORMATION FOR SEQ ID NO: 4945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4945:

GAATAGGTCG ATGTATTTGG CGACCGAAC CAGGAATCTA CCCTTGGTCA GGTTGAAGTT 60
CAGGTAACAC TGAAT 75

(2) INFORMATION FOR SEQ ID NO: 4946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4946:

ATCAGAAGGC ACACCCGAGA ATGAAACATC TAGTACCCGG AGAAGAGAAA GAAATTGAT 60
TCCCTATAGC GGCGnCGAAA CGGAAGAGCC AACCACAGCT GCTTTGGTTT GACCCATCGG 120
TACAGCGCTG ACACT 135

(2) INFORMATION FOR SEQ ID NO: 4947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4947:

GATTTGGGCT CTTCCATTTC GCTCGCCGCT ACTAAGGGAA TCGAATTCC TTTCTCTTCC 60
T 61

(2) INFORMATION FOR SEQ ID NO: 4948:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4948:

GCTTTTGAGG AATTAAATAT CAATATATAT TCTGTGTATGAAAATATTTT TCATAAAAAT	60
TGTTTGAATC	70

(2) INFORMATION FOR SEQ ID NO: 4949:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4949:

CTTCGACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACCAAGT ACTAAACGCC	60
CTATTC	66

(2) INFORMATION FOR SEQ ID NO: 4950:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQID NO: 4950:

GGGTGTTACA AAATATCGTG GTGTGACGGG GCGGTGTGTA CAAGACCCCG GGTACGTTT	60
TCACCGTAGG CATGCTGG	78

(2) INFORMATION FOR SEQ ID NO: 4951:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4951:

CCCGGATAAT AAAAATAAT GGC GGAGGAA GAGGGATTG AAC CCCC GTG GCC CGTTAAG	60
G	61

(2) INFORMATION FOR SEQ ID NO: 4952:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4952:

ACTTATCTAG TTTTCAATGT ACAATGTCTT TTTAGTCAGC GCTCGCATAA GCAATATCAC	60
TGTAACCA	68

(2) INFORMATION FOR SEQ ID NO: 4953:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4953:

ACTGACGCTG ATGTGCGAAA GCGTG G GGAT CAAACAGGAT TAGATACCCT GGTAGTCCA	59
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(2) INFORMATION FOR SEQ ID NO: 4954:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4954:

CGTGAGCGCT AGCTGTACGT GGAGGCGCTG GTGGGATACT ACCCTAGCTG TGTTGGCTTT	60
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(2) INFORMATION FOR SEQ ID NO: 4955:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4955:

AAGGCGTAAC GATTGGGCA CTGTCTAAC GAGAGACTCG GTGAAATCAT AGTACCTGT	59
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(2) INFORMATION FOR SEQ ID NO: 4956:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4956:

AATAGGTGCC CGTACCGCAA ACCGACACAG GTAGTC~~A~~GA TGAGAATTCT AAGGTGAGC 59

(2) INFORMATION FOR SEQ ID NO: 4957:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4957:

ACACGTTAG TTCACCGGGG TTTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT 60

TTTCAATGTA CAATTTC 77

(2) INFORMATION FOR SEQ ID NO: 4958:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4958:

TGTCGTCAGC TCGTGTGCG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCTTAA 59

(2) INFORMATION FOR SEQ ID NO: 4959:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4959:

GACTTGAACC CCCAACCTAC TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 59

(2) INFORMATION FOR SEQ ID NO: 4960:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4960:

TATTAACCTGG TGACTTAGCG AGATGGACAA CGATGGCGAT ATATTTATTA TTGACCGCA 59

(2) INFORMATION FOR SEQ ID NO: 4961:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4961:

ATGATTATCA TATTGCCTTA AATATCGCCA CAATTTAGC GGGTGGTGAT TTACCAAGA 59

(2) INFORMATION FOR SEQ ID NO: 4962:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4962:

CGCCGAAAAT TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACA 59

(2) INFORMATION FOR SEQ ID NO: 4963:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4963:

TTAAGCTTAG TTGCCATCAT TAAGTTGGGC ACTCTAATGT TGACTGCCGG TGACAAACCG 60

(2) INFORMATION FOR SEQ ID NO: 4964:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4964:

TAGTTTGCGTACGGTAACAAATTTATTGAGAACAATCTCAAATAAAGAATTGTTG

59

(2) INFORMATION FOR SEQ ID NO: 4965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4965:

AGTCGGTCCCTATCCGTCGTGGGGCGTAGGAAATTTAGAGGAGCTGTCCTTAGTACG

59

(2) INFORMATION FOR SEQ ID NO: 4966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4966:

TACAAAGGGCAGCGAAACCGTGAGTCAAAGCAAATCCCATAAAGTTGTTCTCAGTCGG

59

(2) INFORMATION FOR SEQ ID NO: 4967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4967:

CCATTGCAGCACCGACAGGCCACACCATTATTTTGCGCTATGTATATCGCATTAACGT

60

TTGTC

65

(2) INFORMATION FOR SEQ ID NO: 4968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4968:

GCTCCGTTACTTTAGAGGCGACGCCAGTCAAATGCCCGCTGACACTGTCTCCCACC

60

(2) INFORMATION FOR SEQ ID NO: 4969:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4969:

CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC GCCGTTACT GGGGCTTCG 59

(2) INFORMATION FOR SEQ ID NO: 4970:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4970:

CATCTGTCAC AGGTACTATG GATTTCACCG AGTCTCTCG TTGAGACAGT GCCCAAATCG 60
TTACG 65

(2) INFORMATION FOR SEQ ID NO: 4971:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4971:

CTAGAGTTGG CATAACCAGTC CGTCGCTAAG GAACCTTTCT TGACTTGATG ACAATCGACT 60
TGCTTCTTTC CTCTCCTTCG GCTCTCACTT nCTCATTAG 100

(2) INFORMATION FOR SEQ ID NO: 4972:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4972:

AGACCCCGTG GAGCTTTACT GTAGCCTGCA TATTCGAATT CGGCACAGCT TGTACAGGAT 60

AGGTAGG

67

(2) INFORMATION FOR SEQ ID NO: 4973:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4973:

TGTGTACTTA AAAATATGAA TACATGAGTA AAACTCATGC ATAAGAAATA CTAATTTC

58

(2) INFORMATION FOR SEQ ID NO: 4974:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4974:

ACCTCCAATA ATCATCACTT GAGGCTAGCC CTAAAGCTAT TTCGGAGAGA ACCAGCTA

58

(2) INFORMATION FOR SEQ ID NO: 4975:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4975:

GACGCCACAT CCTTTCCAC TTGGCGTGTG TTTTGGGACC TTGGCTGGTG GTCTGGCTG

60

TTTCCCTA

68

(2) INFORMATION FOR SEQ ID NO: 4976:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4976:

TCACTAAGTC CGTCTTCGA CCCTGACTCG ACTTGTAGGT CTCGCAGTCA AGCTCCCTT

59

(2) INFORMATION FOR SEQ ID NO: 4977:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4977:

TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG TTTAAAT 58

(2) INFORMATION FOR SEQ ID NO: 4978:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4978:

GTGAGGTACG TCCAGAATGG GGATTGGCTA AAAATGCATC ATTTATAATT GGACGACG 58

(2) INFORMATION FOR SEQ ID NO: 4979:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4979:

TCGCTATCTG AATCCGAGGT CCTATCCGA ATCTGGAGTC GCTATCTGGA GTCTGGAATC 60

(2) INFORMATION FOR SEQ ID NO: 4980:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4980:

AAGAAGGTAA TAATCCTGTA GTCGAAAATG TTGTCTCTCT TGAGTGAGTC CTGAGTAC 58

(2) INFORMATION FOR SEQ ID NO: 4981:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4981:

GTGGTGTGTT AGGGCACTCT ATACGGGTTA CAAAGTACGA CATTAGACGG ATCATCTGGA	60
AAGATGAATC AAAGT	75

(2) INFORMATION FOR SEQ ID NO: 4982:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4982:

GTTTTTCATT TTCATTATA TTTATATTAG TGTTAATCCA ATCATAGATT TATCTATA	58
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(2) INFORMATION FOR SEQ ID NO: 4983:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4983:

TGACAGCTAA CTATTGGCCA GCTTCTATGT TGGGGCCCCG CCAAATGCA TTGTCTGTAG	60
A	61

(2) INFORMATION FOR SEQ ID NO: 4984:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4984:

GGTGTNTTA AGTCTGATGT GAAAACCCAC GGCTCAACCG GTAGAGGTCA TTGGAAACTG	60
GAAA	64

(2) INFORMATION FOR SEQ ID NO: 4985:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4985:

CAGCATACAA TAATGTGCAA GTTGGTCGGG GCCCCAACAT AGAGAATTTC AAAAGAAAT

59

(2) INFORMATION FOR SEQ ID NO: 4986:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4986

TGATGAAGGT CTTCGGATCG TAAAACCTCTG TTATTAGGGA AGAACATATG TGTAAGT

57

(2) INFORMATION FOR SEQ ID NO: 4987:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4987:

AAAGAATTG CGCAAAACGC TATCGATACT GAAGGGCGTT CAATGATTAT CATGGGT

57

(2) INFORMATION FOR SEQ ID NO: 4988:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4988:

TTGTCACAAG TCAAGAAAGG TCTTTAGCGA CGATGGTAGC CAACTTACGT TCCGCTA

57

(2) INFORMATION FOR SEQ ID NO: 4989:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4989:

TAGGACCGTT ATAGTTACGG CCGCCGTTA CTGGGGCTTC GATTCGTAGC TTTCGCAG

57

(2) INFORMATION FOR SEQ ID NO: 4990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4990:

AAAGTCAACG TTAATTCAA AAAACGTAAC TATAAGTTAC TAACATTATT TAGTATTTAT

60

G 61

(2) INFORMATION FOR SEQ ID NO: 4991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4991:

TCCACGGGGT CTTCCATCC TGTCTGGGT AACCTGCATC TTCACAGGTA CTATGATTTC

60

ACCGA 65

(2) INFORMATION FOR SEQ ID NO: 4992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4992:

GTGCGGCTGG ATCACCTCCT TTCTAAGGAT ATATTCGGAA CATCTTCTTC AGAAGAT

57

(2) INFORMATION FOR SEQ ID NO: 4993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4993:

CCAATGCGGC TCATCGCATH CATTTCGGTCTGCTGACGCTGGCAACGT TTACTCTAG CGGAACG

57

(2) INFORMATION FOR SEQ ID NO: 4994:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4994:

CTGGTTTCGG GTCTACGACA AATACTAAAC GCCTATTAG ACTCGCTTTC GCTACGG

57

(2) INFORMATION FOR SEQ ID NO: 4995:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4995:

CAAACCTCTCG TGGTGTGACG GGCGGTGTGG TACAAGCCCC GGGAACGTAT TCACCGTAGC

60

ATGCCGGTCT ACG

73

(2) INFORMATION FOR SEQ ID NO: 4996:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4996:

ACTAATTCT ATAGGAAAAG TATTCTTAT CGTCGTCCCA CCCCAACTCG CACATTATTG

60

TAAGC

65

(2) INFORMATION FOR SEQ ID NO: 4997:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4997:

ATTGGATTCC CAATTCTAC AGACAATGCA GTTGGGTGG GACGTCGAAA TAAATTT

58

(2) INFORMATION FOR SEQ ID NO: 4998:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4998:

AACTTCAACA GGTTTGCAG GTGGCGGTGC GACTGCAGGA AGACGTTAAA TTAATG

56

(2) INFORMATION FOR SEQ ID NO: 4999:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4999:

GGGCAGGCGT CAGCCCTATA CATCACCTTA CGGTTAGCA GAGACCTGTG TTTTG

56

(2) INFORMATION FOR SEQ ID NO: 5000:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5000:

TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG GAAACCTTAG TCAATC

56

(2) INFORMATION FOR SEQ ID NO: 5001:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5001:

GACGGGATTC TCACCCGTCT TTGCTACTC ACACCGGCAT TCTCACTTCT AAGCGC

56

(2) INFORMATION FOR SEQ ID NO: 5002:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5002:

CCTGTCGGCC TCAGCTTAGG ACCCGACTAA CCCAGAGCGG ACGAGCCTTC CTCTGG

56

(2) INFORMATION FOR SEQ ID NO: 5003:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5003:

TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTCT CGTTTCGTCA GATTCA

56

(2) INFORMATION FOR SEQ ID NO: 5004:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5004:

AATCCTTGTT TCGTTTTACG TCCGAGTGCAG CCATTGTCAG ACAACGTATT TACAATT

57

(2) INFORMATION FOR SEQ ID NO: 5005:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5005:

GACATAGATT AAGTTATTAA GGGCGCACGG TGGATGCCTT GGCACTAGAA GCCGATG

57

(2) INFORMATION FOR SEQ ID NO: 5006:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5006:

GGAACCACTA CATAATAAAT CATTAGTGGC TCTTTATCAT TCTGTCCCAC TCCCCCTG

57

(2) INFORMATION FOR SEQ ID NO: 5007:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5007:

CGCTACGTTT TTCCTCAACA TTTAAGAAAA TAAAGA~~A~~GC TACAATTACG ATTGCAATCA

60

AACCAAAGA

69

(2) INFORMATION FOR SEQ ID NO: 5008:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5008:

AAAAGCTTGT TACAAGCGCT ATTTTCGTTTC AGTCAACTAC TGCCAATATA ACTTCGT

57

(2) INFORMATION FOR SEQ ID NO: 5009:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5009:

ACATCTTAGT ACCCGGAGAA GAGAAAGAAA ATTGATTCC CTTAGTAGCG GC~~A~~GC

56

(2) INFORMATION FOR SEQ ID NO: 5010:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5010:

GTTTGGACGA GGGGCCCTCT CGGGTTACGA TTCAGACAAA CTCCGATGCA ATTAATTAC 60
TTGGG 65

(2) INFORMATION FOR SEQ ID NO: 5011:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5011:

TTTACTTGTA TTGGAATAAT TTCATCTTG AACCGACCAT CACGTTGTGC GTCATA 56

(2) INFORMATION FOR SEQ ID NO: 5012:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

CCTTATACAT CACCTTTACG GTTTTAGCAG AAACCTGTGT TTTTGATAA ACAGTCGCTT 60

(2) INFORMATION FOR SEQ ID NO: 5013:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5013:

GGGCCAACAA CAGAAGCTGG CGAAAAGTCA GCATACAAAA TTGTGCAAGT TGGCGGGTCC 60

ACA 63

(2) INFORMATION FOR SEQ ID NO: 5014:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5014:

TAGGGTAGTA TCCCACCACT GGCCTCCACG TAAGCTAGCG CTTCACGTTT CAAAGGCT

58

(2) INFORMATION FOR SEQ ID NO: 5015:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5015:

CAACTCCGAT GCAATTAATT TAACTTGGGA nCAGACATGG GTGATAAGGT CGTGTTCGAA

60

GGGAACAGCC AGACACAGCT AAGTCCAGAT ATATGTAAGT GGAAA

105

(2) INFORMATION FOR SEQ ID NO: 5016

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5016:

CAAACGATT ATTATATATGC TTATTTCTTT ATTATTATTATT ATTACAATTA CATTAA

56

(2) INFORMATION FOR SEQ ID NO: 5017:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5017:

TCTGTAGAAA TTGGGGAATC CAATTTCTCT TGGTTTGGGT CCCATCCCCA ACTTGCACAT

60

TATTG

65

(2) INFORMATION FOR SEQ ID NO: 5018:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5018:

GGGGATGGGC CCCAACAAAG AGAAATTGGA TTCCCAATTCTAAGACAA TGCAAC

56

(2) INFORMATION FOR SEQ ID NO: 5019:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5019:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTC 55

(2) INFORMATION FOR SEQ ID NO: 5020:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5020:

TACGGCGTTT AGTATTTGGT CGTAGCCGGA AACCAGGTGA TCTACCCTTG GTCAGGTT 58

(2) INFORMATION FOR SEQ ID NO: 5021:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5021:

TTGTGCGGGGT CCCCGTCAAT TCCTTGAGT TTCAACCTTG CGGTCGTACT CCCCA 55

(2) INFORMATION FOR SEQ ID NO: 5022:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 5022:

AGAGTTCACA TCGACGGGGA GGTTTGGCAC CTCGATGTCG GCTCATCGCA TCCTG 55

(2) INFORMATION FOR SEQ ID NO: 5023:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5023:

CCTTAGCTGG TGGTCTGGGC TGTTTCCCTT TCGAACACGG ACCTTATCAC CCATGGTC 58

(2) INFORMATION FOR SEQ ID NO: 5024:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5024:

TAAAGGCTAA ACTACCAATG TTTCAATGG ATTTCAAAAA TGAATCATCT GGGAT 55

(2) INFORMATION FOR SEQ ID NO: 5025:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5025:

TCAAACCGGA GGGGTCATTG GAAACTGGAA AACTTGAGTG CAGAAGAGGA AAGTGGATT 60

CCA 63

(2) INFORMATION FOR SEQ ID NO: 5026:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5026:

GCTTGCCTAC CTAAAGAGCA CCCCTCTCC GAATTACGGG GTCATTTGC CGAGTTCTT 60

AACG 64

(2) INFORMATION FOR SEQ ID NO: 5027:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5027:

AATACATAGC ATATCATAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGA

56

(2) INFORMATION FOR SEQ ID NO: 5028:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5028:

GGGCCCTCT CGGGTTACCA ATTTCAGACAA ACTCCGAATG CCAATTAAATT TAACT

55

(2) INFORMATION FOR SEQ ID NO: 5029:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5029:

CGTAACTATA ACGGTCTAA GGTAGCGAA ATTCCCTTGTC GGGTAAGTTC CGAC

54

(2) INFORMATION FOR SEQ ID NO: 5030:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5030:

ATCCCCGGGG CCCAACACA GAGAATTTCG AAAAGAAATT CTACAGGCAA TGCAAGT

57

(2) INFORMATION FOR SEQ ID NO: 5031:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5031:

TGCTTGGTAA AATCTATATT TTACTTACTT ATCTAGTTT CAATGTACAA TTTC

54

(2) INFORMATION FOR SEQ ID NO: 5032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5032:

TCCCTATCCG TCGTGGCGT AGGAAATTG AGAGGAGCT TCCTTAGTAC GAGA

54

(2) INFORMATION FOR SEQ ID NO: 5033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5033:

AGAACACTCA CAAGATTAAT AACGCCTTC CTGTAGGATG GAAACATAGA TTAA

54

(2) INFORMATION FOR SEQ ID NO: 5034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5034:

TATCTGAATC TGAGTCGCTG TCTGAATCTG AATCGCTATC CGAGTCTGAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5035:

CACCAGCAAT TCAATTAGCT AAAGATTATT TAGCAACTAG ACCGGAATGAAAAA

54

(2) INFORMATION FOR SEQ ID NO: 5036:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5036:

CTACCATCGA CGCTAACAGAGC TTAACATTCTG TGTCGGCAT GGGAACAGGT GTGA

54

(2) INFORMATION FOR SEQ ID NO: 5037:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5037:

CGCGCGAGTTA CGATTGATG CAAGGTAAAG CAGTAAATGT GGAGCCGTAG CGGAAG

56

(2) INFORMATION FOR SEQ ID NO: 5038:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5038:

GACCGGGATG GACATAACCTC TGGTGTACCA GTTTGTCGTG CCAACGCATA AGCT

54

(2) INFORMATION FOR SEQ ID NO: 5039:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5039:

TTTCACCGAG TCTCTCGTTG AGCAGTGCCC AAATCGTTAC GCCTTTCGTG CGGG

54

(2) INFORMATION FOR SEQ ID NO: 5040:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5040:

TTATAACACG TATGCTTGGG GAGTGTAATA AGCTTGATCA GAGATTCCnA TGGGAACCAG 60

CATGAGTTAT GTCATTTATC ATATGTGATC ATAGCATATC AAAGG 105

(2) INFORMATION FOR SEQ ID NO: 5041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5041:

GGCACCTATT TTCTATCTAG AGGCTTTCT CGGCAGTGTG GAAATCAACG ACTC 54

(2) INFORMATION FOR SEQ ID NO: 5042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5042:

ACTTATCTAG TTTTCAATGT ACAAAATAATG GTGGAGACTA GCAGGATCGA ACCG 54

(2) INFORMATION FOR SEQ ID NO: 5043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5043:

CGTTCAGTCA ACTACTGCCA ATATAACATC GTAGAGCATA GAACATTGAT TTA 53

(2) INFORMATION FOR SEQ ID NO: 5044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5044:

ACTAGAGAGT ATTTAGACTT AGGAGTGGTC CTCCCCAGATT CCGACGGATT TCACGTGCT 59

(2) INFORMATION FOR SEQ ID NO: 5045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5045:

TTTCGTCGTC CCACCCCAAC TTGCACGCTA TTGTGAGCTG ACTTTTCGCC AGCTTCTGTG 60

TT 62

(2) INFORMATION FOR SEQ ID NO: 5046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5046:

CGTCATCCCC ACCTTCCTCC GGTTTGTAC CCGCAGTCAA CTTAGAGTGC CCA 53

(2) INFORMATION FOR SEQ ID NO: 5047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5047:

TATTTATTAA ACCTAATAAA GATGAATTAG AAGTGATGTT TAATACAACA GTG 53

(2) INFORMATION FOR SEQ ID NO: 5048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5048:

CCTCGGCACC ATTTCAATA AAAACATATG CGCCCGTAGC TCAATTGGAT AGA

53

(2) INFORMATION FOR SEQ ID NO: 5049:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5049:

AAATGGCAA CTTAACAG GATACAATT ACAAAATAGCG ACAATTCTC AATGTGTTT

59

(2) INFORMATION FOR SEQ ID NO: 5050:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5050:

CGAAAGACAC nCACAAAGATT AATAACGCGT TTGAGTCTTT TTATAAAGAC GTACTTCATG

60

TTACGTTGAC TTTAAGATGG TGGAACATAG TTAGTTTAG GGCCACGGGG G

111

(2) INFORMATION FOR SEQ ID NO: 5051:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5051:

ACGTTGACAT ATTGTCATTC AGTTTCAAT GTTCATTAAT GTTCAATCTC TTT

53

(2) INFORMATION FOR SEQ ID NO: 5052:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5052:

CTGAATTCGG TAACCCGAGA GGGCCCCTCG TCCAAACAGT GCTCTACCTC CAA

53

(2) INFORMATION FOR SEQ ID NO: 5053:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5053:

TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC CGG 53

(2) INFORMATION FOR SEQ ID NO: 5054:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5054:

AAATGCGGCT CATCGCATCC ATTTTTGCC TGGCAACGTT CTACTCTAGC GGAC 54

(2) INFORMATION FOR SEQ ID NO: 5055:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5055

TAGGGCTAGC CTCAAGTGAT GATTATTGGA GGTAGAGCAC TGTTGGACG AGG 53

(2) INFORMATION FOR SEQ ID NO: 5056:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5056:

ACTGCTTG AATGTTGTTG TCTCAGTTAA TATTCAATTG CTTTTCTTT GCATAATTGA 60

CAA 63

(2) INFORMATION FOR SEQ ID NO: 5057:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5057:

CTATGTTGGG GCCCGCCAA CTTGCATTGT CTGTAGAATT CCTTTTCGAA ATTC

54

(2) INFORMATION FOR SEQ ID NO: 5058:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5058:

CTGAATCCGA GTCGCTATCC GAGTCTGAGT CGCTATCTGA GTCTGAATCG CTG

53

(2) INFORMATION FOR SEQ ID NO: 5059:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5059:

TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG TGATGTCAA

59

(2) INFORMATION FOR SEQ ID NO: 5060:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5060:

AAATAACTAA TAACATTTAG AGGCTGGAC ATAAATCCCT AAAAAAACAGC AGT

53

(2) INFORMATION FOR SEQ ID NO: 5061:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5061:

TTAAAGAGTG CGTAATAGCT CACTAATCGA GTGACAATGG CGCCGAAAAT GTACC

55

(2) INFORMATION FOR SEQ ID NO: 5062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5062:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTCGC ACATCAGCGT CA

52

(2) INFORMATION FOR SEQ ID NO: 5063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5063:

TCGCCAAGCC ATTTTCTTT GTGTTTCTTT TTATTTAC GTTTAGACA TA

52

(2) INFORMATION FOR SEQ ID NO: 5064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5064:

CTCAAGCTCC CTTGTGCCTT TACACTCTAT GTGTGCTTTC CGACCGTTCT GGGGGGAAC

60

TTGGAGCGCC TCCGTT

76

(2) INFORMATION FOR SEQ ID NO: 5065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5065:

CCACCGCTTG TGCAGGTCCC CGTCAATTCC TTTGAGTCGC AACCTTGCAG TCGT

54

(2) INFORMATION FOR SEQ ID NO: 5066:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5066:

TCCCCGGGCT AAACATATTA CCGAAGCTGT GGATTGTCCT TTGGACAATG GTAGG

55

(2) INFORMATION FOR SEQ ID NO: 5067:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5067:

GCTCATCGCA TCCACTTTT GCCTGGAAC ACCTGAACTCT AGCGGAACGT AA

52

(2) INFORMATION FOR SEQ ID NO: 5068:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5068:

CGGACACCAG AAGTACCAAG CGAGCCGGAA ACACCAACAC CACCGACACC AGACGTACAA

60

GCGAGCGGAA ACAACAACAA CG

82

(2) INFORMATION FOR SEQ ID NO: 5069:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5069:

TCCATAACGT GCTGTATCTG TAGCAATAAC TAATACCTTT TCATTGGTC TA

52

(2) INFORMATION FOR SEQ ID NO: 5070:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5070:

CGACTCGAAG ACTCAATGTC TTCTCCCCAT CACAGCTCAG CCTTAACGAG TA 52

(2) INFORMATION FOR SEQ ID NO: 5071:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5071:

GCGATGGATA ACAGGTTGAT ATTCCCTGTAC CACCTATAAT CGTTTTAACATC GA 52

(2) INFORMATION FOR SEQ ID NO: 5072:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5072:

CACTTCACCA CAGCCGCCAT GGCATGGGCA GTAGGAATCG AACCCACACC AAA 53

(2) INFORMATION FOR SEQ ID NO: 5073:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5073:

GTCCAGACTC CTACGGGAGG CAGCAGTAGG GAATCTTCCG CAATGGCGA AA 52

(2) INFORMATION FOR SEQ ID NO: 5074:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5074:

TGTTGGCTTA GAATCAGCCA TCATTTAAAG AGTGC GTAAT AGCTCACTAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5075:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5075:

AGAATTTCGA ATCCCGCGAC GATCTGCCAA TTCCGCCACA CCGGCTTAAT GGTAAACAAA

60

AAACTTCCCT TTGG

74

(2) INFORMATION FOR SEQ ID NO: 5076:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5076:

TGAGCTAAC TGAGCTAAC ATTATTTATGG AGAGTTGAT CCTGGCTCAA GAT

53

(2) INFORMATION FOR SEQ ID NO: 5077:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5077:

GTAAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTG CGCTAGAGTA GA

52

(2) INFORMATION FOR SEQ ID NO: 5078:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5078:

GGGTAAGTTC CGACCCGCAC GAAAGGCGTA ACGATTTGGG CACTGTCTCA AC

52

(2) INFORMATION FOR SEQ ID NO: 5079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5079:

ATTAATCCAT TGTGCCACAA GTGCCGGACC AGAAATGATG GTATTTAAAT AT

52

(2) INFORMATION FOR SEQ ID NO: 5080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5080:

AATAGCGACG AATCACACCT TCTGCCGCAC CACGGAATAA TACACCATGT GG

52

(2) INFORMATION FOR SEQ ID NO: 5081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5081:

CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAAGCGCTC CACATGTCCT TA

52

(2) INFORMATION FOR SEQ ID NO: 5082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5082:

CAGACAGCGA CTCAGATCAG ATAGCGATCG GACTCAGACA ACGACTCAGA TTCAGA

56

(2) INFORMATION FOR SEQ ID NO: 5083:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQID NO: 5083:

AGGGTATGAT CCATCCGGG TCCTCTCGGT ACTAAGGGAC AGCTCCTCTC AAATTCCTA	60
CG	62

(2) INFORMATION FOR SEQ ID NO: 5084:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5084:

GTGTACCA GT TGTGTGCCA ACGGCATAGC TGGGTAGCTA TGTGTGGACG AG	52
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(2) INFORMATION FOR SEQ ID NO: 5085:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5085:

TTGCTTACGC TTGCTATAGC CAATATATAG ATGTTGGAGG GGGCAGATT C GAATGCGAAC	60
CCGAGGAGCG GATTAACA	78

(2) INFORMATION FOR SEQ ID NO: 5086:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5086:

ACTGACGCTG ATGTGCGAAG CGTGGGGATC ACACAGGATT AGATAACCCTG GT	52
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(2) INFORMATION FOR SEQ ID NO: 5087:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5087:

AAGTTGTTCT CAGTCGGAT TGTAGTCTGC AACTCGACTA CATGAAGCTG G

51

(2) INFORMATION FOR SEQ ID NO: 5088:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5088:

AATACTTAA AAAAATAAGA CACTTGGCC AACTTAAGCC AGGATACAAT T

51

(2) INFORMATION FOR SEQ ID NO: 5089:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5089:

AGAACGTAAA TTTAACCTTG ATTTAGCACC AGGGACAGAA AAAGTAACAA G

51

(2) INFORMATION FOR SEQ ID NO: 5090:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5090:

CCGCTACCC CAGTCATCC GCTCACTTT AACGTAAGT CGGTTGGTC C

51

(2) INFORMATION FOR SEQ ID NO: 5091:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5091:

CATGGGTGAT AAGGTCCGTG TTCGAAAGGG AAACAGCCCCA GACCACCAAGC T

51

(2) INFORMATION FOR SEQ ID NO: 5092:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5092:

TTGTGCGGAT CCCCCGTCAAT TCCTTGAGT TTCAACCTTG CGGTCGTACT CCCCA

55

(2) INFORMATION FOR SEQ ID NO: 5093:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5093:

CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TG~~A~~CGAGCG A

51

(2) INFORMATION FOR SEQ ID NO: 5094:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5094:

ACGAATACTA ATCGATCGAA GACTTAATCA AAATAATGT TTTGCGACAA A

51

(2) INFORMATION FOR SEQ ID NO: 5095:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 77 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5095:

AATCGTTGTT ACCTTCATTA TACCACTTAC TTGTGGAGTG ATCTTCTTCA AAGTAACACT 60

ATTGTGCCAC CGATTGA 77

(2) INFORMATION FOR SEQ ID NO: 5096:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5096:

TTCGTAAGGA CATGTGGAGC GCTTAGAACT GAGAATGCCG GTGTGAGTAG CG 52

(2) INFORMATION FOR SEQ ID NO: 5097:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5097:

GGGTCTGTTT TCTAATTGGA GCACAATCTT CGTTCTCAAT AGAATGATTT A 51

(2) INFORMATION FOR SEQ ID NO: 5098:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5098:

CTGTAGAAAT TGGGAATCCA ATTTCTCTAT GTTGGGGCCC ACACCCCAAC T 51

(2) INFORMATION FOR SEQ ID NO: 5099:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5099

CTGTGGATTG TCCTTGGCA TGAGATAGGA GAGCGTTCTA AGGGCGTTGA A 51

(2) INFORMATION FOR SEQ ID NO: 5100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5100:

GGTCAGAAC GTCGTGAGAC AGTTCGGTCC CTATCCGTCG TGGGCGTAGG A 51

(2) INFORMATION FOR SEQ ID NO: 5101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5101:

TGACTGATAC GATCAATGCG CTTGTAACAA GCTTTTTCA ATTCTAGTCA GGGGCCCAA 60

CACA 64

(2) INFORMATION FOR SEQ ID NO: 5102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5102:

TATTTGCATT TATATTGACG TTTTAAACAT AAAAAAAAGAA ACCTTGCGGT CTCAATGG 58

(2) INFORMATION FOR SEQ ID NO: 5103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5103:

ATTACCATT TGGTATAACCA CATCGTTATT CAACACATTA TCTTTTACTT 50

(2) INFORMATION FOR SEQ ID NO: 5104:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5104:

GGACACTGCT CCCTCAGGAG TCTCGCATT AATACTACGT ATTAACATGT AAT 53

(2) INFORMATION FOR SEQ ID NO: 5105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5105:

ATTTCCTTCTT TTTCTACAAT CGAGTCTCCT TTTACAGGTC CATATTTGT 50

(2) INFORMATION FOR SEQ ID NO: 5106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5106:

TGGTCAAGCG GTTAAGACAC CGCCCTTTCA CGGCGGTAAC ACGGGTTCGA 50

(2) INFORMATION FOR SEQ ID NO: 5107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5107:

TTTTTAGCAG TAATTGCCAC ATCTGTGTGA CGATAATAT ATGCGACAGT 50

(2) INFORMATION FOR SEQ ID NO: 5108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5108:

CAAGCCATTT TTCTTGTGT TTACTTTTA TTTTGACGTT TTAGACATAA

50

(2) INFORMATION FOR SEQ ID NO: 5109:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5109:

AGCCGATGAA GGACGTTACT AACGACGATA TGCTTGAGGG AGCTGTAAGT

50

(2) INFORMATION FOR SEQ ID NO: 5110:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5110:

ATCCATAACG TTTGGTATCT GTAGCAATAA CTAATACTTT TTCATTGGTCTA

53

(2) INFORMATION FOR SEQ ID NO: 5111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5111:

CCCTTAGTAC TGCAGCTAAC GCATTAAGCA CTCCGCCTGA GGAGTACGAC CTC

53

(2) INFORMATION FOR SEQ ID NO: 5112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5112:

GGAGTCAAAG TCCGTTGCCT TACCGCTTGG CTATAGCCCA ATATATAGAT

50

(2) INFORMATION FOR SEQ ID NO: 5113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5113:

AGAnTTTCTT TTCGAAATTC TTTATGTTGG GGCCCCGCCA ACTTGCATTG

50

(2) INFORMATION FOR SEQ ID NO: 5114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5114:

GCTGTGATGG GGAGAAGACA TTGTGTCTTC GAGTCGTTGA TTTCACACTG

50

(2) INFORMATION FOR SEQ ID NO: 5115:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5115:

CTTGATTAAC TCATTATCAA GTTATGCACG TGTAAATGAA TTCGGCTTA TCGAA

55

(2) INFORMATION FOR SEQ ID NO: 5116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5116:

GTACTTAAAA AATGAATACA TGAGTAAAGC TCATGGCATA AGAAATACTA

50

(2) INFORMATION FOR SEQ ID NO: 5117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5117:

CAGAACATCAGA TAGCGACTCA GAATCAGATA GTGAGTCAGA TTCAGCAGTn

50

(2) INFORMATION FOR SEQ ID NO: 5118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5118:

CGAAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACnAA

50

(2) INFORMATION FOR SEQ ID NO: 5119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5119:

AATCGTCGAA ACTTAATCAA AATAAATGTT TTGCGACAAA TCACCTTTAC TTACTATCTA

60

(2) INFORMATION FOR SEQ ID NO: 5120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5120:

CCGAAGTTA CGGGGTCTATT TTGCCGAGTT CCTTAACGAG AGTCGCTCG

50

(2) INFORMATION FOR SEQ ID NO: 5121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5121:

ATAATCCTGT AGTCGAAAAT GTTGTCTCTC TTGAGTGGAT CCTTAGTACG CCGGGGCACG 60
T 61

(2) INFORMATION FOR SEQ ID NO: 5122

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5122:

TAGCGACTCA GATTCAAGACA GCGATTCAAGA CAGCGACTCA GACTCAGATA 50
(2) INFORMATION FOR SEQ ID NO: 5123:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5123:

TATTTGTAAA TTGTATCCTG GCTTAAGTTG GCCATTTTC ATATGGTCTT 50
(2) INFORMATION FOR SEQ ID NO: 5124:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5124:

CACGAGCTGA CGACAACCAT GCACCACCTG TCACTTGTC CCCCGAGAAAG GTCTCTATCT 60
(2) INFORMATION FOR SEQ ID NO: 5125:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5125:

AGAACACATT GCAGTCTTCG AGTCGTTGAT TTCACACTGCCGTAGTAAAA GCCTCTAGAT 60
AGAA 64

(2) INFORMATION FOR SEQ ID NO: 5126:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5126:

GGACGACATT AGACGAATCA TCTGGAAAAG ATGAGTCAAA GAAGGTAATA GTCCTGT 57

(2) INFORMATION FOR SEQ ID NO: 5127:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5127:

GTCCTTAGTA CGAGATGACC GGGATGGACA TACCTCTGGT GTACCAGTTG 50

(2) INFORMATION FOR SEQ ID NO: 5128:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 5128:

GCCGATTTA GCAGTTGTTG CTTCGTTCAA TTTTATGGGG CCATTTATGG 50

(2) INFORMATION FOR SEQ ID NO: 5129:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5129:

TCCACACATA GCTACCCAGT CTATGCCGTT TGCACTACAA CTGGTACACC A 51

(2) INFORMATION FOR SEQ ID NO: 5130:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5130:

CTCAGTTGGT TGAGCATCTG ACTTTAACAA AAAGGGTCAA GGGTCGAATC CTCTTTT 57

(2) INFORMATION FOR SEQ ID NO: 5131:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5131:

TGATATTCAC TTCAATGTTA TCAATATTAG TGCCATCTAT GACATCTGCC A 51

(2) INFORMATION FOR SEQ ID NO: 5132:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5132:

TCCTGTAGTC GAACGTGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG A 51

(2) INFORMATION FOR SEQ ID NO: 5133:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5133:

ACTCAGACAT TGGATTCAAGA TTCAGACAGC GACTCAGATT CAGATAGCGA CTCAGATTC 59

(2) INFORMATION FOR SEQ ID NO: 5134:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5134:

CCACCCCCAAC GTTGCATTGT CTGTAGAAAT TGGGAATCCA ATTTCTCTTT

50

(2) INFORMATION FOR SEQ ID NO: 5135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5135:

CAATAACnAAG GGCAGCGAAA CCGTGATTCA AGCAAATCCC ATAAAGTTGG

50

(2) INFORMATION FOR SEQ ID NO: 5136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5136:

GAAGCTGGCG AAAAGTCAGC TTACAAAATG TGCCAGTTGG CGGGGGGCCA AC

52

(2) INFORMATION FOR SEQ ID NO: 5137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5137:

TTGTAAGGAA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGAnT

50

(2) INFORMATION FOR SEQ ID NO: 5138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5138:

CTGTACAAGC TGTGCCGATA TTTCAATATC AnGnTACAGT AnAGCTCCAC

50

(2) INFORMATION FOR SEQ ID NO: 5139:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5139:

GGTCGAATC CTGTCTCCC GATATACTGT AATTATTATG GGGGCTTG C TC

52

(2) INFORMATION FOR SEQ ID NO: 5140:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5140:

GCTACTGAAC CTATAAAATG TATGATGGCG GTCTCGAGGG AATCGAACCC AGATCT

56

(2) INFORMATION FOR SEQ ID NO: 5141:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5141:

AGGAGGCTCG TCCGCTCTAG GTTAGTCGGG TCCTAAGCTG AGGCCGACAG TA

52

(2) INFORMATION FOR SEQ ID NO: 5142:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5142:

CACGCTTCG ACATCAGCGT CAGTTACAGA CCAGAAAGTC GCCTTCGCAC TGGTGT

56

(2) INFORMATION FOR SEQ ID NO: 5143:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5143:

CTCCTAAAC AATTTACATC CAAACCTTCA TCACTCACGC GCGTTGCTC CGTCAGCTT 60
CGCCATTGCG AAGAT 75

(2) INFORMATION FOR SEQ ID NO: 5144:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:

GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT 55

(2) INFORMATION FOR SEQ ID NO: 5145:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:

GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG 53

(2) INFORMATION FOR SEQ ID NO: 5146:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:

AGCTGTGGAT TGTCTTTG GCATGGTAA GGAGAACGTT CTAAGGGCGT T 51

(2) INFORMATION FOR SEQ ID NO: 5147:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5147:

CTCTTGATC CGTAGTCAAA CGCTCTATCC AATTGAGCTA CGGGCGCATA

50

(2) INFORMATION FOR SEQ ID NO: 5148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5148:

GAACTAACATTG TCCAAAATAA TGACTCCTAC AGGAACCTCGA ACCCGTATAA CCGCCGTAAA

60

(2) INFORMATION FOR SEQ ID NO: 5149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5149:

AAAGCACACC CGGAAACTG AAACATCTTA AGTACCCGGA GnAAGAGAAA

50

(2) INFORMATION FOR SEQ ID NO: 5150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5150:

GTAAGTCGC ACTACCATCG ACGCTAAGGG AGCTTAACCTT CTGTGGTTCG GCATGG

56

(2) INFORMATION FOR SEQ ID NO: 5151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5151:

GGACTACCTG TGTCGAGTTT GCGGTAGGGG TCACCTGATT TTCTATCTAG AGGCTC

56

(2) INFORMATION FOR SEQ ID NO: 5152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5152:

CTATTCTCTG TGTCGGGCTC ACCCCAACTT GCACACTATT GTAAGCTGAC TTTCCTCCA

59

(2) INFORMATION FOR SEQ ID NO: 5153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5153:

TAACCACATC ATTGGGATAC TGTCATGGA AGTAATTCT CTATTCTCG GACCAGGAAA

60

ATACA

65

(2) INFORMATION FOR SEQ ID NO: 5154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5154:

CCATATGTGT CAGTCACTGT GCAATCTTG ACGGTACCTA ATCAGACAGC CACGGCTAAC

60

TCCGTGCCAG CCGCCGCGGT ACTACGTGGT G

91

(2) INFORMATION FOR SEQ ID NO: 5155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5155:

GGGAAAAGGA TGTGGTCGTT GCCCAGACAA CTAGGATGTT GGCTTATAAT CA

52

(2) INFORMATION FOR SEQ ID NO: 5156:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5156:

GACTCTGGGA GGACCATCTC CTAAGGCTAA ACTACTCTCGTGACCGAT AGTGAACC

58

(2) INFORMATION FOR SEQ ID NO: 5157:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5157:

TTGTAACTCC GGTATAAGGAG TGTCTACAA CCCCAACAAG CAAGCTTGTT G

51

(2) INFORMATION FOR SEQ ID NO: 5158:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5158:

TAGTnACCGn TAGTGAACCA TTACCGTGAG GGAAAGGTGA AAAGCACCCC

50

(2) INFORMATION FOR SEQ ID NO: 5159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5159:

TTCGCTCGCC GCTACTCAAG GGAATCGCAT TTCCTTCTC TTCCTCCGGG T

51

(2) INFORMATION FOR SEQ ID NO: 5160:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5160:

AACTGGAGAA ACAACTTAT GGGGTTTGCT TGAACCTCGC GGTTTCGCTG CCCTTTGTAT 60
T 61

(2) INFORMATION FOR SEQ ID NO: 5161:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5161:

AGACCTCTGC CTTACCACTT GGCTATGCGC CAATAACTGG GCTACCTGGA T 51

(2) INFORMATION FOR SEQ ID NO: 5162:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5162:

CCGCTCACTT TTCAACGTAA GTCGGATCGG TCCTCCATTC AGTGTCACCT GAACT 55

(2) INFORMATION FOR SEQ ID NO: 5163:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5163:

CTTGATCTGT ATTTAAAATG ATATTTCTA TCTTTCTTT ATTATTAACG TCTATGACGT 60
CGTAGTATAA GATTCCGTGT A 81

(2) INFORMATION FOR SEQ ID NO: 5164:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5164:

GTTCGAACATCC CGTCTTCTGC TCCATTATTT TGCCGGGGTG GCGGCAACTC TCACACGCAC 60
AG 62

(2) INFORMATION FOR SEQ ID NO: 5165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5165:

CAGGGGTCTT TCGTCCTGTG TGGGTAAC TG CATCTTCACA GGTACTATGA TTTCA 55
55

(2) INFORMATION FOR SEQ ID NO: 5166

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5166:

AAGCTGAGGC CGACAGCGTA GGCGATGGAT GACAGGTTGA TATTGCCGGT ACCACCCGAT 60
AA 62

(2) INFORMATION FOR SEQ ID NO: 5167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5167:

CTTGCCTCTC CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA CG 52
52

(2) INFORMATION FOR SEQ ID NO: 5168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5168:

TCGTCCGCTA TCTCCACCAT TATTTGTACA TTGAAACTAG ATA~~A~~TAGTA AATATA

56

(2) INFORMATION FOR SEQ ID NO: 5169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5169:

CTTGGACGTC GGTGGGTAGT CGAAACTTAC GTTCCGCTAG AGTAGAACGT TGCCA

55

(2) INFORMATION FOR SEQ ID NO: 5170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5170:

CTACTGCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCA TA

52

(2) INFORMATION FOR SEQ ID NO: 5171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5171:

GGGCTTnGGA CATTAAGTTC TnAGGCAATG TAAAAAAAGCT GATTCTATT

50

(2) INFORMATION FOR SEQ ID NO: 5172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 5172:

AAATTACATG TTAATACGTA ATTAATGGCG AGACTCCTGA GGAACCATTG CCATTCGAAG 60

(2) INFORMATION FOR SEQ ID NO: 5173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5173:

GTTTATTCTT TTTAAAGTAT GTAAAAGTAA AATTACATGn TAATACGTAn 50

(2) INFORMATION FOR SEQ ID NO: 5174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5174:

CAACTCTCGT TAAGGAACTC GGCAAAATAC CCCGTAACCT CGGAGTAGGT CTCTTTA 57

(2) INFORMATION FOR SEQ ID NO: 5175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5175:

GGAAACTGGA ATAAATAAAC ATTCAATTGA GCGCATCAGT ATTAGGATTC ACTCTAAAAA 60

(2) INFORMATION FOR SEQ ID NO: 5176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5176:

GTAACGGACG CGCTCAAAGG TTCCCTCACCA ATGGTTGGAA ATCATTCTATA 50

(2) INFORMATION FOR SEQ ID NO: 5177:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5177:

AGTTACGTTTC TTTTATAAAG AGGTTTGAGA CGCGTTATTA ATCTTGTGAG

50

(2) INFORMATION FOR SEQ ID NO: 5178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5178:

GTGTGGATCC TGAGTACGAC GGAGCACGTG ACAATTCCGT CGGCAATCTG GGG

53

(2) INFORMATION FOR SEQ ID NO: 5179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 83 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5179:

CGGTAACCTTC ATACCTTTA ACATATTTG CATTGATTG CGTTTACCTT TTTTACCTTT

60

ACCGCCACCA GTGAACGTGTT TCA

83

(2) INFORMATION FOR SEQ ID NO: 5180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5180:

TTAAACCCTT TTAATTGTTT GCCCAGAACCA CCATCGCTAT GGATGAAATT TAAAAAGCCG

60

TTTAAA

66

(2) INFORMATION FOR SEQ ID NO: 5181:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 67 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5181:

GTTCGGTAAC TCGAGCGGGT CTCATAACCC GTAGGTCGGG TGGTTCAAAT CCGTCCTCCC	60
GCAATAT	67

(2) INFORMATION FOR SEQ ID NO: 5182:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5182:

TAGCGGTGAA ATGCGCAGAG ATATGGAGGA ACACCAGTAG CGAAGGCAAC TTTCT	55
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(2) INFORMATION FOR SEQ ID NO: 5183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5183:

GAATTCCATG TGTAGCGGTG AAATGCGCAG AGATATGnAC GAACACCAAT	50
--	----

(2) INFORMATION FOR SEQ ID NO: 5184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5184:

GAATCAGAGT TGGGGTGTGG GCCCGACGAA AGAGAAATTG GATTCCCGAA TTTCACGAG	60
CC	62

(2) INFORMATION FOR SEQ ID NO: 5185:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5185:

GAGACCTTGT CGGTCCATAT GCGGCTCATC GCATCCATT TTTGCCTGGC AACGT

55

(2) INFORMATION FOR SEQ ID NO: 5186:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5186:

CCATCATTAA GTTGGGCACT CTAAGTTGAC TGCCGGnGnC ACCnAAGAAG

50

(2) INFORMATION FOR SEQ ID NO: 5187:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5187

TTAATACGTT GCAATCCAAT CGCACGCTTC GCCTATCCTA CTGCCnTCCC

50

(2) INFORMATION FOR SEQ ID NO: 5188:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5188:

AGTCGCTATC CGAATCTGAG TCGCTATCTG AGTCTnAGTC GCTAnnCCAG

50

(2) INFORMATION FOR SEQ ID NO: 5189:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5189:

ATAGATGCC C TTACCGCAAA CCGACACATG TAGTCAATAT GATAATTCTA AGGT

54

(2) INFORMATION FOR SEQ ID NO: 5190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5190:

CTTTAATGGG CGAACAGnAC CCTTGGACCG ACTACAGCCC AGATCGATGA

50

(2) INFORMATION FOR SEQ ID NO: 5191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5191:

ACATAGCACC CAGCGAGCCG TTGGACGACA ACTGGTACAC CAGAGGATGC CATCCGGCCT

60

(2) INFORMATION FOR SEQ ID NO: 5192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5192:

Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu
1 5 10 15

Leu Leu Gly Ala Cys Gly Ala Ser Ala Thr Asp Ser Lys Glu Asn Thr
20 25 30

Leu Ile Ser Ser Lys Ala Gly Asp Val Thr Val Ala Asp Thr Met Lys
35 40 45

Lys Ile Gly Lys Asp Gln Ile Ala Asn Ala Ser Phe Thr Glu Met Leu
50 55 60

Asn	Lys	Ile	Leu	Ala	Asp	Lys	Tyr	Lys	Asn	Lys	Val	Asn	Asp	Lys	Lys
65					70				75					80	
Ile	Asp	Glu	Gln	Ile	Glu	Lys	Met	Gln	Lys	Gln	Tyr	Gly	Gly	Lys	Asp
					85				90					95	
Lys	Phe	Glu	Lys	Ala	Leu	Gln	Gln	Gly	Leu	Thr	Ala	Asp	Lys	Tyr	
					100				105				110		
Lys	Glu	Asn	Leu	Arg	Thr	Ala	Ala	Tyr	His	Lys	Glu	Leu	Leu	Ser	Asp
					115				120				125		
Lys	Ile	Lys	Ile	Ser	Asp	Ser	Glu	Ile	Lys	Glu	Asp	Ser	Lys	Lys	Ala
					130				135				140		
Ser	His	Ile	Leu	Ile	Lys	Val	Lys	Ser	Lys	Lys	Ser	Asp	Xaa	Glu	Gly
					145				150				155		160
Leu	Asp	Asp	Lys	Glu	Ala	Lys	Gln	Lys	Ala	Glu	Glu	Ile	Gln	Lys	Glu
					165				170				175		
Val	Ser	Lys	Asp	Pro	Ser	Lys	Phe	Gly	Glu	Ile	Ala	Lys	lys	Glu	Ser
					180				185				190		
Met	Asp	Thr	Gly	Ser	Ala	Lys	Lys	Asp	Gly	Glu	Leu	Gly	Tyr	Val	Leu
					195				200				205		
Lys	Gly	Gln	Thr	Asp	Lys	Asp	Phe	Glu	Lys	Ala	Leu	Phe	Lys	Leu	Lys
					210				215				220		
Asp	Gly	Glu	Val	Ser	Glu	Val	Val	Lys	Ser	Ser	Phe	Gly	Tyr	His	Ile
					225				230				235		240
Ile	Lys	Ala	Asp	Lys	Pro	Thr	Asp	Phe	Asn	Ser	Glu	Lys	Gln	Ser	Leu
					245				250				255		
Lys	Glu	Lys	Leu	Val	Asp	Gln	Lys	Val	Gln	Lys	Asn	Pro	Lys	Leu	Leu
					260				265				270		
Thr	Asp	Ala	Tyr	Lys	Asp	Leu	Leu	Lys	Glu	Tyr	Asp	Val	Asp	Phe	Lys
					275				280				285		
Asp	Arg	Asp	Ile	Lys	Ser	Val	Val	Glu	Asp	Lys	Ile	Leu	Asn	Pro	Glu
					290				295				300		
Lys	Leu	Lys	Gln	Gly	Gly	Ala	Gln	Gly	Gly	Gln	Ser	Gly	Met	Ser	Gln
					305				310				315		320

(2) INFORMATION FOR SEQ ID NO:5193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5193:

Met Asn Lys Val Ile Lys Met Leu Val Val Thr Leu Ala Phe Leu Leu
1 5 10 15

Val Leu Ala Gly Cys Ser Gly Asn Ser Asn Lys Gln Ser Ser Asp Asn
20 25 30

Lys Asp Lys Glu Thr Thr Ser Ile Lys His Ala Met Gly Thr Thr Glu
35 40 45

Ile Lys Gly Lys Pro Lys Arg Val Val Thr Leu Tyr Gln Gly Ala Thr
50 55 60

Asp Val Ala Val Ser Leu Gly Val Lys Pro Val Gly Ala Val Glu Ser
65 70 75 80

Trp Thr Gln Lys Pro Lys Phe Glu Tyr Ile Lys Asn Asp Leu Lys Asp
85 90 95

Thr Lys Ile Val Gly Gln Glu Pro Ala Pro Asn Leu Glu Glu Ile Ser
100 105 110

Lys Leu Lys Pro Asp Leu Ile Val Ala Ser Lys Val Arg Asn Glu Lys
115 120 125

Val Tyr Asp Gln Leu Ser Lys Ile Ala Pro Thr Val Ser Thr Asp Thr
130 135 140

Val Phe Lys Phe Lys Asp Thr Thr Lys Le Met Gly Lys Ala Leu Gly
145 150 155 160

Lys Glu Lys Glu Ala Glu Asp Leu Leu Lys Lys Tyr Asp Asp Lys Val
165 170 175

Ala Ala Phe Gln Lys Asp Ala Lys Ala Lys Tyr Lys Asp Ala Trp Pro
180 185 190

Leu Lys Ala Ser Val Val Asn Phe Arg Ala Asp His Thr Arg Ile Tyr
195 200 205

Ala Gly Gly Tyr Ala Gly Glu Ile Leu Asn Asp Leu Gly Phe Lys Arg
210 215 220

Asn Lys Asp Leu Gln Lys Gln Val Asp Asn Gly Lys Asp Ile Ile Gln
225 230 235 240

Leu Thr Ser Lys Glu Ser Ile Pro Leu Met Asn Ala Asp His Ile Phe
245 250 255

Val Val Lys Ser Asp Pro Asn Ala Lys Asp Ala Ala Leu Val Lys Lys
260 265 270

Thr Glu Ser Glu Trp Thr Ser Ser Lys Glu Trp Lys Asn Leu Asp Ala
275 280 285

Val Lys Asn Asn Gln Val Ser Asp Asp Leu Asp Glu Ie Thr Trp Asn
290 295 300

Leu Ala Gly Gly Tyr Lys Ser Ser Leu Lys Leu Ile Asp Asp Leu Tyr
305 310 315 320

Glu Lys Leu Asn Ile Glu Lys Gln Ser Lys
325 330

(2) INFORMATION FOR SEQ ID NO:5194:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5194:

Met Thr Arg Lys Phe Arg Thr Leu Ile Leu Ile Leu Ile Ala Thr Ile
1 5 10 15

Ala Leu Ser Gly Cys Ala Asn Asp Asp Gly Ile Tyr Ser Asp Lys Gly
20 25 30

Gln Val Phe Arg Lys Ile Leu Ser Ser Asp Leu Thr Ser Leu Asp Thr
35 40 45

Ser Leu Ile Thr Asp Glu Ile Ser Ser Glu Val Thr Ala Gln Thr Phe
50 55 60

Glu Gly Leu Tyr Thr Leu Gly Lys Gly Asp Lys Pro Val Leu Gly Val
65 70 75 80

Ala Lys Ala Phe Pro Glu Lys Ser Lys Asp Gly Lys Thr Leu Lys Val
85 90 95

Lys Leu Arg Ser Asp Ala Lys Trp Ser Asn Gly Asp Lys Val Thr Ala
100 105 110

Gln Asp Phe Val Tyr Ala Trp Arg Lys Thr Val Asp Pro Lys Thr Gly
115 120 125

Ser Glu Phe Ala Tyr Ile Met Gly Asp Ile Lys Asn Ala Ser Asp Ile
130 135 140

Ser Thr Gly Lys Lys Pro Val Glu Gln Leu Gly Ile Lys Ala Leu Asn
145 150 155 160

Asp Glu Thr Leu Gln Ile Glu Leu Glu Lys Pro Val Pro Tyr Ile Asn
165 170 175

Gln Leu Leu Ala Leu Asn Thr Phe Ala Pro Gln Asn Glu Lys Val Ala
180 185 190

Lys Lys Tyr Gly Lys Asn Tyr Gly Thr Ala Ala Asp Arg Ala Val Tyr
195 200 205

Asn Gly Pro Phe Lys Val Asp Asp Trp Lys Gln Glu Asp Lys Thr Leu

210	215	220	
Leu Ser Lys Asn Gln Tyr Tyr Trp Asp Lys Lys Asn Val Lys Leu Asp			
225	230	235	240
Lys Val Asn Tyr Lys Val Ile Lys Asp Leu Gln Ala Gly Ala Ser Leu			
245	250	255	
Tyr Asp Thr Glu Ser Val Asp Asp Ala Phe Ile Thr Ala Asp Gln Val			
260	265	270	
Asn Lys Tyr Lys Asp Asn Lys Gly Leu Asn Phe Val Leu Thr Mr Gly			
275	280	285	
Thr Phe Phe Val Lys Met Asn Glu Lys Gln Tyr Pro Asp Phe Lys Asn			
290	295	300	
Lys Asn Leu Arg Leu Xaa Ser HisLys Gln			
305	310		

(2) INFORMATION FOR SEQ ID NO:5195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5195:

Met Lys Arg Leu Ile Gly Leu Val Ile Val Ala Leu Val Leu Leu Ala			
1	5	10	15
Ala Cys Gly Gly Asn Asn Asp Lys Lys Val Thr Ile Gly Val Ala Ser			
20	25	30	
Asn Asp Thr Lys Ala Trp Glu Lys Val Lys Glu Leu Ala Lys Lys Asp			
35	40	45	
Asp Ile Asp Val Glu Ile Lys His Phe Ser Asp Tyr Asn Leu Pro Asn			
50	55	60	
Lys Ala Leu Asn Asp Gly Asp Ile Asp Met Asn Ala Phe Gln His Phe			
65	70	75	80
Ala Phe Leu Asp Gln Tyr Lys Lys Ala His Lys Gly Thr Lys Ile Ser			
85	90	95	
Ala Leu Ser Thr Thr Val Leu Ala Pro Leu Gly Ile Tyr Ser Asp Lys			
100	105	110	
Ile Lys Asp Val Lys Lys Val Lys Asp Gly Ala Lys Val Val Ile Pro			
115	120	125	
Asn Asp Val Ser Asn Gln Ala Arg Ala Leu Lys Leu Leu Gl Ala Ala			
130	135	140	

Gly Leu Ile Lys Leu Lys Lys Asp Phe Gly Leu Ala Gly Thr Val Lys
 145 150 155 160
 Asp Ile Thr Ser Asn Pro Lys His Leu Lys Ile Thr Ala Val Asp Ala
 165 170 175
 Gln Gln Thr Ala Arg Ala Leu Ser Asp Val Asp Ile Ala Val Ile Asn
 180 185 190
 Asn Gly Val Ala Thr Lys Ala Gly Lys Asp Pro Lys Asn Asp Pro Ile
 195 200 205
 Phe Leu Glu Lys Ser Asn Ser Asp Ala Val Lys Pro Tyr Ile Asn Ile
 210 215 220
 Val Ala Val Asn Asp Lys Asp Leu Asp Asn Lys Thr Tyr Ala Lys Ile
 225 230 235 240
 Val Glu Leu Tyr His Ser Lys Glu Ala Gln Lys Ala Leu Gln Glu Asp
 245 250 255
 Val Lys Asp Gly Glu Lys Pro Val Asn Leu Ser Lys Asp Glu Ile Lys
 260 265 270
 Ala Ile Glu Thr Ser Leu Ala Lys
 275 280

(2) INFORMATION FOR SEQ ID NO:5196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5196: -

Met Lys Lys Leu Phe Gly Leu Ile Leu Val Leu Thr Phe Ala Val Val
 1 5 10 15
 Leu Ala Ala Cys Gly Asn Gly Asn Lys Ser Gly Ser Asp Asp Lys Lys
 20 25 30
 Ile Thr Val Ser Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys
 35 40 45
 Ala Lys Pro Leu Leu Glu Lys Lys Gly Tyr Gu Leu Asp Ile Lys Thr
 50 55 60
 Ile Asn Asp Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile
 65 70 75 80
 Asp Ala Asn Tyr Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Lys Lys
 85 90 95

Asp Lys Gly Tyr Lys Ile Val Ser Ala Gly Asp Val His Leu Glu Pro
100 105 110

Met Ala Val Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Glu Leu Pro Lys
115 120 125

Gly Ala Thr Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe
130 135 140

Leu Lys Phe Phe Val Asp Ala Gly Leu Ile Lys Ile Lys Lys Gly Val
145 150 155 160

Lys Ile Glu Asp Ala Lys Phe Ser Asp Ile Thr Glu Asn Lys Lys Asp
165 170 175

Ile Lys Phe Asn Asn Lys Gln Ser Ala Glu Phe Leu Pro Lys Ile Tyr
180 185 190

Gln Asn Glu Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Phe Ala Ile
195 200 205

Glu Gln Lys Leu Asn Pro Lys Lys Asp Ser Ile Ala Val Glu Ser Ala
210 215 220

Lys Asp Asn Pro Tyr Ala Asn Leu Ile Ala Val Lys Glu Gly His Gln
225 230 235 240

Asp Asp Lys Ile Lys Ala Leu Ile Glu Val Leu Gln Ser Lys Asp
245 250 255

Ile Gln Asp Phe Ile Asn Glu Lys Tyr Asn Gly Ala Val Ile Pro Ala
260 265 270

Lys

(2) INFORMATION FOR SEQ ID NO:5197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5197:

Met Lys Lys Ile Lys Tyr Ile Leu Val Val Phe Val Leu Ser Ile Thr
1 5 10 15

Val Leu Ser Gly Cys Ser Leu Pro Gly Leu Gly Ser Lys Ser Thr Lys
20 25 30

Asn Asp Val Lys Ile Thr Ala Leu Ser Thr Ser Glu Ser Gln Ile Ile
35 40 45

Ser His Met Leu Arg Leu Leu Ile Glu His Asp Thr His Gly Lys Ile

50	55	60
Lys Pro Thr Leu Val Asn Asn Leu Gly Ser Ser Thr Ile Gln His Asn		
65	70	75
Ala Leu Ile Asn Gly Asp Ala Asn Ile Ser Gly Val Arg Tyr Asn Gly		
85	90	95
Thr Asp Leu Thr Gly Ala Leu Lys Glu Ala Pro Ile Lys Asn Pro Lys		
100	105	110
Lys Ala Met Ile Ala Thr Gln Gln Gly Phe Lys Lys Phe Asp Gln		
115	120	125
Thr Phe Phe Asp Ser Tyr Gly Phe Ala Asn Thr Tyr Ala Phe Met Val		
130	135	140
Thr Lys Glu Thr Ala Lys Lys Tyr His Leu Glu Thr Val Ser Asp Leu		
145	150	155
Ala Lys His Ser Lys Asp Leu Arg Leu Gly Met Asp Ser Ser Trp Met		
165	170	175
Asn Arg Lys Gly Asp Gly Tyr Glu Gly Phe LysLys Glu Tyr Gly Phe		
180	185	190
Asp Phe Gly Thr Val Arg Pro Met Gln Ile Gly Leu Val Tyr Asp Ala		
195	200	205
Leu Asn Ser Glu Lys Leu Asp Val Ala Leu Gly Tyr Ser Thr Asp Gly		
210	215	220
Arg Ile Ala Ala Tyr Asp Leu Lys Val Leu Lys Asp Asp Lys Gln Phe		
225	230	235
Phe Pro Pro Tyr Ala Ala Ser Ala Val Ala Thr Asn Glu Leu Leu Arg		
245	250	255
Gln His Pro Glu Leu Lys Thr Thr Ile Asn Lys Leu Thr Gly Lys Ile		
260	265	270
Ser Thr Ser Glu Met Gln Arg Leu Asn Tyr Glu Ala Asp Gly Lys Gly		
275	280	285
Lys Glu Pro Ala Val Val Ala Glu Glu Phe Leu Lys Lys His His Tyr		
290	295	300
Phe Asp Lys Gln Lys Gly Gly His Lys		
305	310	

(2) INFORMATION FOR SEQ ID NO:5198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5198:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala
1 5 10 15

Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys
20 25 30

Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln AlaThr Lys Ala Tyr
35 40 45

Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu
50 55 60

Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala
65 70 75 80

Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala
85 90 95

Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp
100 105 110

Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile
115 120 125

Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys
130 135 140

Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala
145 150 155 160

Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp
165 170 175

Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu GluIle
180 185 190

Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala
195 200 205

Gln Lys Ile Tyr Asp Leu Phe Lys Ro Ile Leu Glu Lys Lys Asp Lys
210 215 220

Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
225 230 235 240

Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
245 250 255

Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
260 265 270

Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
275 280

(2) INFORMATION FOR SEQ ID NO:5199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5199:

Met	Lys	Lys	Leu	Thr	Thr	Leu	Leu	Leu	Ala	Ser	Thr	Leu	Leu	Ile	Ala
1															15
Ala	Cys	Gly	Asn	Asp	Asp	Ser	Lys	Lys	Asp	Asp	Ser	Lys	Thr	Ser	Lys
															30
Lys	Asp	Asp	Gly	Val	Lys	Ala	Glu	Leu	Lys	Gln	Ala	Thr	Lys	Ala	Tyr
															45
Asp	Lys	Tyr	Thr	Asp	Glu	Gln	Leu	Asn	Glu	Phe	Leu	Lys	Gly	Thr	Glu
															60
Lys	Phe	Val	Lys	Ala	Ile	Glu	Asn	Asn	Asp	Met	Ala	Gln	Ala	Lys	Ala
															80
Leu	Tyr	Pro	Lys	Val	Arg	Met	Tyr	Tyr	Glu	Arg	Ser	Glu	Pro	Val	Ala
															95
Glu	Ala	Phe	Gly	Asp	Leu	Asp	Pro	Lys	Ile	Asp	Ala	Arg	Leu	Ala	Asp
															110
Met	Lys	Glu	Glu	Lys	Lys	Glu	Lys	Glu	Trp	Ser	Gly	Tyr	His	Lys	Ile
															125
Glu	Lys	Ala	Leu	Tyr	Glu	Asp	Lys	Lys	Ile	Asp	Asp	Val	Thr	Lys	Lys
															140
Asp	Ala	Gln	Gln	Leu	Leu	Lys	Asp	Ala	Lys	Glu	Leu	His	Ala	Lys	Ala
															160
Asp	Thr	Leu	Asp	Ile	Thr	Pro	Lys	Leu	Met	Leu	Gln	Gly	Ser	Val	Asp
															175
Leu	Leu	Asn	Glu	Val	Ala	Thr	Ser	Lys	Ile	Thr	Gly	Glu	Glu	Ile	
															190
Tyr	Ser	His	Thr	Asp	Leu	Tyr	Asp	Phe	Lys	Ala	Asn	Val	Glu	Gly	Ala
															205
Gln	Lys	Ile	Tyr	Asp	Leu	Phe	Lys	Pro	Ile	Leu	Glu	Lys	Lys	Asp	Lys
															220
Lys	Leu	Ser	Asp	Asp	Ile	Gln	Met	Asn	Phe	Asp	Lys	Val	Asn	Gln	Leu
															240
Leu	Asp	Lys	Tyr	Lys	Asp	Asn	Asn	Gly	Gly	Tyr	Glu	Ser	Phe	Glu	Lys
															255
Val	Ser	Lys	Lys	Asp	Arg	Lys	Ala	Phe	Ala	Asp	Ala	Val	Asn	Ala	Leu

260

265

270

Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
275 280

(2) INFORMATION FOR SEQ ID NO:5200:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5200:

Met Lys Phe Lys Ala Ile Val Ala Ile Thr Leu Ser Leu Ser Leu Leu
1 5 10 15

Thr Ala Cys Gly Ala Asn Gln His Lys Glu Asn Ser Ser Lys Ser Asn
20 25 30

Asp Thr Asn Lys Lys Thr Gln Gln Thr Asp Asn Thr Thr Gln Ser Asn
35 40 45

Thr Glu Lys Gln Met Thr Pro Gln Glu Ala Glu Asp Ile Val Arg Asn
50 55 60

Asp Tyr Lys Ala Arg Gly Val Asn Glu Tyr Gln Thr Leu Asn Tyr Lys
65 70 75 80

Thr Asn Leu Glu Arg Ser Asn Glu His Glu Tyr Tyr Val Glu His Leu
85 90 95

Val Arg Asp Ala Val Gly Thr Pro Leu Lys Arg Cys Ala Ile Val Asn
100 105 110

Arg His Asn Gly Thr Ile Ile Asn Ile Phe Asp Asp Met Ser Glu Lys
115 120 125

Asp Lys Glu Glu Phe Glu Ala Phe Lys Lys Arg Ser Pro Lys Tyr Asn
130 135 140

Pro Gly Met Asn Asn His Asp Glu Thr Asp Gly Glu Ser Glu Asp Ile
145 150 155 160

Gln His His Asp Ile Asp Asn Asn Lys Ala Ile Gln Asn Asp Ile Pro
165 170 175

Asp Gln Lys Val Asp Asp Lys Asn Asp Lys Asn Ala Val Asn Lys Glu
180 185 190

Glu Lys His Asp Asn Gly Ala Asn Asn Ser Glu Glu Thr Lys Val Lys
195 200 205

(2) INFORMATION FOR SEQ ID NO:5201:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5201:

Met	Leu	Lys	Gly	Cys	Gly	Gly	Cys	Leu	Ile	Ser	Phe	Ile	Leu	Leu	Ile
1				5					10						15
Ile	Leu	Leu	Ser	Ala	Cys	Ser	Met	Met	Phe	Ser	Asn	Asn	Asp	Asn	Ser
							20		25						30
Thr	Asn	Asn	Gln	Ser	Ser	Lys	Thr	Gln	Leu	Thr	Gln	Lys	Asp	Glu	Asn
						35		40							45
Lys	Asn	Glu	Asp	Lys	Pro	Glu	Glu	Lys	Ser	Glu	Thr	Ala	Thr	Asp	Glu
					50		55								60
Asp	Leu	Gln	Ser	Thr	Glu	Glu	Val	Pro	Ala	Asn	Glu	Asn	Thr	Glu	Asn
					65		70			75					80
Asn	Gln	His	Glu	Ile	Asp	Glu	Ile	Thr	Thr	Lys	Asp	Gln	Ser	Asp	Asp
					85			90							95
Asp	Ile	Asn	Thr	Pro	Asn	Val	Ala	Glu	Asp	Lys	Ser	Gln	Asp	Asp	Leu
					100			105							110
Lys	Asp	Asp	Leu	Lys	Glu	Lys	Gln	Gln	Ser	Ser	Asn	His	His	Gln	Ser
					115			120							125
Thr	Gln	Pro	Lys	Thr	Ser	Pro	Ser	Thr	Glu	Thr	Asn	Thr	Gln	Gln	Ser
					130			135							140
Phe	Ala	Asn	Cys	Lys	Gln	Leu	Arg	Gln	Val	Tyr	Pro	Asn	Gly	Val	Thr
					145		150		155						160
Ala	Asp	His	Pro	Ala	Tyr	Arg	Pro	His	Leu	Asp	Arg	Asp	Lys	Asp	Lys
					165			170							175
Arg	Ala	Cys	Glu	Pro	Asp	Lys	Tyr								
					180										

(2) INFORMATION FOR SEQ ID NO:5202:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5202:

Met Lys Lys Arg Leu Leu Leu Ser Thr Phe Leu Ala Ser Thr Leu Ile
1 5 10 15

Leu Thr Gly Cys Ala Ser Asp Gln Ser Asp Asn Glu Asp His His Thr
20 25 30

Ser Thr Gly Ile His Ala Pro Lys Ser Ala Lys Lys Leu Glu Thr Lys
35 40 45

Asp Ile Phe Xaa Ser Asp Lys Lys Asn Ser Asp Ile Ser Asp Ala Glu
50 55 60

Met Lys Gln Ala Ile Glu Lys Tyr Leu Ser Val Asn Ser Asp Ile Leu
65 70 75 80

Asp Asn Lys Tyr Ile Met Gln His Lys Leu Asp Lys Gln Ile Asp Ser
85 90 95

Gln Thr Lys Val Thr Glu Lys Gln Ala Glu Thr Leu Ser His Leu Ser
100 105 110

Asn Leu Ala Val Lys Asn Asp Leu His Phe Lys Lys Phe Val Thr Glu
115 120 125

Asn Asn Ile Pro Lys Glu Tyr Lys Lys Pro Val Glu Leu MetMet Asn
130 135 140

Tyr Phe Lys Ala Leu Asn Ser Thr Ile Ala Asn Val Asp Glu Asp Ile
145 150 155 160

Glu Lys Leu Ser Tyr Gln Pro Gh Asn Lys Ile Asn Val Val Asp Val
165 170 175

Pro Thr Lys Tyr Ala Gly Asp Val Asn Lys Lys Gln Gln Asp Lys Ile
180 185 190

Lys Asp Phe Leu Lys Ser Lys Gly Ile Lys Ser Asp Val Ile Asp Lys
195 200 205

(2) INFORMATION FOR SEQ ID NO:5203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 283 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5203:

Met Lys Ser Lys Ile Tyr Ile Leu Leu Leu Xaa Leu Ile Phe Leu Ser
1 5 10 15

Ala Cys Ala Asn Thr Arg His Ser Glu Ser Asp Lys Asn Val Leu Thr
 20 25 30

Val Tyr Ser Pro Tyr Gln Ser Asn Leu Ile Arg Pro Ile Leu Asn Glu
 35 40 45

Xaa Glu Lys Gln Glu His Val Lys Ile Glu Ile Lys His Gly Ser Thr
 50 55 60

Gln Val Leu Leu Ser Asn Leu His Asn Glu Asp Phe Ser Glu Arg Gly
 65 70 75 80

Asp Val Phe Met Gly Gly Val Leu Ser Glu Thr Ile Asp His Pro Glu
 85 90 95

Asp Phe Val Pro Tyr Gln Asp Thr Ser Val Thr Gln Gln Leu Glu Asp
 100 105 110

Tyr Arg Ser Asn Asn Lys Tyr Val Thr Ser Phe Leu Leu Met Pro Thr
 115 120 125

Val Ile Val Val Asn Ser Asp Leu Gln Gly Asp Ile Lys Ile Arg Gly
 130 135 140

Tyr Gln Asp Leu Leu Gln Pro Ile Leu Lys Gly Lys Ile Ala Tyr Ser
 145 150 155 160

Asn Pro Asn Thr Thr Thr Gly Tyr Gln His Met Arg Ala Ile Tyr
 165 170 175

Ser Met His His Arg Val Ser Asp Val His Gln Phe Gln Asn His Ala
 180 185 190

Met Gln Leu Ser Lys Thr Ser Lys Val Ile Glu Asp Val Ala Lys Gly
 195 200 205

Lys Tyr Tyr Ala Gly Leu Ser Tyr Glu Gln Asp Ala Arg Thr Trp Lys
 210 215 220

Asn Lys Gly Tyr Pro Val Ser Ile Val Tyr Pro Ile Glu Gly Thr Met
 225 230 235 240

Leu Asn Val Asp Gly Ile Ala Leu Val Lys Asn Ala His Pro His Pro
 245 250 255

Lys Arg Lys Lys Leu Val Gln Tyr Leu Thr Ser Arg Ser Val Gln Gln
 260 265 270

Arg Leu Val Ala Glu Phe Asp Ala Lys Ser Ile
 275 280

(2) INFORMATION FOR SEQ ID NO:5204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5204:

Met Lys Lys Phe Ile Gly Ser Val Leu Ala Thr Thr Leu Ile Leu Gly
1 5 10 15

Gly Cys Ser Thr Met Glu Asn Glu Ser Lys Lys Asp Thr Lys Thr Glu
20 25 30

Thr Lys Ser Val Pro Glu Glu Met Glu Ala Ser Lys Tyr Val Gly Gln
35 40 45

Gly Phe Gln Pro Pro Ala Glu Lys Asn Ala Ile Glu Phe Ala Lys Lys
50 55 60

His Arg Lys Glu Phe Glu Lys Val Gly Glu Gln Phe Phe LysAsp Asn
65 70 75 80

Phe Gly Leu Lys Val Lys Ala Thr Asn Val Val Gly Lys Asp Asp Gly
85 90 95

Val Glu Val Tyr Val His Cys Glu Asp His Gly Ile Val Phe Asn Ala
100 105 110

Ser Leu Pro Leu Tyr Lys Asp Ala Ile His Gln Lys Gly Ser Met Arg
115 120 125

Ser Asn Asp Asn Gly Asp Asp Met Ser Met Met Val Gly Thr Val Leu
130 135 140

Ser Gly Phe Glu Tyr Arg Ala Gln Lys Glu Lys Tyr Asp Asn Leu Tyr
145 150 155 160

Lys Phe Phe Lys Glu Asn Glu Lys Lys Tyr Gln Tyr Thr Gly Phe Thr
165 170 175

Lys Glu Ala Ile Asn Lys Thr Gln Asn Val Gly Tyr Lys Asn Glu Tyr
180 185 190

Phe Tyr Ile Thr Tyr Ser Ser Arg Ser Leu Lys Glu Tyr Arg Lys Tyr
195 200 205

Tyr Glu Pro Leu Ile Arg Lys Asn Asp Lys Glu Phe Lys Glu Gly Met
210 215 220

Glu Arg Ala Arg Lys Glu Val Asn Tyr Ala Ala Asn Thr Asp Ala Val
225 230 235 240

Ala Thr Leu Phe Ser Thr Lys Lys Asn Phe Thr Lys Asp Asn Thr Val
245 250 255

Asp Asp Val Ile Glu Leu Ser Asp Lys Leu Tyr Asn Leu Lys Asn Lys
260 265 270

Pro Asp Lys Ser Thr Ile Thr Ile Gln Ile Gly Lys Pro Thr Ile Asn
275 280 285

Thr Lys Lys Ala Phe Tyr Asp Asp Asn Arg Pro Ile Glu Tyr Gly Val

290

295

300

His Ser Lys Asp Glu
305

(2) INFORMATION FOR SEQ ID NO:5205:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5205:

Met Lys Lys Leu Val Ser Ile Val Gly Ala Thr Leu Leu Leu Ala Gly
1 5 10 15

Cys Gly Ser Gln Asn Leu Ala Pro Leu Glu Glu Lys Thr Thr Asp Leu
20 25 30

Arg Glu Asp Asn His Gln Leu Lys Leu Asp Ile Gln Glu Leu Asn Gln
35 40 45

Gln Ile Ser Asp Ser Lys Ser Lys Ile Lys Gly Leu Glu Lys Asp Lys
50 55 60

Glu Asn Ser Lys Lys Thr Ala Ser Asn Asn Thr Lys Ile Lys Leu Met
65 70 75 80

Asn Val Thr Ser Thr Tyr Tyr Asp Lys Val Ala Lys Ala Leu Lys Ser
85 90 95

Tyr Asn Asp Ile Glu Lys Asp Val Ser Lys Asn Lys Gly Asp Lys Asn
100 105 110

Val Gln Ser Lys Leu Asn Gln Ile Ser Asn Asp Ile Gln Ser Ala His
115 120 125

Thr Ser Tyr Lys Asp Ala Ile Asp Gly Leu Ser Leu SerAsp Asp Asp
130 135 140

Lys Lys Thr Ser Lys Asn Ile Asp Lys Leu Asn Ser Asp Leu Asn His
145 150 155 160

Ala Phe Asp Asp Ile Lys Asn Gly Tyr Gln Asn Lys Asp Lys Lys Gln
165 170 175

Leu Thr Lys Gly Gln Gln Ala Leu Ser Lys Leu Asn Leu Asn Ala Lys
180 185 190

Ser

(2) INFORMATION FOR SEQ ID NO:5206:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5206:

Met Lys Arg Leu Leu Phe Val Met Ile Ala Phe Val Phe Ile Leu Ala
1 5 10 15

Ala Cys Gly Asn Asn Ser Ser Lys Asp Lys Glu Ala Ser Lys Asp Ser
20 25 30

Lys Thr Ile Asn Val Gly Thr Glu Gly Thr Tyr Ala Pro Phe Ser Phe
35 40 45

His Asp Lys Asp Gly Lys Leu Thr Gly Tyr Asp Ile Asp Val Ile Lys
50 55 60

Ala Val Ala Lys Glu Glu Gly Leu Lys Leu Lys Phe Asn Glu Thr Ser
65 70 75 80

Trp Asp Ser Met Phe Ala Gly Leu Asp Ala Gly Arg Phe Asp Val Ile
85 90 95

Ala Asn Gln Val Gly Ile Asn Pro Asp Arg Glu Lys Lys Tyr Lys Phe
100 105 110

Ser Lys Pro Tyr Thr Phe Ser Ser Ala Val Leu Val Ile Arg Glu Asn
115 120 125

Glu Lys Asp Ile Lys Asp Phe Asp Asp Val Lys Gly Lys Lys Leu Ala
130 135 140

Gln Thr Phe Thr Ser Asn Tyr Gly Lys Leu Ala Lys Asp Lys Gly Ala
145 150 155 160

Asp Ile Thr Lys Val Asp Gly Phe Asn Gln Ser Met Asp Leu Leu
165 170 175

Ser Lys Arg Val Asp Gly Thr Phe Asn Asp Ser Leu Ser Tyr Leu Asp
180 185 190

Tyr Lys Lys Gln Lys Pro Asn Ala Lys Ile Lys Ala Ile Lys Gly Asn
195 200 205

Ala Glu Gln Ser Arg Ser Ala Phe Ala Phe Ser Lys Lys Ala Asp Asp
210 215 220

Glu Thr Val Gln Lys Phe Asn Asp Gly Leu Lys Lys Ile Glu Glu Asn
225 230 235 240

Gly Glu Leu Ala Lys Ile Gly Lys Lys Trp Phe Gly Gln Asp Val Ser
245 250 255

Lys Ser Lys

(2) INFORMATION FOR SEQ ID NO:5207:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5207:

Met	Gly	Val	His	Ser	Met	Lys	Leu	Lys	Arg	Leu	Phe	Ala	Val	Val	Ile	
1					5				10						15	
Ala	Met	Leu	Leu	Val	Leu	Ala	Gly	Qs	Ser	Asn	Ser	Asn	Asp	Asn	Asn	
				20				25					30			
Glu	Ser	Lys	Lys	Asp	Asp	Ala	Asp	Asn	Gly	Lys	Lys	Gln	Glu	Ile	Gln	
				35			40						45			
Val	Ala	Ala	Ala	Ala	Ser	Leu	Thr	Asp	Val	Thr	Lys	Lys	Leu	Ala	Ser	
				50		55				60						
Glu	Phe	Lys	Lys	Glu	His	Ser	Lys	Asn	Ala	Asp	Ile	Lys	Phe	Asn	Tyr	Gly
				65		70				75				80		
Gly	Ser	Gly	Ala	Leu	Arg	Lys	Gln	Ile	Glu	Ser	Gly	Ala	Pro	Val	Asp	
				85				90					95			
Val	Phe	Met	Ser	Ala	Asn	Thr	Lys	Asp	Val	Asp	Ala	Leu	Lys	Asp	Lys	
				100			105						110			
Asn	Lys	Ala	His	Asp	Thr	Tyr	Lys	Tyr	Ala	Lys	Asn	Ser	Leu	Val	Leu	
				115			120					125				
Ile	Gly	Asp	Lys	Asp	Ser	Asn	Tyr	Thr	Ser	Val	Lys	Asp	Leu	Lys	Asp	
				130		135				140						
Asn	Asp	Lys	Leu	Ala	Leu	Gly	Glu	Val	Lys	Thr	Val	Pro	Ala	Gly	Lys	
				145		150			155				160			
Tyr	Ala	Lys	Gln	Tyr	Leu	Asp	Asn	Asn	Leu	Phe	Lys	Glu	Val	Glu		
				165			170					175				
Ser	Xaa	Ile	Val	Tyr	Ala	Lys	Asp	Val	Lys	Gln	Val	Leu	Asn	Tyr	Val	
				180			185					190				
Xaa	Lys	Gly	Asn	Ala	Lys	Gln	Gly	Phe	Val	Tyr						
				195		200										

(2) INFORMATION FOR SEQ ID NO:5208:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5208:

Met Lys Lys Trp Gln Phe Val Gly Thr Thr Ala Leu Gly Ala Thr Leu
1 5 10 15

Leu Leu Gly Ala Cys Gly Gly Asn Gly Gly Ser Gly Asn Ser Asp
20 25 30

Leu Lys Gly Glu Ala Lys Gly Asp Gly Ser Ser Thr Val Ala Pro Ile
35 40 45

Val Glu Lys Leu Asn Glu Lys Trp Ala Gln Asp His Ser Asp Ala Lys
50 55 60

Ile Ser Ala Gly Gln Ala Gly Thr Gly Ala Gly Phe Gln Lys Phe Ile
65 70 75 80

Ala Gly Asp Ile Asp Phe Ala Asp Ala Ser Arg Pro Ile Lys Asp Glu
85 90 95

Glu Lys Gln Lys Leu Gln Asp Lys Asn Ile Lys Tyr Lys Glu Phe Lys
100 105 110

Ile Ala Gln Asp Gly Val Thr Val Ala Val Asn Lys Glu Asn Asp Phe
115 120 125

Val Asp Glu Leu Asp Lys Gln Gln Leu Lys Ala Ile Tyr Ser Gly Lys
130 135 140

Ala Lys Thr Trp Lys Asp Val Asn Ser Lys Trp Pro Asp Lys Lys Ile
145 150 155 160

Asn Ala Val Ser Pro Asn Ser Ser His Gly Thr Tyr Asp Phe Phe Glu
165 170 175

Asn Glu Val Met Asn Lys Glu Asp Ile Lys Ala Glu Lys Asn Ala Asp
180 185 190

Thr Asn Ala Ile Val Ser Ser Val Thr Lys Asn Lys Glu Gly Ile Gly
195 200 205

Tyr Phe Gly Tyr Asn Phe Tyr Val Gln Asn Lys Asp Lys Leu Lys Glu
210 215 220

Val Lys Ile Lys Asp Glu Asn Gly Lys Ala Thr Glu Pro Thr Lys Lys
225 230 235 240

Thr Ile Gln Asp Asn Ser Tyr Ala Leu Ser Arg Pro Leu Phe Ile Tyr
245 250 255

Val Asn Glu Lys Ala Leu Lys Asp Asn Lys Val Met Ser Glu Phe Ile
260 265 270

Lys	Phe	Val	Leu	Glu	Asp	Lys	Gly	Lys	Ala	Ala	Glu	Glu	Ala	Gly	Tyr
275						280								285	
Val	Ala	Ala	Pro	Glu	Lys	Thr	Tyr	Lys	Ser	Gln	Leu	Asp	Asp	Leu	Lys
290					295									300	
Ala	Phe	Ile	Asp	Lys	Asn	Gln	Lys	Ser	Asp	Asp	Lys	Lys	Ser	Asp	Asp
305				310					315					320	
Lys	Lys	Ser	Glu	Asp	Lys	Lys									
				325											

(2) INFORMATION FOR SEQ ID NO:5209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5209:

Met	Lys	Arg	Leu	Ser	Ile	Ile	Val	Ile	Ile	Gly	Ile	Phe	Ile	Ile	Thr
1					5				10					15	
Gly	Cys	Asp	Trp	Gln	Arg	Thr	Ser	Lys	Glu	Arg	Ser	Lys	Asn	Ala	Gln
				20				25				30			
Asn	Gln	Gln	Val	Ile	Lys	Ile	Gly	Tyr	Leu	Pro	Ile	Thr	His	Ser	Ala
				35			40				45				
Asn	Leu	Met	Met	Thr	Lys	Lys	Leu	Leu	Ser	Gln	Tyr	Asn	His	Pro	Lys
			50			55				60					
Tyr	Lys	Leu	Glu	Leu	Val	Lys	Phe	Asn	Asn	Trp	Pro	Asp	Leu	Met	Asp
	65				70				75				80		
Ala	Leu	Asn	Ser	Gly	Arg	Ile	Asp	Gly	Ala	Ser	Thr	Leu	Ile	Glu	Leu
				85				90				95			
Ala	Met	Lys	Ser	Lys	Gln	Lys	Gly	Ser	Asn	Ile	Lys	Ala	Val	Ala	Leu
				100				105			110				
Gly	His	His	Glu	Gly	Asn	Val	Ile	Met	Gly	Gln	Lys	Gly	Met	His	Leu
				115			120			125					
Asn	Glu	Phe	Asn	Asn	Asn	Gly	Asp	Asp	Tyr	His	Phe	Gly	Ile	Pro	His
				130			135			140					
Arg	Tyr	Ser	Thr	His	Tyr	Leu	Leu	Leu	GluGlu	Leu	Arg	Lys	Gln	Leu	
	145				150				155			160			
Lys	Ile	Lys	Pro	Gly	His	Phe	Ser	Tyr	His	Glu	Met	Ser	Pro	Ala	Glu
				165				170			175				

(2) INFORMATION FOR SEQ ID NO:5210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5210:

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Met Lys Lys Thr Leu Gly Cys Leu Leu Leu Ile Met Leu Leu Val Val
1 5 10 15

Ala Gly Cys Ser Phe Gly Gly Asn His Lys Leu Ser Ser Lys Ly Ser
20 25 30

Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Glu Lys
35 40 45

Asp Pro Asp Leu Glu Lys Tyr GluGlu Ile Glu Lys Lys Met Lys Gly
50 55 60

Ile Lys Asp Ala Pro Ser Leu Asp Lys Leu Asp Pro Leu Met Thr Glu
65 70 75 80

Lys Ser Phe Thr Asn Ser Lys Gly Ile Gln Gly Trp Lys Asp Tyr Lys

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85	90	95
Glu Leu Met Gly Lys Val Glu Leu Ala Asp Tyr Arg Phe Thr Lys Asp		
100	105	110
Ser Lys Gly Ser Ser Ile Lys Asp Val Asp Ala Phe Phe Lys Gly Lys		
115	120	125
Lys Gly Ile Lys Arg Lys Val Ile Glu Thr His Asp Asp Val Lys Gln		
130	135	140
Val Asp Tyr Trp		
145		

(2) INFORMATION FOR SEQ ID NO:5211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5211:

Trp Pro Cys Ala Thr Xaa Gln Glx Glu	Trp Trp Ser Arg His Xaa Trp		
1	5	10	15
Cys Val Cys Asx Met Val Arg Asn Leu Ile Lys Asp Glx Glu Glu Leu			
20	25	30	
His			

(2) INFORMATION FOR SEQ ID NO:5212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 490 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5212:

Met Ser Ile Ile Met Glu Val Ala Thr Met Gln AlaLys Leu Thr Lys			
1	5	10	15
Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn			
20	25	30	
Val Asp Leu Trp Tyr Gy Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly			
35	40	45	

Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp
 50 55 60

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
 65 70 75 80

Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
 85 90 95

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
 100 105 110

Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Trp
 115 120 125

Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
 130 135 140

Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asp Phe
 145 150 155 160

Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr Gln Ala Pro
 165 170 175

Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile
 180 185 190

Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Ser Asn
 195 200 205

Pro Lys Gly Ile Val Ile His Asn Asp Ala Gly Ser Lys Gly Ala Thr
 210 215 220

Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Leu Ser Arg Leu
 225 230 235 240

Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp Gln
 245 250 255

Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile Gly
 260 265 270

Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala Asp
 275 280 285

Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys Ala
 290 295 300

Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile Arg
 305 310 315 320

Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser Val
 325 330 335

Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu Asp
 340 345 350

Lys Arg Leu Gln Ile Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala Tyr
 355 360 365

Met	Asp	Gly	Lys	Ile	Pro	Val	Ala	Thr	Val	Ser	Asn	Glu	Ser	Ser	Ala
370						375									380
Ser	Ser	Asn	Thr	Val	Lys	Pro	Val	Ala	Ser	Ala	Trp	Lys	Arg	Asn	Lys
385						390					395				400
Tyr	Gly	Thr	Tyr	Tyr	Met	Glu	Glu	Ser	Ala	Arg	Phe	Thr	Asn	Gly	Asn
					405					410					415
Gln	Pro	Ile	Thr	Val	Arg	Lys	Val	Gly	Pro	Phe	Leu	Ser	Cys	Pro	Val
					420			425							430
Gly	Tyr	Gln	Phe	Gln	Pro	Gly	Gly	Tyr	Cys	Asp	Tyr	Thr	Glu	Val	Met
					435		440								445
Leu	Gln	Asp	Gly	His	Val	Trp	Val	Gly	Tyr	Thr	Trp	Glu	Gly	Gln	Arg
					450		455								460
Tyr	Tyr	Leu	Pro	Ile	Arg	Thr	Trp	Asn	Gly	Ser	Ala	Pro	Phe	Asn	Gln
					465		470								480
Ile	Leu	Gly	Asp	Leu	Trp	Gly	Glu	Ile	Ser						
					485			490							

(2) INFORMATION FOR SEQ ID NO:5213:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 299 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5213:

Gly	Asp	Lys	Met	Asn	Lys	Ile	Ser	Lys	Tyr	Ile	Ala	Ile	Ala	Ser	Leu
1				5					10					15	
Ser	Val	Ala	Val	Thr	Val	Ser	Ala	Pro	Gln	Thr	Thr	Asn	Ser	Thr	Ala
			20					25					30		
Phe	Ala	Lys	Ser	Ser	Ala	Glu	Val	Gln	Gln	Thr	Gln	Gln	Ala	Ser	Ile
		35				40						45			
Pro	Ala	Ser	Gln	Lys	Ala	Asn	Leu	Gly	Asn	Gln	Asn	Ile	Met	Ala	Val
		50				55					60				
Ala	Trp	Tyr	Gln	Asn	Ser	Ala	Glu	Ala	Lys	Ala	Leu	Tyr	Leu	Gln	Gly
		65				70				75				80	
Tyr	Asn	Ser	Ala	Lys	Thr	Gln	Leu	Asp	Lys	Glu	Ile	Lys	Lys	Asn	Lys
				85				90					95		
Gly	Lys	His	Lys	Leu	Ala	Ile	Ala	Leu	Asp	Leu	Asp	Glu	Thr	Val	Leu
				100				105					110		
Asp	Asn	Ser	Pro	Tyr	Gln	Gly	Tyr	Ala	Ser	Ile	His	Asn	Lys	Pro	Phe

115	120	125
Pro Glu Gly Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val		
130	135	140
Tyr Gly Ala Lys Glu Phe Leu Lys Tyr Ala Asp Lys LysGly Val Asp		
145	150	155
Ile Tyr Tyr Ile Ser Asp Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr		
165	170	175
Gln Lys Asn Leu Lys Gln Gln Gly Ile Pro Gln Ala Lys Lys Ser His		
180	185	190
Ile Leu Leu Lys Gly Lys Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln		
195	200	205
Met Val Gln Lys Asp His Lys Leu Val Met Leu Phe Gly Asp Asn Leu		
210	215	220
Leu Asp Phe Thr Asp Pro Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala		
225	230	235
Leu Ile Glu Lys His Lys Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe		
245	250	255
Pro Asn Pro Met Tyr Gly Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn		
260	265	270
Tyr Lys Ala Ser Xaa Lys Ala Lys Asp Lys Leu Arg Lys Asn Ala Ile		
275	280	285
Lys Gln Phe Asp Pro Lys Thr Gly Glu Val Lys		
290	295	

(2) INFORMATION FOR SEQ ID NO:5214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 178 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5214:

Leu Asn Lys Cys Lys Ile Ile Ile Trp Arg Ile Ile Asn Met Lys Asn		
1	5	10
15		
Lys Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile Gly Ile Thr		
20	25	30
Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro		
35	40	45
Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn		
50	55	60

Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro
 65 70 75 80
 Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp
 85 90 95
 Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala
 100 D5 110
 Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln
 115 120 125
 Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg
 130 135 140
 Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys
 145 150 155 160
 Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu LysGln Gly Leu
 165 170 175
 Val Lys

(2) INFORMATION FOR SEQ ID NO:5215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 173 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5215:

Lys Glu Arg Val Leu Met Lys Lys Leu Leu Thr Ala Ser Ile Ile Ala
 1 5 10 15
 Cys Ser Val Val Met Gly Val Gly Leu Val Asn Thr Ser Ala Glu Ala
 20 25 30
 Ala Ser Gly Asn Ser Ile Asp Thr Val Lys Gln Leu Ile Lys Gly Asp
 35 40 45
 Gln Ser Leu Glu Asn Val Lys Ile Gly Glu Ser Ile Lys Asp Val Leu
 50 55 60
 Thr Lys Tyr Lys Asn Pro Met Tyr Ser Tyr Asn Glu Ap Gly Thr Glu
 65 70 75 80
 His Tyr Tyr Glu Phe His Thr Lys Lys Gly Met Leu Leu Val Thr Thr
 85 90 95
 Asp Gly Lys Lys Asn Asn Gly Lys Val Thr His Ile Ser Met Met Tyr
 100 105 110

Asn	Asp	Ala	Asn	Gly	Pro	Thr	Tyr	Gln	Ala	Val	Lys	Asn	Tyr	Val	Gly
115								120				125			
Lys	Ala	Val	Thr	His	Thr	Glu	Tyr	Ser	Lys	Val	Ala	Gly	Asn	Phe	Gly
130						135						140			
Tyr	Ile	Glu	Lys	Gly	Lys	Thr	Thr	Tyr	Gln	Phe	Ala	Ser	Ala	Pro	Lys
145					150				15			160			
Asp	Lys	Asn	Ile	Lys	Leu	Tyr	Arg	Ile	Asp	Leu	Glu	Lys			
					165				170						

(2) INFORMATION FOR SEQ ID NO:5216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5216:

Phe	Glu	Val	Arg	Glu	Ser	Met	Ser	Asn	Gln	Asn	Tyr	Asp	Tyr	Asn	Lys
1				5					10					15	
Asn	Glu	Asp	Gly	Ser	Lys	Lys	Met	Ser	Thr	Thr	Ala	Lys	Val	Val	
					20			25				30			
Ser	Ile	Ala	Thr	Val	Leu	Leu	Leu	Gly	Gly	Leu	Val	Phe	Ala	Ile	
					35			40				45			
Phe	Ala	Tyr	Val	Asp	His	Ser	Asn	Lys	Ala	Lys	Glu	Arg	Met	Leu	Asn
					50			55			60				
Glu	Gln	Lys	Gln	Glu	Gln	Lys	Glu	Lys	Arg	Gln	Lys	Glu	Asn	Ala	Glu
					65			70			75		80		
Lys	Glu	Arg	Lys	Lys	Gln	Gln	Glu	Glu	Lys	Glu	Gln	Asn	Glu	Leu	
					85			90				95			
Asp	Ser	Gln	Ala	Asn	Gln	Tyr	Gln	Gln	Leu	Pro	Gln	Gln	Asn	Gln	Tyr
					100			105				110			
Gln	Tyr	Val	Pro	Pro	Gln	Gln	Ala	Pro	Thr	Lys	Gln	Arg	Pro	Ala	
					115			120			125				
Lys	Glu	Glu	Asn	Asp	Asp	Lys	Ala	Ser	Lys	Asp	Glu	Ser	Lys	Asp	Lys
						130		135			140				
Asp	Asp	Lys	Ala	Ser	Gln	Asp	Lys	Ser	Asp	Asp	Asn	Gln	Lys	Lys	Thr
					145			150			155		160		
Asp	Asp	Asn	Lys	Gln	Pro	Ala									
					165										

(2) INFORMATION FOR SEQ ID NO:5217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5217:

Met Lys Arg Asn Phe Pro Lys Leu Ile Ala Leu Ser Leu Ile Phe Ser
1 5 10 15

Leu Ser Val Thr Pro Ile Ala Asn Ala Glu Ser Asn Ser Asn Ile Lys
20 25 30

Ala Lys Asp Lys Lys His Val Gln Val Asn Val Glu Asp Lys Ser Val
35 40 45

Pro Thr Asp Val Arg Asn Leu Ala Gln Lys Asp Tyr Leu Ser Tyr Val
50 55 60

Thr Ser Leu Asp Lys Ile Tyr Asn Lys Glu Lys Ala Ser Tyr Thr Leu
65 70 75 80

Gly Glu Pro Phe Lys Ile Tyr Lys Phe Asn Lys Lys Ser Asp Gly Asn
85 90 95

Tyr Tyr Phe Pro Val Leu Asn Thr Glu Gly Asn Ile Asp Tyr Ile Val
100 105 110

Thr Ile Ser
115

(2) INFORMATION FOR SEQ ID NO:5218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 173 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5218:

Asn Phe Lys Met Gln Glu Val Lys Tyr Met Thr Glu Ile Thr Phe Lys
1 5 10 15

Gly Gly Pro Ile His Leu Lys Gly Gln Gln Ile Asn Glu Gly Asp Phe
20 25 30

Ala Pro Asp Phe Thr Val Leu Asp Asn Asp Leu Asn Gln Val Thr Leu
35 40 45

Ala Asp Tyr Ala Gly Lys Lys Lys Leu Ile Ser Val Val Pro Ser Ile
 50 55 60

Asp Thr Gly Val Cys Asp Gln Gln Thr Arg Lys Phe Asn Ser Asp Ala
 65 70 75 80

Ser Lys Glu Glu Gly Ile Val Leu Thr Ile Ser Ala Asp Leu Pro Phe
 85 90 95

Ala Gln Lys Arg Trp Cys Ala Ser Ala Gly Leu Asp Asn Val Ile Thr
 100 105 110

Leu Ser Asp His Arg Asp Leu Ser Phe Gly Glu Asn Tyr Gly Val Val
 115 120 125

Met Glu Glu Leu Arg Leu Leu Ala Arg Ala Val Phe Val Leu Asp Ala
 130 135 140

Asp Asn Lys Val Val Tyr Lys Glu Ile Val Ser Glu Gly Thr Asp Phe
 145 150 155 160

Pro Asp Phe Asp Ala Ala Leu Ala Ala Tyr Lys Asn Ile
 165 170

(2) INFORMATION FOR SEQ ID NO:5219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5219:

Ile Glu Ser Arg Phe Ile Met Ala Lys Ile Asn Phe Asp Ala Ala Thr
 1 5 10 15

Lys Gly Asn Pro Gly Ile Ser Thr Cys Ala Ile Val Ile Lys Glu Asp
 20 25 30

Glu Gln His Tyr Thr Tyr Thr His Glu Leu Gly Glu Met Asp Asn His
 35 40 45

Thr Ala Glu Trp Ala Ala Cys Ile Tyr Ala Leu Glu His Ala Arg Glu
 50 55 60

Leu Asn Val Gln Asn Ala Leu Leu Tyr Thr Asp Ser Lys Leu Ile Ala
 65 70 75 80

Asp Ser Ile Glu Ala Gly Tyr Val Lys Asn Ala Asn Phe Lys Pro Tyr
 85 90 95

Phe Asp Gln Ile Glu Ile Phe Glu Lys Asp Phe Asp Leu Leu Phe Val
 100 105 110

Lys Trp Ile Pro Arg Glu Gln Asn Lys Glu Ala Asn Gln His Ala Gln
115 120 125
Gln Ala Leu Tyr Lys Leu Ile Lys Lys Asn Lys
130 135

(2) INFORMATION FOR SEQ ID NO:5220:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5220:

Met Pro Gly Thr Val Leu Asp Pro Gln Met Ile LysAsn Glu Asp Val
1 5 10 15
Ser Glu Lys Glu Tyr Ala Ala Val Ser Gln Gln Leu Ser Lys Leu Pro
20 25 30
Gly Val Asn Thr Ser Met Asp Trp Asp Arg Lys Tyr Pro Tyr Gly Asp
35 40 45
Thr Leu Arg Gly Ile Phe Gly Asp Val Ser Thr Pro Ala Glu Gly Ile
50 55 60
Pro Lys Glu Leu Thr Glu His Tyr Leu Ser Lys Gly Tyr Ser Arg Asn
65 70 75 80
Asp Arg Val Gly Lys Ser Tyr Leu Glu Tyr Gln Tyr Glu Asp Val Leu
85 90 95
Arg Gly Lys Lys Lys Glu Met Lys Tyr Thr Thr Asp Lys Ser Gly Lys
100 105 110
Val Thr Ser Ser Glu Val Leu Xaa Pro Gly Ala Arg Gly Gln Asp Leu
115 120 125
Lys Leu Thr Ile Asp Ile Asp Leu Gln Lys Glu Val Glu Ala Leu Leu
130 135 140
Asp Lys Gln Ile Lys Lys Leu Ala Val Lys Val Pro Lys Ile Tyr Ile
145 150 155 160
Met Gln

(2) INFORMATION FOR SEQ ID NO:5221:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5221:

Ile Met Ala Tyr Asp Gly Leu Phe Thr Lys Lys Met Val Glu Ser Leu
1 . 5 10 15

Gln Phe Leu Thr Thr Gly Arg Val His Lys Ile Asn Gln Pro Asp Asn
20 25 30

Asp Thr Ile Leu Met Val Val Arg Gln Asn Arg Gln Asn His Gln Leu
35 40 45

Leu Leu Ser Ile His Pro Asn Phe Ser Arg Leu Gln Leu Thr Thr Lys
50 55 60

Lys Tyr Asp Asn Pro Phe Asn Pro Pro Met Phe Ala Arg ValPhe Arg
65 70 75 80

Lys His Leu Glu Gly Gly Ile Ile Glu Ser Ile Lys Gln Ile Gly Asn
85 90 95

Asp Arg Arg Ile Glu Ile Asp Ile Lys Ser Lys Asp Glu Ile Gly Asp
100 105 110

Thr Ile Tyr Arg Thr Val Ile Leu Glu Ile Met Gly Lys His Ser Asn
115 120 125

Leu Ile Leu Val Asp Glu Asn Arg Lys Ile Ile Glu Gly Phe Lys His
130 135 140

Leu Thr Pro Asn Thr Asn His Tyr Arg Thr Val Met Pro Gly Phe Asn
145 150 155 160

Tyr Glu Ala Pro Pro Thr Gln His Lys Ile Asn Pro Tyr Asp Ile Thr
165 170 175

Gly Ala Glu Val Leu Lys Tyr Ile Asp Phe Asn Ala Gly Asn Ile Ala
180 185 190

Lys Gln Leu Leu Asn Gln Phe Glu Gly Phe Ser Pro Leu Ile Thr Asn
195 200 205

Glu Ile Val Ser Arg Arg Gln Phe Met Thr Ser Ser Thr Leu Pro Glu
210 215 220

Ala Phe Asp Glu Val Met Ala Glu Thr Lys Leu Pro Pro Thr Pro Ile
225 230 235 240

Phe His Lys Asn His Glu Thr Gly Lys Glu Asp Phe Tyr Phe Ile Lys
245 250 255

Leu Asn Gln Phe Asn Asp Asp Thr Val Thr Tyr Asp Ser Leu Asn Asp
260 265 270

Leu Leu Asp Arg Phe Tyr Asp Ala Arg Gly Glu Arg Glu Arg Val Lys
275 280 285

Gln Arg Ala Asn Asp Leu Val Arg Phe Val Gln Gln Gln Leu His Lys
290 295 300

Tyr Gln Asn Lys Leu Ala Ser
305 310

(2) INFORMATION FOR SEQ ID NO:5222:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5222:

Ile Ser Glu Leu Ile Glu Glu Tyr Glu Gln Ser Lys Asn Lys Asp Thr
1 5 10 15

Glu Gln Leu Tyr Gly Glu Leu Ile Thr Ala Asn Ile Tyr Arg Ile Lys
20 25 30

Gln Gly Asp Lys Glu Val Thr Ala Leu Asn Tyr Tyr Asn Glu Glu
35 40 45

Val Val Ile Pro Leu Asn Pro Thr Lys Ser Pro Ser Ala Asn Ala Gln
50 55 60

Tyr Tyr Tyr Lys Gln Tyr Xaa Arg Met Lys Thr Arg Xaa Arg Glu Leu
65 70 75 80

Gln His Gln Ile Gln Leu Thr Lys Asp Asn Ile Asp Tyr Phe Ser Thr
85 90 95

Ile Glu Gln Gln Leu His His Ile Ser Val His Asp Ile Asp Glu Ile
100 105 110

Arg Asp Glu Leu Ala Glu Gln Gly Phe Met Lys Gln Arg Lys Asn Gln
115 120 125

Thr Lys Lys Lys Ala Gln Ile Gln Leu Gln His Tyr Val Ser Thr
130 135 140

Asp Gly Asp Asp Ile Tyr Val Gly Lys Asn Asn Lys Gln Asn Asp Tyr
145 150 155 160

Leu Thr Asn Lys Lys Ala Lys Lys Thr His Thr Trp Leu His Thr Lys
165 170 175

Asp Ile Pro Gly Ser His Val Val Ile Phe Asn Asp Ala Pro Ser Asp
180 185 190

Thr Thr Ile Lys Glu Ala Ala Met Leu Ala Gly Tyr Phe Ser Lys Ala
195 200 205

Gly Asn Ser Gly Gln Ile Pro Val Asp Tyr Thr Leu Ile Lys Asn Val
210 215 220

His Lys Pro Ser Gly Ala Lys Pro Gly Phe Val Thr Tyr Asp Asn Gln
225 230 235 240

Lys Thr Leu Tyr Ala
245

(2) INFORMATION FOR SEQ ID NO:5223:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ IDNO:5223:

Tyr Ile Thr Asn Pro Gln Asn Pro Lys Ile Lys Ile Thr Gly Ile Ser
1 5 10 15

Leu Ser Ser Gly Val Gly Asn Phe Phe Ile Ile Thr Asn Gly Lys Arg
20 25 30

Ile Ile Val Ala Lys Ile Lys Arg Asn Ala Asp Asn Asp Ser Ala Leu
35 40 45

Lys Ser Phe Asn Ala Ile Phe Ile Ile Gly Asn Ala Asp Pro His Asn
50 55 60

Met Ile Val Asn Lys Tyr Asp Arg Lys Val Val Ser Arg Ser Leu Phe
65 70 75 80

Ile Asn Ile Ile Thr Pro Leu Ile Met Cys Phe TyrIle Lys Lys Tyr
85 90 95

Asp Leu Lys

(2) INFORMATION FOR SEQ ID NO:5224:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5224:

Glu Asn Val Leu Ala Lys Glu Tyr Ala Val Lys Tyr Asn Ala Val Glu

1	5	10	15												
Ala	Ile	Gln	His	Arg	Gly	Glu	Thr	Val	Thr	Glu	Gly	Ser	Ser	Ser	Asn
			20			25				30					
Ala	Tyr	Ala	Ile	Lys	Asp	Gly	Val	Ile	Tyr	Thr	His	Pro	Ile	Asn	Asn
	35				40				45						
Tyr	Ile	Leu	Asn	Gly	Ile	Thr	Arg	Ile	Val	Ile	Lys	Lys	Ile	Ala	Glu
	50				55				60						
Asp	Tyr	Asn	Ile	Pro	Phe	Lys	Glu	Glu	Th	Phe	Thr	Val	Asp	Phe	Leu
	65				70				75				80		
Lys	Asn	Ala	Asp	Glu	Val	Ile	Val	Ser	Ser	Thr	Ser	Ala	Glu	Val	Thr
					85				90				95		
Pro	Val	Ile	Lys	Leu	Asp	Gly	Glu	Pro	Val	Asn	Asp	Gly	Lys	Val	Gly
					100				105				110		
Pro	Ile	Thr	Arg	Gln	Leu	Gln	Glu	Gly	Phe	Glu	Lys	Tyr	Ile	Glu	Ser
	115					120						125			
His	Ser	Ile													
		130													

(2) INFORMATION FOR SEQ ID NO:5225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5225:

Asn	His	Leu	Thr	Ala	Arg	Ile	Ile	Asn	Gln	Glu	Asp	Asp	Leu	Met	Asn
1					5			10					15		
Leu	Phe	Arg	Gln	Gln	Lys	Phe	Ser	Ile	Arg	Lys	Phe	Asn	Val	Gly	Ile
					20			25					30		
Phe	Ser	Ala	Leu	Ile	Ala	Thr	Val	Thr	Phe	Ile	Ser	Thr	Asn	Pro	Thr
					35			40				45			
Thr	Ala	Ser	Ala	Ala	Glu	Gln	Asn	Gln	Pro	Ala	Gln	Asn	Gln	Pro	Ala
					50			55			60				
Gln	Pro	Ala	Asp	Ala	Asn	Thr	Gln	Pro	Asn	Ala	Asn	Ala	Gly	Ala	Gln
					65			70			75		80		
Ala	Asn	Pro	Thr	Ala	Gln	Pro	Ala	Ala	Pro	Ala	Asn	Gln	Gly	Gln	Pro
						85			90				95		
Ala	Val	Gln	Pro	Ala	Asn	Gln	Gly	Gly	Gln	Ala	Asn	Pro	Ala	Gly	Gly
						100			105				110		

Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
 115 120 125

Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
 130 135 140

Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala
 145 150 155 160

Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Gln
 165 170 175

Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
 180 185 190

Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
 195 200 205

Pro Ala Ile Ser Thr Asp Glu Asn Arg Gln Asp Pro Thr Val Thr Val
 210 215 220

Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly
 225 230 235 240

Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn
 245 250 255

Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val
 260 265 270

Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys
 275 280 285

Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr
 290 295 300

Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp
 305 310 315 320

Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly
 325 330 335

Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu
 340 345 350

Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr
 355 360 365

Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly
 370 375 380

Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro
 385 390 395 400

Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn
 405 410 415

Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu
 420 425 430

Val	Thr	Leu	Pro	Gln	Gly	Val	Thr	Tyr	Val	Asn	Asn	Ser	Leu	Thr	Thr
435						440							445		
Thr	Phe	Pro	Asn	Gly	Asn	Glu	Asp	Ser	Thr	Val	Leu	Lys	Asn	Met	Mr
450						455						460			
Val	Asn	Tyr	Asp	Gln	Asn	Ala	Asn	Lys	Val	Thr	Phe	Thr	Ser	Gln	Gly
465						470				475			480		
Val	Thr	Thr	Ala	Arg	Gly	Thr	His	Thr	Lys	Glu	Val	Leu	Phe	Pro	Asp
485								490					495		
Lys	Ser	Leu	Lys	Leu	Ser	Tyr	Lys	Val	Asn	Val	Ala	Asn	Ile	Asp	Thr
500								505					510		
Pro	Lys	Asn	Ile	Asp	Phe	Asn	Glu	Lys	Leu	Thr	Tyr	Arg	Thr	Ala	Ser
515						520						525			
Asp	Val	Val	Ile	Asn	Asn	Ala	Gln	Pro	Glu	Val	His				
530						535						540			

(2) INFORMATION FOR SEQ ID NO:5226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5226:

Tyr	Lys	Glu	Leu	Ser	His	Gly	Arg	Leu	Ile	Gly	Gly	Thr	Lys	Met	His
1						5				10			15		
Lys	Lys	Tyr	Phe	Ile	Gly	Thr	Ser	Ile	Leu	Ile	Ala	Val	Phe	Val	Val
						20			25			30			
Ile	Phe	Asp	Gln	Val	Thr	Lys	Tyr	Ile	Ile	Ala	Thr	Thr	Met	Lys	Ile
						35			40			45			
Gly	Asp	Ser	Phe	Glu	Val	Ile	Pro	His	Phe	Leu	Asn	Ile	Thr	Ser	His
						50			55			60			
Arg	Asn	Asn	Gly	Ala	Ala	Trp	Gly	Ile	Leu	Ser	Gly	Lys	Met	Thr	Phe
65						70				75			80		
Phe	Phe	Ile	Ile	Thr	Ile	Ile	Ile	Leu	Ile	A ^h	Leu	Val	Tyr	Phe	Phe
									85		90		95		
Ile	Lys	Asp	Ala	Gln	Tyr	Asn	Leu	Phe	Met	Gln	Val	Ala	Ile	Ser	Leu
									100		105		110		
Leu	Phe	Ala	Gly	Ala	Leu	Gly	Asn	Phe	Ile	Asp	Arg	Ile	Leu	Thr	Gly
									115		120		125		
Glu	Val	Val	Asp	Phe	Ile	Asp	Thr	Asn	Ile	Phe	Gly	Tyr	Asp	Phe	Pro

130	135	140
Ile Phe Asn Ile Ala Asp Ser Ser Leu Thr Ile Gly Val Ile Leu Ile		
145	150	155
Ile Ile Ala Leu Leu Lys Asp Thr Ser Asn Lys Lys Glu Lys Glu Val		
165	170	175
Lys		

(2) INFORMATION FOR SEQ ID NO:5227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5227:

Ala	Gly	Lys	Ser	Ser	Leu	Ile	Lys	Ser	Leu	Ile	Gly	Glu	Phe	Asn	Ala
1				5					10					15	
Thr	Gly	Thr	Lys	Leu	Leu	Tyr	Asn	Lys	Pro	Ile	Gln	Gln	Gln	Leu	Gln
				20				25						30	
His	Ile	Thr	Tyr	Ile	Pro	Gln	Lys	Ala	His	Ile	Asp	Leu	Asp	Phe	Pro
				35			40				45				
Ile	Ser	Val	Glu	Gln	Val	Ile	Leu	Ser	Gly	Cys	Tyr	Lys	Glu	Ile	Gly
				50			55				60				
Trp	Phe	Arg	Arg	Pro	Asn	Lys	Ser	Ala	Arg	Asp	Lys	Leu	Lys	Gln	Leu
				65			70			75			80		
Leu	Ser	Asp	Leu	Glu	Leu	Glu	Ser	Leu	Arg	His	Arg	Gln	Ile	Ser	Glu
				85				90				95			
Leu	Ser	Gly	Gly	Gln	Leu	Gln	Arg	Val	Leu	Val	Ala	Arg	Ala	Leu	Met
				100			105				110				
Ser	Xaa	Ser	Glu	Val	Tyr	Phe	Leu	Asp	Glu	Pro	Phe	Val	Gly	Ile	Asp
				115			120				125				
Phe	Ser	Ser	Glu	Lys	Leu	Ile	Met	Thr	Lys	Ile	Glu	Asn	Leu	LysGln	
				130			135				140				
Gln	Gly	Lys	Leu	Ile	Leu	Ile	Ile	His	His	Asp	Leu	Ser	Lys	Ala	Lys
				145			150			155			160		
Gln	Tyr	Phe	Asp	Arg	Ile	Ile	Leu	Leu	Asn	Gln	Thr	Leu	Arg	Tyr	Phe
				165				170			175				
Gly	Asp	Ser	Glu	Glu	Ala	Met	Ser	Val	Thr	Arg	Leu	Asn	Glu	Thr	Phe
				180				185			190				

Met Ser Ser Thr Asp Cys Ser Asp Pro Ser Gln Arg Ser Asn Ile Thr
195 200 205

Cys

(2) INFORMATION FOR SEQ ID NO:5228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5228:

Thr Phe Arg Ile Ile Phe Leu Leu Ser Ile Arg Lys Arg Ser Asn Arg
1 5 10 15

Thr His Val Ser Ile His Trp Ser Thr Val Asn Lys Glu Glu Ile Cys
20 25 30

Leu Arg Val Lys Asp Asn Leu Gln Gln IleSer Thr Gln Ile Asn Asp
35 40 45

Lys Ser Glu Lys Asn Asn Phe Ser Thr Lys Pro Asn Val Ile Ala Val
50 55 60

Thr Lys Tyr Val Thr Ile Glu Arg Ala Lys Glu Ala Tyr Glu Ala Gly
65 70 75 80

Ile Arg His Phe Gly Glu Asn Arg Leu Glu Gly Phe Phe Gln Lys Lys
85 90 95

Glu Ala Leu Pro Ser Asp Ala Val Ile His Phe Ile Gly Ser Leu Gln
100 105 110

Ser Arg Lys Val Lys Asp Val Ile Asn Asp Val Asp Tyr Phe His Ala
115 120 125

Leu Asp Arg Leu Ser Leu Ala Lys Glu Ile Asn Lys Arg Ala Glu His
130 135 140

Lys Ile Lys Cys Phe Leu Gln Val Asn Val Ser Gly Glu Ala Ser Lys
145 150 155 160

His Gly Ile Ala Leu Glu Asp Val Asp Gln Phe Ile Asp Asp Leu Lys
165 170 175

Lys Tyr Asp Lys Ile Glu Ile Val Gly Leu Met Thr Met Ala Pro Leu
180 185 190

Thr Asp Asp Glu Ala Tyr Ile Arg Ser Leu Phe Lys Gln Leu Arg Leu
195 200 205

Lys	Lys	Glu	Glu	Ile	Gln	Arg	Leu	Asn	Leu	Glu	Tyr	Ala	Pro	Cys	Asp
210							215					220			
Glu	Leu	Ser	Met	Gly	Met	Ser	Asn	Asp	Tyr	Leu	Ile	Ala	Val	Glu	Glu
225					230					235				240	
Gly	Ala	Thr	Phe	Val	Arg	Ile	Gly	Thr	Lys	Leu	Val	Gly	Glu	Glu	Glu
						245			250				255		

(2) INFORMATION FOR SEQ ID NO:5229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5229:

Lys	His	Lys	Leu	Thr	Ile	Ile	Thr	Gly	Gly	Phe	Phe	Thr	Met	Lys	Lys
1						5			10				15		
Thr	Ile	Met	Ala	Ser	Ser	Leu	Ala	Val	Ala	Leu	Gly	Val	Thr	Gly	Tyr
						20			25				30		
Ala	Ala	Gly	Thr	Gly	His	Gln	Ala	His	Ala	Ala	Glu	Và	Asn	Val	Asp
						35			40			45			
Gln	Ala	His	Leu	Val	Asp	Leu	Ala	His	Asn	His	Gln	Asp	Gln	Leu	Asn
						50			55			60			
Ala	Ala	Pro	Ile	Lys	Asp	Gly	Ala	Tyr	Asp	Ile	His	Phe	Val	Lys	Asp
						65			70			75			80
Gly	Phe	Gln	Tyr	Asn	Phe	Thr	Ser	Asn	Gly	Thr	Thr	Trp	Ser	Trp	Ser
						85				90			95		
Tyr	Glu	Ala	Ala	Asn	Gly	Gln	Thr	Ala	Gly	Phe	Ser	Asn	Val	Ala	Gly
						100			105			110			
Ala	Asp	Tyr	Thr	Thr	Ser	Tyr	Asn	Gln	Gly	Ser	Asn	Val	Gln	Ser	Val
						115			120			125			
Ser	Tyr	Asn	Ala	Gln	Ser	Ser	Asn	Ser	Asn	Val	Glu	Ala	Val	Ser	Ala
						130			135			140			
Pro	Thr	Tyr	His	Asn	Tyr	Ser	Thr	Ser	Thr	Thr	Ser	Ser	Ser	Val	Arg
						145			150			155			160
Leu	Ser	Asn	Gly	Asn	Thr	Ala	Gly	Ala	Thr	Gly	Ser	Ser	Ala	Ala	Gln
						165				170			175		
Ile	Met	Ala	Gln	Arg	Thr	Gly	Val	Ser	Ala	Ser	Thr	Trp	Ala	Ala	Ile
						180			185			190			

Ile	Ala	Arg	Glu	Ser	Asn	Gly	Gln	Val	Asn	Ala	Tyr	Asn	Pro	Ser	Gly
195							200							205	
Ala	Ser	Gly	Leu	Phe	Gln	Thr	Met	Pro	Gly	Trp	Gly	Pro	Thr	Asn	Thr
210							215							220	
Val	Asp	Gln	Gln	Ile	Asn	Ala	Ala	Val	Lys	Ala	Tyr	Lys	Ala	Gln	Gly
225								230						235	
Leu	Gly	Ala	Trp	Gly	Phe										
					245										

(2) INFORMATION FOR SEQ ID NO:5230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5230:

Lys	Glu	Pro	His	Lys	Met	Lys	Lys	Ile	Tyr	Lys	Ser	Leu	Thr	Val	Ser
1					5									10	15
Ala	Ile	Val	Ala	Thr	Val	Ser	Leu	Ser	Ala	Leu	Pro	Gln	Ser	Leu	Ala
					20									25	30
Ile	Thr	His	Glu	Ser	Gln	Pro	Thr	Lys	Gln	Gln	Arg	Thr	Val	Leu	Phe
					35			40						45	
Asp	Arg	Ser	His	Gly	Gln	Thr	Ala	Gly	Ala	Ala	Asp	Trp	Val	Ser	Asp
					50			55						60	
Gly	Ala	Phe	Ser	Asp	Tyr	Ala	Asp	Ser	Ile	Gln	Lys	Gln	Gly	Tyr	Asp
					65			70			75			80	
Val	Lys	Ala	Ile	Asp	Gly	His	Ser	Asn	Ile	Thr	Glu	Ala	Ser	Leu	Lys
					85					90				95	
Ser	Ser	Lys	Ile	Phe	Val	Ile	Pro	Glu	Ala	Asn	Ile	Pro	Phe	Lys	Glu
					100					105				110	
Ser	Glu	Gln	Ala	Ala	Ile	Val	Lys	Tyr	Val	Lys	Gln	Gly	Gly	Asn	Val
					115			120						125	
Val	Phe	Ile	Ser	Asp	His	Tyr	Asn	Ala	Asp	Arg	Asn	Leu	Asn	Arg	Ile
					130			135						140	
Asp	Ser	Ser	Glu	Ala	Met	Asn	Gly	Tyr	Arg	Arg	Gly	Ala	Tyr	Glu	Asp
					145			150			155			160	
Met	Ser	Lys	Gly	Met	Asn	Ala	Glu	Glu	Lys	Ser	Ser	Thr	Ala	Met	Gln
					165			170						175	
Gly	Val	Lys	Ser	Ser	Asp	Trp	Leu	Ser	Thr	Asn	Phe	Gly	Val	Arg	Phe

180	185	190
Arg Tyr Asn Ala Leu Gly Asp Leu Asn Thr Ser Asn Ile Val Ser Ser		
195	200	205
Lys Glu Ser Phe Gly Ile Thr Glu Gly Val Lys Ser Val Ser Met His		
210	215	220
Ala Gly Ser Thr Leu Ala Ile Thr Asn Pro Glu Lys Ala Lys Gly Ile		
225	230	235
Val Tyr Thr Pro Glu Gln Leu Pro Ala Lys Ser Lys Trp Ser His Ala		
245	250	255
Val Asp Gln Gly Ile Tyr Asn Gly Gly Lys Ala Glu Gly Pro Tyr		
260	265	270
Val Ala Ile Ser Lys Val Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp		
275	280	285
Ser Ser Leu Val Glu Asp Ser Ser Pro Lys Tyr Val Arg Glu Asp Asn		
290	295	300
Gly Glu Lys Lys Lys Thr Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly		
305	310	315
Lys Leu Leu Asn Asn Ile Thr Ala Trp Met Ser Lys Asp Asn Asp Gly		
325	330	335
Lys Ser Leu Lys Ala Ser Ser Leu Thr Leu Asp Thr Lys Thr Lys Leu		
340	345	350
Leu Asp Phe Glu Arg Pro Glu Arg Ser Thr Glu Pro Glu Lys Glu Pro		
355	360	365
Trp Ser Gln Pro Pro Ser Gly Tyr Lys Trp Tyr Asp Pro Thr Thr Phe		
370	375	380
Lys Ala Gly Ser Tyr Gly Ser Glu Lys Gly Ala Asp Pro Gln Pro Asn		
385	390	39
400		
Thr Pro Asp Asp His Thr Pro Pro Asn Gln Asn Glu Lys Val Thr Phe		
405	410	415
Asp Ile Pro Gln Asn Val Ser Val Asn Glu Pro Phe Glu Met Thr Ile		
420	425	430
His Leu Lys Gly Phe Glu Ala Asn Gln Thr Leu Glu Asn Leu Arg Val		
435	440	445
Gly Ile Tyr Lys Glu Gly Gly Arg Gln Ile Gly Gln Phe Ser Ser Lys		
450	455	460
Asp Asn Asp Tyr Asn Pro Pro Gly Tyr Ser Thr Leu Pro Thr Val Lys		
465	470	475
480		
Ala Asp Glu Asn Gly Asn Val Thr Ile Lys Val Asn Ala Lys Val Leu		
485	490	495
Glu Ser Met Glu Gly Ser Lys Ile Arg Leu Lys Leu Gly Asp Lys Thr		
500	505	510

Leu Ile Thr Thr Asp Phe Lys
515

(2) INFORMATION FOR SEQ ID NO:5231:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5231:

Arg	Asp	Glu	Arg	Ile	Lys	Thr	Met	Thr	Asn	Ser	Ser	Lys	Ser	Phe	Thr
1				5					10						15
Lys	Phe	Met	Ala	Ala	Ser	Ala	Val	Phe	Thr	Met	Gly	Phe	Leu	Ser	Val
							20		25					30	
Pro	Thr	Ala	Gly	Ala	Glu	Gln	Thr	Asn	Gln	Ile	Ala	Asn	Lys	Pro	Gln
							35		40					45	
Ala	Ile	Gln	Trp	His	Thr	Asn	Leu	Thr	Asn	Glu	Arg	Phe	Thr	Thr	Ile
							50		55					60	
Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Ala	Pro	Glu	His	Thr	Phe	Gln	Ala
							65		70					80	
Tyr	Asp	Lys	Ser	His	Asn	Glu	Leu	Lys	Ala	Ser	Tyr	Ile	Glu	Ile	Asp
							85		90					95	
Leu	Gln	Arg	Thr	Lys	Asp	Gly	His	Leu	Val	Ala	Met	His	Asp	Glu	Thr
							100		105					110	
Val	Asn	Arg	Thr	Thr	Asn	Gly	His	Gly	Lys	Val	Glu	Asp	Tyr	Thr	Leu
							115		120					125	
Asp	Glu	Leu	Lys	Gln	Leu	Asp	Ala	Gly	Ser	Trp	Phe	Asn	Lys	Lys	Tyr
							130		135					140	
Pro	Lys	Tyr	Ala	Arg	Ala	Ser	Tyr	Lys	Asn	Ala	Lys	Val	Pro	Thr	Leu
							145		150					160	
Asp	Glu	Ile	Leu	Glu	Arg	Tyr	Gly	Pro	Asn	Ala	Asn	Tyr	Tyr	Ile	Glu
							165		170					175	
Thr	Lys	Ser	Pro	Asp	Val	Tyr	Pro	Gly	Met	Glu	Glu	Gln	Leu	Leu	Ala
							180		185					190	
Ser	Leu	Lys	Lys	His	His	Leu	Leu	Asn	Asn	Asn	Lys	Leu	Lys	Asn	Gly
							195		200					205	
His	Val	Met	Ile	Gln	Ser	Phe	Ser	Asp	Glu	Ser	Leu	Lys	Lys	Ile	His
							210		215					220	

Arg	Gln	Asn	Lys	His	Val	Pro	Leu	Val	Lys	Leu	Val	Asp	Lys	Gly	Glu
225					230					235					240
Leu	Gln	Gln	Phe	Asn	Asp	Gln	Arg	Leu	Lys	Glu	Ile	Arg	Ser	Tyr	Ala
			245						250						255
Ile	Gly	Leu	Gly	Pro	Asp	Tyr	Thr	Asp	Leu	Thr	Glu	Gln	Asn	Thr	His
			260					265							270
His	Leu	Lys	Asp	Leu	Gly	Phe	Ile	Val	His	Pro	Tyr	Thr	Val	Asn	Glu
			275					280							285
Lys	Ala	Asp	Met	Leu	Arg	Leu	Asn	Lys	Tyr	Gly	Val	Asp	Gly	Val	Phe
			290				295								300
Thr	Asn	Phe	Ala	Asp	Lys	Tyr	Lys	Glu	Val	Ile	Lys				
			305				310				315				

(2) INFORMATION FOR SEQ ID NO:5232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 433 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5232:

Arg	Phe	Met	Lys	Asn	Leu	Ile	Ser	Ile	Ile	Ile	Ile	Lys	Cys	Leu	Thr
1					5				10						15
Leu	Ser	Ile	Met	Thr	Pro	Tyr	Ala	Gln	Ala	Thr	Asn	Ser	Asp	Val	Thr
					20				25						30
Pro	Val	Gln	Ala	Ala	Asn	Gln	Tyr	Gly	Tyr	Ala	Gly	Leu	Ser	Ala	Ala
					35			40				45			
Tyr	Glu	Pro	Thr	Ser	Ala	Val	Asn	Val	Ser	Gln	Thr	Gly	Gln	Leu	Leu
					50			55			60				
Tyr	Gln	Tyr	Asn	Ile	Asp	Thr	Lys	Trp	Asn	Pro	Ala	Ser	Met	Thr	Lys
					65		70		75						80
Leu	Met	Thr	Met	Tyr	Leu	Thr	Leu	Glu	Ala	Val	Asn	Lys	Gly	Gln	Leu
					85				90						95
Ser	Leu	Asp	Asp	Thr	Val	Thr	Met	Thr	Asn	Lys	Glu	Tyr	Ile	Met	Ser
					100			105					110		
Thr	Leu	Pro	Glu	Leu	Ser	Asn	Thr	Lys	Leu	Tyr	Pro	Gly	Gln	Val	Trp
							115		120					125	
Thr	Ile	Ala	Asp	Leu	Leu	Gln	Ile	Thr	Val	Ser	Asn	Ser	Ser	Asn	Ala
							130		135					140	
Ala	Ala	Leu	Ile	Leu	Ala	Lys	Lys	Val	Ser	Lys	Asn	Thr	Ser	Asp	Phe

145	150	155	160
Val Asp Leu Met Asn Asn Lys Ala Lys Ala Ile Gly Met Lys Asn Thr			
165	170	175	
His Phe Val Asn Pro Thr Gly Ala Glu Asn Ser Arg Leu Arg Thr Phe			
180	185	190	
Ala Pro Thr Lys Tyr Lys Asp Gln Glu Arg Thr Val Thr Ala Arg			
195	200	205	
Asp Tyr Ala Ile Leu Asp Leu His Val Ile Lys Glu Thr Pro Lys Ile			
210	215	220	
Leu Asp Phe Thr Lys Gln Leu Ala Pro Thr Thr His Ala Val Thr Tyr			
225	230	235	240
Tyr Thr Phe Asn Phe Ser Leu Glu Gly Ala Lys Met Ser Leu Pro Gly			
245	250	255	
Thr Asp Gly Leu Lys Thr Gly Ser Ser Asp Thr Ala Asn Tyr Asn His			
260	265	270	
Thr Ile Thr Thr Lys Arg Gly Lys Phe Arg Ile Asn Gln Val Ile Met			
275	280	285	
Gly Ala Gly Asp Tyr Lys Asn Leu Gly Gly Glu Lys Gln Arg Asn Met			
290	295	300	
Met Gly Asn Ala Leu Met Glu Arg Ser Phe Asp Gln Tyr Lys Tyr Val			
305	310	315	320
Lys Ile Leu Ser Lys Gly Glu Gln Arg Ile Asn Gly Lys Lys Tyr Tyr			
325	330	335	
Val Glu Asn Asp Leu Tyr Asp Val Leu Pro Ser Asp Phe Ser Lys Lys			
340	345	350	
Asp Tyr Lys Leu Val Val Glu Asp Gly Lys Val His Ala Asp Tyr Pro			
355	360	365	
Arg Glu Phe Ile Asn Lys Asp Tyr Gly Pro Pro Thr Val Glu Val His			
370	375	380	
Gln Pro Ile Ile Gln Lys Ala Asn Thr Val Ala Lys Ser Met Trp Glu			
385	390	395	400
Glu His Pro Leu Phe Thr Ile Ile Gly Gly Thr Cys Leu Val Ala Gly			
405	410	415	
Leu Ala Leu Ile Val His Met Ile Ile Asn Arg Leu Phe Arg Lys Arg			
420	425	430	
Lys			

(2) INFORMATION FOR SEQ ID NO:5233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5233:

Leu Thr Lys Glu Arg Glu Tyr Met Lys Leu Lys Ser Phe Ile Thr Val
1 5 10 5

Thr Leu Ala Leu Gly Met Ile Ala Thr Thr Gly Ala Thr Val Ala Gly
20 25 30

Asn Glu Val Ser Ala Ala Glu Lys Asp Lys Leu Pro Ala Thr Gln Lys
35 40 45

Ala Lys Glu Met Gln Asn Val Pro Tyr Thr Ile Ala Val Asp Gly Ile
50 55 60

Met Ala Phe Asn Gln Ser Tyr Leu Asn Leu Pro Lys Asp Ser Gln Leu
65 70 75 80

Ser Tyr Leu Asp Leu Gly Asn Lys Val Lys Ala Leu Leu Tyr Asp Glu
85 90 95

Arg Gly Val Thr Pro Glu Lys Ile Arg Asn Ala Lys Ser Ala Val Tyr
100 105 110

Thr Ile Thr Trp Lys Asp Gly Ser Lys Lys Glu Val Asp Leu Lys Lys
115 120 125

Asp Ser Tyr Thr Ala Asn Leu Phe Asp Ser Asn Ser Ile Lys Gln Ile
130 135 140

Asp Ile Asn Val Lys Thr Lys
145 150

(2) INFORMATION FOR SEQ ID NO:5234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 497 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5234:

Asn His Cys Asn Arg Ile Glu Arg Lys Met Ala Met Ser Asn Asn Phe
1 5 10 15

Lys Asp Asp Phe Glu Lys Asn Arg Gln Ser Ile Asp Thr Asn Ser His
20 25 30

Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln Ser Glu Leu Glu His
35 40 45

Gln Asp Thr Ile Glu Asn Thr Glu Gln Gln Phe Pro Pro Arg Asn Ala
50 55 60

Gln Arg Arg Lys Arg Arg Arg Asp Leu Ala Thr Asn His Asn Lys Gln
65 70 75 80

Val His Asn Glu Ser Gln Thr Ser Glu Asp Asn Val Gln Asn Glu Ala
85 90 95

Gly Thr Ile Asp Asp Arg Gln Val Glu Ser Ser His Ser Thr Glu Ser
100 105 110

Gln Glu Pro Ser His Gln Asp Ser Thr Pro Gln His Glu Glu Glu Tyr
115 120 125

Tyr Asn Lys Asn Ala Phe Ala Met Asp Lys Ser His Pro Glu Pro Ile
130 135 140

Glu Asp Asn Asp Lys His Asp Thr Ile Lys Asn Ala Glu Asn Asn Thr
145 150 155 160

Glu His Ser Thr Val Ser Asp Lys Ser Glu Ala Glu Gln Ser Gln Gln
165 170 175

Pro Lys Pro Tyr Phe Thr Thr Gly Ala Asn Gln Ser Glu Thr Ser Lys
180 185 190

Asn Glu His Asp Asn Asp Ser Val Lys Gln Asp Gln Asp Glu Pro Lys
195 200 205

Glu His His Asn Gly Lys Lys Ala Ala Ala Ile Gly Ala Gly Thr Ala
210 215 220

Gly Val Ala Gly Ala Ala Gly Ala Met Ala Ala Ser Lys Ala Lys Lys
225 230 235 240

His Ser Asn Asp Ala Gln Asn Lys Ser Asn Ser Gly Lys Ala Asn Asn
245 250 255

Ser Thr Glu Asp Lys Ala Ser Gln Asp Lys Ser Lys Asp His His Asn
260 265 270

Gly Lys Lys Gly Ala Ala Ile Gly Ala Gly Thr Ala Gly Leu Ala Gly
275 280 285

Gly Ala Ala Ser Lys Ser Ala Ser Ala Ala Ser Lys Pro His Ala Ser
290 295 300

Asn Asn Ala Ser Gln Asn His Asp Glu His Asp Asn His Asp Arg Asp
305 310 315 320

Lys Glu Arg Lys Lys Gly Gly Met Ala Lys Val Leu Leu Pro Leu Ile
325 330 335

Ala Ala Val Leu Ile Ile Gly Ala Leu Ala Ile Phe Gly Gly Met Ala
340 345 350

Leu Asn Asn His Asn Asn Gly Thr Lys Glu Asn Lys Ile Ala Asn Thr

355	360	365
Asn Lys Asn Asn Ala Asp Glu Ser Lys Asp Lys Asp Thr Ser Lys Asp		
370	375	380
Ala Ser Lys Asp Lys Ser Lys Ser Thr Asp Ser Asp Lys Ser Lys Glu		
385	390	395
Asp Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp Asn Asp Gln Asn Asn		
405	410	415
Ala Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn Gln Asn Gln Gln		
420	425	430
Ala Asn Gln Asn Gln Gln Gln Gln Arg Gln Gly Gly Gly Gln		
435	440	445
Arg His Thr Val Asn Gly Gln Glu Asn Leu Tyr Arg Ile Ala Ile Gln		
450	455	460
Tyr Tyr Gly Ser Gly Ser Pro Glu Asn ValGlu Lys Ile Arg Arg Ala		
465	470	475
Asn Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly Gln Gln Ile Val Ile		
485	490	495
Pro		

(2) INFORMATION FOR SEQ ID NO:5235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 886 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5235:

Leu	Leu	Ser	Ile	Lys	Tyr	Asn	Leu	Ile	Gly	Val	Val	Asn	Asn	Met	Asn
1				5				10						15	
Lys His His Pro Lys Leu Arg Ser Phe Tyr Ser Ile Arg Lys Ser Thr															
	20				25				30						
Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile Thr Ser															
	35				40			45							
Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Th Ser Asp Lys Ile															
	50				55			60							
Ser Glu Asn Gln Asn Asn Asn Ala Thr Thr Thr Gln Pro Pro Lys Asp															
	65				70			75			80				
Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Ala Asn Thr Ala Lys Asn															
	85				90			95							

Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp Pro Ala
 100 105 110
 Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val Asn Phe
 115 120 125
 Gln Leu Leu Asp Lys Asn Asn Glu Thr Gln Tyr Tyr His Phe Phe Ser
 130 135 140
 Ile Lys Asp Pro Ala Asp Val Tyr Tyr Thr Lys Lys Lys Ala Glu Val
 145 150 155 160
 Glu Leu Asp Ile Asn Thr Ala Ser Thr Trp Lys Lys Phe Glu Val Tyr
 165 170 175
 Glu Asn Asn Gln Lys Leu Pro Val Arg Leu Val Ser Tyr Ser Pro Val
 180 185 190
 Pro Glu Asp His Ala Tyr Ile Arg Phe Pro Val Ser Asp Gly Mr Gln
 195 200 205
 Glu Leu Lys Ile Val Ser Ser Thr Gln Ile Asp Asp Gly Glu Glu Thr
 210 215 220
 Asn Tyr Asp Tyr Thr Lys Leu Val Phe Ala Lys Pro Ile Tyr Asn Asp
 225 230 235 240
 Pro Ser Leu Val Lys Ser Asp Thr Asn Asp Ala Val Val Thr Asn Asp
 245 250 255
 Gln Ser Ser Ser Val Ala Ser Asn Gln Thr Asn Thr Asn Ser Asn
 260 265 270
 Gln Asn Ile Ser Thr Ile Asn Asn Ala Asn Asn Gln Pro Gln Ala Thr
 275 280 28
 Thr Asn Met Ser Gln Pro Ala Gln Pro Lys Ser Ser Thr Asn Ala Asp
 290 295 300
 Gln Ala Ser Ser Gln Pro Ala His Glu Thr Asn Ser Asn Gly Asn Thr
 305 310 315 320
 Asn Asp Lys Thr Asn Glu Ser Ser Asn Gln Ser Asp Val Asn Gln Gln
 325 330 335
 Tyr Pro Pro Ala Asp Glu Ser Leu Gln Asp Ala Ile Lys Asn Pro Ala
 340 345 350
 Ile Ile Asp Lys Glu His Thr Ala Asp Asn Trp Arg Pro Ile Asp Phe
 355 360 365
 Gln Met Lys Asn Asp Lys Gly Glu Arg Gln Ph Tyr His Tyr Ala Ser
 370 375 380
 Thr Val Glu Pro Ala Thr Val Ile Phe Thr Lys Thr Gly Pro Ile Ile
 385 390 395 400
 Glu Leu Gly Leu Lys Thr Ala Ser Thr Trp Lys Lys Phe Glu Val Tyr
 405 410 415

Glu Gly Asp Lys Lys Leu Pro Val Glu Leu Val Ser Tyr Asp Ser Asp
420 425 430

Lys Asp Tyr Ala Tyr Ile Arg Phe Pro Val Ser Asn Gly Thr Arg Glu
435 440 445

Val Lys Ile Val Ser Ser Ile Glu Tyr Gly Glu Asn Ile His Glu Asp
450 455 460

Tyr Asp Tyr Thr Leu Met Val Phe Ala Gln Pro Ile Thr Asn Asn Pro
465 470 475 480

Asp Asp Tyr Val Asp Glu Glu Thr Tyr Asn Leu Gln Lys Leu Leu Ala
485 490 495

Pro Tyr His Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Glu
500 505 510

Lys Leu Gln Glu Lys Leu Pro Glu Lys Tyr Lys Ala Glu Tyr Lys Lys
515 520 525

Lys Leu Asp Gln Thr Arg Val Glu Leu Ala Asp Gln Val Lys Ser Ala
530 535 540

Val Thr Glu Phe Glu Asn Val Thr Pro Thr Asn Asp Gln Leu Thr Asp
545 550 555 560

Leu Gln Glu Ala His Phe Val Val Phe Glu Ser Glu Glu Asn Ser Glu
565 570 575

Ser Val Met Asp Gly Phe Val Glu His Pro Phe Tyr Thr Ala Thr Leu
580 585 590

Asn Gly Gln Lys Tyr Val Val Met Lys Thr Lys Asp Asp Ser Tyr Trp
595 600 605

Lys Asp Leu Ile Val Glu Gly Lys Arg Val Thr Thr Val Ser Lys Asp
610 615 620

Pro Lys Asn Asn Ser Arg Thr Leu Ile Phe Pro Tyr Ile Pro Asp Lys
625 630 635 640

Ala Val Tyr Asn Ala Ile Val Lys Val Val Val Ala Asn Ile Gly Tyr
645 650 655

Glu Gly Gln Tyr His Val Arg Ile Ile Asn Gln Asp Ile Asn Thr Lys
660 665 670

Asp Asp Asp Thr Ser Gln Asn Asn Thr Ser Glu Pro Leu Asn Val Gln
675 680 685

Thr Gly Gln Glu Gly Lys Val Ala Asp Thr Asp Val Ala Glu Asn Ser
690 695 700

Ser Thr Ala Thr Asn Pro Lys Asp Ala Ser Asp Lys Ala Asp Val Ile
705 710 715 720

Glu Pro Glu Ser Asp Val Val Lys Asp Ala Asp Asn Asn Ile Asp Lys
725 730 735

Asp Val Gln His Asp Val Asp His Leu Ser Asp Met Ser Asp Asn Asn

740	745	750
His Phe Asp Lys Tyr Asp Leu Lys Glu Met Asp Thr Gln Ile Ala Lys		
755	760	765
Asp Thr Asp Arg Asn Val Asp Lys Asp Ala Asp Asn Ser Val Gly Met		
770	775	780
Ser Ser Asn Val Asp Thr Asp Lys Asp Ser Asn Lys Asn Lys Asp Lys		
785	790	795
Val Ile Gln Leu Asn His Ile Ala Asp Lys Asn Asn His Thr Gly Lys		
805	810	815
Ala Ala Lys Leu Asp Val Val Lys Gln Asn Tyr Asn Asn Thr Asp Lys		
820	825	830
Val Thr Asp Lys Lys Thr Thr Glu His Leu Pro Ser Ap Ile His Lys		
835	840	845
Thr Val Asp Lys Thr Val Lys Thr Lys Glu Lys Ala Gly Thr Pro Ser		
850	855	860
Lys Glu Asn Lys Leu Ser Gln Ser Lys Met Leu Thr Lys Asn Trp Arg		
865	870	875
Asn Asn Xaa Gln Ala Asn		
885		

(2) INFORMATION FOR SEQ ID NO:5236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 236 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5236:

Asn Met Asn Lys Asn Val Met Val Lys Gly Bu Thr Ala Leu Thr Ile		
1	5	10
Leu Thr Ser Leu Gly Phe Ala Glu Asn Ile Ser Asn Gln Xaa His Ser		
20	25	30
Ile Ala Lys Ala Glu Lys Asn Val Lys Glu Ile Thr Asp Ala Thr Lys		
35	40	45
Glu Pro Tyr Asn Ser Val Val Ala Phe Val Gly Gly Thr Gly Val Val		
50	55	60
Val Gly Lys Asn Thr Ile Val Thr Asn Lys His Ile Ala Lys Ser Asn		
65	70	75
Asp Ile Phe Lys Asn Arg Val Ser Ala His His Ser Ser Lys Gly Lys		
85	90	95

Gly Gly Gly Asn Tyr Asp Val Lys Asp Ile Val Glu Tyr Pro Gly Lys
 100 105 110
 Glu Asp Leu Ala Ile Val His Val His Glu Thr Ser Thr Glu Gly Leu
 115 120 125
 Asn Phe Asn Lys Asn Val Ser Tyr Thr Lys Phe Ala Asp Gly Ala Lys
 130 135 140
 Val Lys Asp Arg Ile Ser Val Ile Gly Tyr Pro Lys Gly Ala Gln Thr
 145 150 155 160
 Lys Tyr Lys Met Phe Glu Ser Thr Gly Thr Ile Asn His Ile Ser Gly
 165 170 175
 Thr Phe Met Glu Phe Asp Ala Tyr Ala Gln Pro Gly Asn Ser Gly Ser
 180 185 190
 Pro Val Leu Asn Ser Lys His Xaa Leu Ile Gly Ile Leu Tyr Ala Gly
 195 200 205
 Ser Gly Lys Asp Glu Ser Glu Lys Asn Phe Gly Val Tyr Phe Thr Pro
 210 215 220
 Gln Leu Xaa Xaa Phe Ile Pro Asn Asn Ile Glu Lys
 225 230 235

(2) INFORMATION FOR SEQ ID NO:5237:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5237:

Tyr Arg Leu Glu His Thr Ile Met Lys Met Arg Thr Ile Ala Lys Thr
 1 5 10 15
 Ser Leu Ala Leu Gly Leu Leu Thr Thr Gly Ala Ile Thr Val Thr Thr
 20 25 30
 Gln Ser Val Lys Ala Glu Lys Ile Gln Ser Thr Lys Val Asp Lys Val
 35 40 45
 Pro Thr Leu Lys Ala Glu Arg Leu Ala Met Ile Asn Ile Thr Ala Gly
 50 55 60
 Ala Asn Ser Ala Thr Thr Gln Ala Ala Asn Thr Arg Gln Glu Arg Thr
 65 70 75 80
 Pro Lys Leu Glu Lys Ala Pro Asn Thr Asn Glu Glu Lys Thr Ser Ala
 85 90 95

Ser Lys Ile Glu Lys Ile Ser Gln Pro Lys Gln Glu Glu Gln Lys Thr
 100 105 110

Leu Asn Ile Ser Ala Thr Pro Ala Pro Lys Gln Glu Gln Ser Gln Thr
 115 120 125

Thr Thr Glu Ser Thr Thr Pro Lys Thr Lys Val Thr Thr Pro Pro Ser
 130 135 140

Thr Asn Thr Pro Gln Pro Met Gln Ser Thr Lys Ser Asp Thr Pro Gln
 145 150 155 160

Ser Pro Thr Ile Lys Gln Ala Gln Thr Asp Met Thr Pro Lys Tyr Glu
 165 170 175

Asp Leu Arg Ala Tyr Tyr Thr Lys Pro Ser Phe Glu Phe Glu Lys Gln
 180 185 190

Phe Gly Phe Met Leu Lys Pro Trp Thr Thr Val Arg Phe Met Asn Val
 195 200 205

Ile Pro Asn Arg Phe Ile Tyr Lys Ile Ala Leu Val Gly Lys Asp Glu
 210 215 220

Lys Lys Tyr Lys Asp Gly Pro Tyr Asp Asn IleAsp Val Phe Ile Val
 225 230 235 240

Leu Glu Asp Asn Lys Tyr Gln Leu Lys Lys Tyr Ser Val Gly Gly Ile
 245 250 255

Thr Lys Thr Asn Ser Lys Lys Val Asn His Lys Val Glu Leu Ser Ile
 260 265 270

Thr Lys Lys Asp Asn Gln Gly Met Ile Ser Arg Asp Val Ser Glu Tyr
 275 280 285

Met Ile Thr Lys Glu Glu Ile Ser Leu Lys Glu Leu Asp Phe Lys Leu
 290 295 300

Arg Lys Gln Leu Ile Glu Lys His Asn Leu Tyr Gly Asn Met Gly Ser
 305 310 315 320

Gly Thr Ile Val Ile Lys Met Lys Asn Gly Gly Lys Tyr Thr Phe Glu
 325 330 335

Leu His Lys Leu Gln Glu His Arg Met Ala Asp Val Ile Asp Gly
 340 345 350

Thr Asn Ile Asp Asn Ile Glu Val Asn Ile Lys
 355 360

(2) INFORMATION FOR SEQ ID NO:5238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5238:

Phe Met Lys Phe Lys Ser Leu Ile Thr Thr Thr Leu Ala Leu Gly Val
1 5 10 15

Leu Ala Ser Thr Gly Ala Asn Phe Asn Asn Asn Glu Ala Ser Ala Ala
20 25 30

Ala Lys Pro Leu Asp Lys Ser Ser Ser Ser Leu His His Gly Tyr Ser
35 40 45

Lys Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn
50 55 60

Ile Leu Ser Ser Leu Thr Phe Asn Lys Asn Gln Asn Ile Ser Tyr Lys
65 70 75 80

Asp Leu Glu Asp Arg Val Lys Ser Val Leu Lys Ser Asp Arg Gly Ile
85 90 95

Ser Asp Ile Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Tyr
100 105 110

Phe Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr
115 120 125

Thr Ala Asp Leu Ile Asn Thr Ser Glu Ile Lys Ala Ile Asn Ile Asn
130 135 140

Val Asp Thr Lys Lys Gln
145 150

(2) INFORMATION FOR SEQ ID NO:5239:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 239 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5239:

Glu Lys Arg Phe Met Gln Met Ala Arg Lys Val Val Val Val Asp Asp
1 5 10 15

Glu Lys Pro Ile Ala Asp Ile Leu Glu Phe Asn Leu Lys Lys Glu Gly
20 25 30

Tyr Asp Val Tyr Cys Ala Tyr Asp Gly Asn Asp Ala Val Asp Leu Ile
35 40 45

Tyr Glu Glu Glu Pro Asp Ile Val Leu Leu Asp Ile Met Leu Pro Gl
50 55 60

Arg Asp Gly Met Glu Val Cys Arg Glu Val Arg Lys Lys Tyr Glu Met
 65 70 75 80
 Pro Ile Ile Met Leu Thr Ala Lys Asp Ser Glu Ile Asp Lys Val Leu
 85 90 95
 Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys Pro Phe Ser Thr
 100 105 110
 Arg Glu Leu Ile Ala Arg Val Lys Ala Asn Leu Arg Arg His Tyr Ser
 115 120 125
 Gln Pro Ala Gln Asp Thr Gly Asn Val Thr Asn Glu Ile Thr Ile Lys
 130 135 140
 Asp Ile Val Ile Tyr Pro Asp Ala Tyr Ser Ile Lys Lys Arg Gly Glu
 145 150 155 160
 Asp Ile Glu Leu Thr His Arg Glu Phe Glu Leu Phe His Tyr Leu Ser
 165 170 175
 Lys His Met Gly Gln Val Met Thr Arg Glu His Leu Leu Gln Thr Val
 180 185 190
 Trp Gly Tyr Asp Tyr Phe Gly Asp Val Arg Thr Val Asp Val Thr Ile
 195 200 205
 Arg Arg Leu Arg Glu Lys Ile Glu Asp Asp Pro Ser His Pro Glu Tyr
 210 215 220
 Ile Val Thr Arg Arg Gly Val Gly Tyr Phe Leu Gln Gln His Glu
 225 230 235

(2) INFORMATION FOR SEQ ID NO:5240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5240:

Xaa Leu Ser Thr Val Ile Gly Ala Xaa Leu Phe Phe Lys Ser Ser Val
 1 5 10 15
 Ser Leu Val Phe Lys Met Val Lys Lys Phe Arg Xaa Gly Val Ile Ser
 20 25 30
 Val Asn Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys
 35 40 45
 Asn Ala Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val
 50 55 60

Ser Val Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu
 65 70 75 80
 Ile Lys Tyr Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys
 85 90 95
 Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile ProHis Phe
 100 105 110
 Tyr Asn Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu
 115 120 125
 Phe Asp Val Lys Ala
 130

(2) INFORMATION FOR SEQ ID NO:5241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:

Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val
 1 5 10 15
 Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe IleAsn Gly
 20 25 30
 Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro
 35 40 45
 Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp
 50 55 60
 Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser
 65 70 75 80
 Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp
 85 90 95
 Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn
 100 105 110
 Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala
 115 120 125
 Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly
 130 135 140
 Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu
 145 150 155 160
 Pro Ile Gly Val Val Gly Ala Val Val Ala Trp Asn Phe Pro Met Leu

165	170	175
Leu Ala Ala Trp Lys Ile Ala Pro Ala Ile Ala Ala Gly Asn Thr Ile		
180	185	190
Val Ile Gln Pro Ser Ser Ser Thr Pro Leu Sr Leu Leu Glu Val Ala		
195	200	205
Lys Ile Phe Gln Glu Val Leu Pro Lys Gly Val Val Asn Ile Leu Thr		
210	215	220
Gly Lys Gly Ser Glu Ser Gly Asn Ala Ile Phe Asn His Asp Gly Val		
225	230	235
240		
Asp Lys Leu Ser Phe Thr Gly Ser Thr Asp Val Gly Tyr Gln Val Ala		
245	250	255
Glu Ala Ala Ala Lys His Leu Val Pro Ala Thr Leu Glu Leu Gly Gly		
260	265	270
Lys Ser Ala Asn Ile Ile Leu Asp Asp Ala Asn Leu Asp Leu Ala Val		
275	280	285
Glu Gly Ile Gln Leu Gly Ile Leu Phe Asn Gln Gly Glu Val Cys Ser		
290	295	300
Ala Gly Ser Arg Leu Leu Val His Glu Lys Ile Tyr Asp Gln Leu Val		
305	310	315
320		
Pro Arg Leu Gln Glu Ala Phe Ser Asn Ile Lys Val Gly Asn Pro Gln		
325	330	335
Asp Glu Ala Thr Gln Met Gly Ser Gln Thr Gly Lys AspGln Leu Asp		
340	345	350
Lys Ile Gln Ser Tyr Ile Asp Ala Ala Lys Glu Ser Asp Ala Gln Ile		
355	360	365
Leu Ala Gly Gly His Arg Leu Thr Glu Asn Gly Leu Asp Lys Gly Phe		
370	375	380
Phe Phe Glu Pro Thr Leu Ile Ala Val Pro Asp Asn His His Lys Leu		
385	390	395
400		
Ala Gln Glu Glu Ile Phe Gly Pro Val Leu Thr Val Ile Lys Val Lys		
405	410	415
Asp Asp Gln Glu Ala Ile Asp Ile Ala Asn Asp Ser Glu Tyr Gly Leu		
420	425	430
Ala Gly Gly Val Phe Ser Gln Asn Ile Thr Arg Ala Leu Asn Ile Ala		
435	440	445
Lys Ala Val Arg Thr Gly Arg Ile Trp Ile Asn Thr Tyr Asn Gln Val		
450	455	460
Pro Glu Gly Ala Pro Phe Gly Gly Tyr Lys Lys Ser Gly Ile Gly Arg		
465	470	475
480		
Glu Thr Tyr Lys Gly Ala Leu Ser Asn Tyr Gln Gln Val Lys Asn Ile		
485	490	495

Tyr Ile Asp Thr Ser Asn Ala Leu Lys Gly Leu Tyr
500 505

(2) INFORMATION FOR SEQ ID NO:5242:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 540 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5242:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn
1 5 10 15

Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile
20 25 30

Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr
35 40 45

Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala
50 55 60

Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln
65 70 75 80

Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro
85 90 95

Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly
100 105 110

Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
115 120 125

Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
130 135 140

Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Ala
145 150 155 160

Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Gln
165 170 175

Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
180 185 190

Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
195 200 205

Pro Ala Ile Ser Thr Asp Glu Asn Arg Gln Asp Pro Thr Val Thr Val
210 215 220

Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly
 225 230 235 240

Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn
 245 250 255

Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val
 260 265 270

Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys
 275 280 285

Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr
 290 295 300

Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp
 305 310 315 320

Ala Lys Lys Asn Thr Glu Leu Aa Thr Val Asn Val Ala Lys Thr Gly
 325 330 335

Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu
 340 345 350

Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr
 355 360 365

Thr Asn Lys Asp Gly Tyr Lys Tyr Ser Phe Ile Asp Asn Val Gly
 370 375 380

Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro
 385 390 395 400

Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn
 405 410 415

Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu
 420 425 430

Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr
 435 440 445

Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr
 450 455 460

Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly
 465 470 475 480

Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp
 485 490 495

Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr
 500 505 510

Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser
 515 520 525

Asp Val Val Ile Asn Asn Ala Gln Pro Glu Val His
 530 535 540

(2) INFORMATION FOR SEQ ID NO:5243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 274 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5243:

Ile Thr Leu Lys Thr Val Ser Gln Leu Ile Asp Met Lys Gln Lys Gln
1 5 10 15

Thr Lys Ile Ser Met Val Thr Ala Tyr Asp Phe Pro Ser Ala Lys Gln
20 25 30

Val Glu Ala Ala Gly Ile Asp Met Ile Leu Val Gly Asp Ser Leu Gly
35 40 45

Met Thr Val Leu Gly Tyr Glu Ser Thr Val Gln Val Thr Leu Ala Asp
50 55 60

Met Ile His His Gly Arg Ala Val Arg Arg Gly AlaPro Asn Thr Phe
65 70 75 80

Val Val Val Asp Met Pro Ile Gly Ala Val Gly Ile Ser Met Thr Gln
85 90 95

Asp Leu Asn His Ala Ieu Lys Leu Tyr Gln Glu Thr Asn Ala Asn Ala
100 105 110

Ile Lys Ala Glu Gly Ala His Ile Thr Pro Phe Ile Glu Lys Ala Thr
115 120 125

Ala Ile Gly Ile Pro Val Val Ala His Leu Gly Leu Thr Pro Gln Ser
130 135 140

Val Gly Val Met Gly Tyr Lys Leu Gln Gly Ala Thr Lys Glu Ala Ala
145 150 155 160

Glu Gln Leu Ile Leu Asp Ala Lys Asn Val Glu Gln Ala Gly Ala Val
165 170 175

Ala Leu Val Leu Glu Ala Ile Pro Asn Asp Leu Ala Glu Glu Ile Ser
180 185 190

Lys His Leu Thr Ile Pro Val Ile Gly Ile Gly Ala Gly Lys Gly Thr
195 200 205

Asp Gly Gln Val Leu Val Tyr His Asp Met Leu Asn Tyr Gly Val Glu
210 215 220

His Lys Ala Lys Phe Val Lys Gln Phe Ala Asp Phe Ser Val Gly Val
225 230 235 240

Asp Gly Leu Lys Gln Tyr Asp GlnGlu Val Lys Ser Gly Ala Phe Pro
245 250 255

Ser Glu Glu Tyr Thr Tyr Lys Lys Lys Ile Met Asn Glu Val Asn Asn
260 265 270

Asn Asp

(2) INFORMATION FOR SEQ ID NO:5244:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 430 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5244:

Ser Asp Asp Trp Pro Lys Ser Ile Thr Ser Leu Ser Ile Arg Gly Val
1 5 10 15

Arg Met Lys His Gln Glu Thr Thr Ser Gln Gln Tyr Asn Phe Ser Ile
20 25 30

Ile Lys His Gly Asp Ile Ser Thr Pro Gln Gly Phe Thr Ala Gly Gly
35 40 45

Met His Ile Gly Leu Arg Ala Asn Lys Asp Phe Gly Trp Ile Tyr
50 55 60

Ser Ser Ser Leu Ala Ser Ala Ala Val Tyr Thr Leu Asn Gln Phe
65 70 75 80

Lys Ala Ala Pro Leu Ile Val Thr Glu Asp Thr Leu Gln Lys Ser Lys
85 90 95

Gly Lys Leu Gln Ala Leu Val Val Asn Ser Ala Asn Ala Asn Ser Cys
100 105 110

Thr Gly Gln Gln Gly Ile Asp Asp Ala Arg Gln Thr Gln Thr Trp Val
115 120 125

Ala Gln Gln Leu Gln Ile Pro Ser Glu His Val Ala Val Ala Ser Thr
130 135 140

Gly Val Ile Gly Glu Tyr Leu Pro Met Asp Lys Ile Lys Thr Gly Thr
145 150 155 160

Glu His Ile Lys Asp Ala Asn Phe Ala Thr Pro Gly Ala Phe Asn Glu
165 170 175

Ala Ile Leu Thr Thr Asp Thr Cys Thr Lys His Ile Ala Val Ser Leu
180 185 190

Lys Ile Asp Gly Lys Thr Val Thr Ile Gly Gy Ser Thr Lys Gly Ser
195 200 205

Gly Met Ile His Pro Asn Met Ala Thr Met Leu Ala Phe Ile Thr Thr
 210 215 220
 Asp Ala Ser Ile Glu Ser Asn Thr Leu His Gln Leu Leu Lys Ser Ser
 225 230 235 240
 Thr Asp His Thr Phe Asn Met Ile Thr Val Asp Gly Asp Thr Ser Thr
 245 250 255
 Asn Asp Met Val Leu Val Met Ala Asn His Gln Val Glu His Gln Ile
 260 265 270
 Leu Ser Gln Asp His Pro Gln Trp Glu Thr Phe Val Asp Ala Phe Asn
 275 280 285
 Phe Val Cys Thr Phe Leu Ala Lys Ala Ile Ala Arg Asp Gly Glu Gly
 290 295 300
 Ala Thr Lys Leu Ile Ser Val Asn Val Ser Gly Ala Lys Ser Ile Ser
 305 310 315 320
 Asp Ala Arg Lys Ile Gly Lys Thr Ile Val Ser Ser Asn Leu Val Lys
 325 330 335
 Ser Ala Ile Phe Gly Glu Asp Ala Asn Phe Gly Arg Ile Ile Thr Ala
 340 345 350
 Ile Gly Tyr Ser Gly Cys Glu Ile Asp Pro Asn Cys Thr Tyr Val Gln
 355 360 365
 Leu Asn Gln Ile Pro Val Val Asp Lys Gly Met Ala Val Leu Phe Asp
 370 375 380
 Glu Gln Ala Met Ser Asn Thr Leu Thr His Glu Asn Val Thr Ile Asp
 385 390 395 400
 Val Gln Leu Gly Leu Gly Asn Ala Ala Ala Thr Ala Tyr Gly Cys Asp
 405 410 415
 Leu Ser Tyr Asp Tyr Val Arg Ile Asn Ala Ser Tyr Arg Thr
 420 425 430

(2) INFORMATION FOR SEQ ID NO:5245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 469 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5245:

Asn Pro Ala Leu Thr Val Phe Ala Phe Ile Met Ile Ile Ser Ile Leu
 1 5 10 15
 Leu Ala Tyr Val Phe Lys Trp Leu Gly Leu Val Asp Asp Val Leu Leu

20

25

30

Met Val Ile Ile Ile Ser Thr Ile Ser Leu Gly Val Val Val Pro Thr		
35	40	45
Leu Lys Glu Met Asn Ile Met Arg Thr Thr Ile Gly Gln Phe Ile Leu		
50	55	60
Leu Val Ala Val Leu Ala Asp Leu Val Thr Met Ile Leu Leu Thr Val		
65	70	75
Tyr Gly Ala Ile Asn Gly Gln Gly Ser Thr Ile Trp Leu Ile Gly		
85	90	95
Ile Leu Val Val Phe Thr Ala Ile Ser Tyr Ile Leu Gly Val Gln Phe		
100	105	110
Lys Arg Met Ser Phe Leu Gln Lys Leu Met Asp Gly Thr Thr Gln Ile		
115	120	125
Gly Ile Arg Ala Val Phe Ala Leu Ile Ile Leu Val Ala Leu Ala		
130	135	140
Glu Gly Val Gly Ala Glu Asn Ile Leu Gly Ala Phe Leu Ala Gly Val		
145	150	155
Val Val Ser Leu Leu Asn Pro Asp Glu Glu Met Val Glu Lys Leu Asp		
165	170	175
Ser Phe Gly Tyr Gly Phe Phe Ile Pro Ile Phe Phe Ile Met Xaa Gly		
180	185	190
Val Asp Leu Asn Ile Pro Ser Leu Ile Lys Glu Pro Lys Le Leu Ile		
195	200	205
Ile Ile Pro Ile Leu Ile Val Ala Phe Ile Ile Ser Lys Leu Ile Pro		
210	215	220
Val Met Phe Ile Arg Arg Trp Phe Asp Met Lys Thr Thr Ile Ala Ser		
225	230	235
Ala Phe Leu Leu Thr Ser Thr Leu Ser Leu Val Ile Ala Ala Lys		
245	250	255
Ile Ser Glu Arg Leu Asn Ala Ile Ser Ala Glu Thr Ser Gly Ile Leu		
260	265	270
Ile Leu Ser Ala Val Ile Thr Cys Val Phe Val Pro Ile Ile Phe Lys		
275	280	285
Lys Leu Phe Pro Val Pro Asp Glu Phe Asn Arg Lys Ile Glu Val Ser		
290	295	300
Leu Ile Gly Lys Asn Gln Leu Thr Ile Pro Ile Ala Gln Asn Leu Thr		
305	310	315
Ser Gln Leu Tyr Asp Val Thr Leu Tyr Tyr Arg Lys Asp Leu Ser Asp		
325	330	335
Arg Arg Gln Leu Ser Asp Asp Ile Thr Met Ile Glu Ile Ala Asp Tyr		
340	345	350

Glu Gln Asp Val Leu Glu Arg Leu Gly Leu Phe Asp Arg Asp Ile Val
 355 360 365
 Val Cys Ala Thr Asn Asp Asp Asp Ile AsnArg Lys Val Ala Lys Leu
 370 375 380
 Ala Lys Ala His Gln Val Glu Arg Val Ile Cys Arg Leu Glu Ser Thr
 385 390 395 400
 Thr Asp Asp Thr Glu Leu Val Asp Ser Gly Ile Glu Ile Phe Ser Ser
 405 410 415
 Tyr Leu Ser Asn Lys Ile Leu Leu Lys Gly Leu Ile Glu Thr Pro Asn
 420 425 430
 Met Leu Asn Leu Leu Ser Asn Val Glu Thr Ser Leu Tyr Glu Ile Gln
 435 440 445
 Met Leu Asn Tyr Lys Tyr Glu Asn Ile Gln Leu Arg Asn Phe Pro Phe
 450 455 460
 Gly Gly Asp Ile Ile
 465

(2) INFORMATION FOR SEQ ID NO:5246:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 414 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5246:

Ala Ile Ile Val Ile Leu Leu Phe Leu Arg Asn Ile Arg Thr Thr Ala
 1 5 10 15
 Ile Ser Ile Ile Ser Ile Pro Leu Ser Leu Leu Met Ala Leu Ile Ala
 20 25 30
 Leu Lys Leu Ser Asp Val Ser Leu Asn Ile Leu Thr Leu Gly Ala Leu
 35 40 45
 Thr Val Ala Ile Gly Arg Val Ile Asp Asp Ser Ile Val Val Val Glu
 50 55 60
 Asn Ile Tyr Arg Arg Leu Thr Asp Ser Glu Glu Gln Leu Lys Gly Glu
 65 70 75 80
 Asn Leu Ile Ile Ser Ala Thr Thr Glu Val Phe Lys Pro Ile Met Ser
 85 90 95
 Ser Thr Leu Val Thr Ile Ile Val Phe Leu Pro Leu Val Phe Val Ser
 100 105 110

Gly Ser Val Gly Glu Met Phe Arg Pro Phe Ala Leu Ala Ile Ala Phe
 115 120 125
 Ser Leu Leu Ala Ser Leu Leu Val Ser Ile Thr Leu Val Pro Ala Leu
 130 135 140
 Ala Ala Thr Leu Phe Lys Lys Gly Val Lys Arg Arg Asn Lys Gln His
 145 150 155 160
 Gln Glu Gly Leu Gly Val Val Ser Thr Thr Tyr Lys Lys Val Leu His
 165 170 175
 Trp Ser Leu Asn His Lys Trp Ile Val Ile Ile Leu Ser Thr Leu Ile
 180 185 190
 Leu Val Ala Thr Ile Val Phe Gly Gly Pro Arg Leu Gly Thr Ser Phe
 195 200 205
 Ile Ser Ala Gly Asp Asp Lys Phe Leu Ala Ile Thr Tyr Thr Pro Lys
 210 215 220
 Pro Gly Glu Thr Glu Gln Ala Val Leu Asn His Ala Lys Asp Val Glu
 225 230 235 240
 Lys Tyr Leu Lys Gln Lys Lys His Val Lys Thr Ile Gln Tyr Ser Al
 245 250 255
 Gly Gly Ser Ser Pro Val Asp Pro Thr Gly Ser Thr Asn Ser Met Ala
 260 265 270
 Ile Met Val Glu Tyr Asp Asn Asp Thr Pro Asn Phe Asp Val Glu Ala
 275 280 285
 Asp Lys Val Ile Lys His Ala Asp Gly Phe Lys His Pro Gly Glu Trp
 290 295 300
 Lys Asn Gln Asp Leu Gly Thr Gly Ala Gly Asn Lys Ser Val Glu Val
 305 310 315 320
 Thr Val Lys Gly Pro Ser Met Asp Ala Ile Lys Ser Thr Val Lys Asp
 325 330 335
 Ile Glu Gln Lys Met Lys Gln Val Lys Gly Leu Ala Asn Val Lys Ser
 340 345 350
 Asp Leu Ser Gln Thr Tyr Asp Gln Tyr Glu Ile Lys Val Asp Gln Asn
 355 360 365
 Lys Ala Ala Glu Asn Gly Ile Ser Ala Ser Gln Leu Ala Met His Leu
 370 375 380
 Asn Glu Asn Leu Pro Glu Lys Thr Val Thr Thr Val Lys Glu Asn Gly
 385 390 395 400
 Lys Thr Val Asp Val Lys Val Lys Gln Asn Lys Gln Thr Ala
 405 410

(2) INFORMATION FOR SEQ ID NO:5247:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5247:

Gly Lys Pro Phe Ile Ile Gly Leu Gly Asp Ile Ile Val Lys Lys Leu
1 5 10 15

Thr Thr Ile Leu Phe Gln Tyr Lys Ile Phe Pro Val Leu Met Phe Leu
20 25 30

Val Ser Thr Gly Leu Gly Ile Ile Val Ile Thr Gln Asn Ile Leu Ile
35 40 45

Ala Asp Phe Leu Ala Lys Ile Ile Arg His Gln Phe Gln Gly Leu Trp
50 55 6

Ile Val Leu Phe Ile Leu Gly Val Leu Leu Leu Arg Ala Thr Val
65 70 75 80

Gln Phe Leu Asn Gln Trp Leu Gly Asp Thr Leu Ala Phe Lys Val Lys
85 90 95

His Met Leu Arg Gln Arg Val Ile Tyr Lys Asn Asn Gly His Pro Ile
100 105 110

Gly Glu Gln Met Thr Ile Leu Thr Glu Asn Ile Asp Gly Leu Ala Pro
115 120 125

Phe Tyr Lys Ser Tyr Leu Pro Gln Val Phe Lys Ser Met Met Val Pro
130 135 140

Leu Ile Ile Ile Ile Ala Met Phe Phe Ile His Phe Asn Thr Ala Leu
145 150 155 160

Ile Met Leu Ile Thr Ala Pro Phe Ile Pro Leu Phe Tyr Ile Ile Phe
165 170 175

Gly Leu Lys Thr Arg Asp Glu Ser Lys Asp Gln Met Thr Tyr Leu Asn
180 185 190

Gln Phe Ser Gln Arg Phe Leu Asn Ile Ala Lys Gly Leu Val Thr Leu
195 200 205

Lys Leu Phe Asn Arg Thr Glu Gln Thr Glu Lys His Ile Tyr Asp Asp
210 215 220

Ser Thr Gln Phe Arg Thr Leu Thr Met Arg Ile Leu Arg Ser Ala Phe
225 230 235 240

Leu Ser Gly Leu Met Leu Glu Phe Ile Ser Met Leu Gly Ile Gly Leu
245 250 255

Val Ala Leu Glu Ala Thr Leu Ser Leu Val Val Phe His Asn Ile Asp
260 265 270

Phe Lys Thr Ala Ala Ile Ala Ile Ile Leu Ala Pro Glu Phe Tyr Asn
 275 280 285
 Ala Ile Lys Asp Leu Gly Gln Ala Phe His Thr Gly Lys Gln Ser Glu
 290 295 300
 Gly Ala Ser Asp Val Val Phe Glu Phe Leu Glu Gln Pro Asn Tyr Asn
 305 310 315 320
 Asn Glu Phe Leu Leu Lys Tyr Glu Glu Asn Gln Lys Pro Phe Ile Gln
 325 330 335
 Leu Thr Asp Ile Ser Phe Arg Tyr Asp Asp Ser Asp Arg Leu Val Leu
 340 345 350
 Asn Asp Leu Asn Leu Glu Ile Phe Lys Gly Asp Gln Ile Ala Leu Val
 355 360 365
 Gly Pro Ser Gly Ala Gly Lys Ser Thr Leu Thr His Leu Ile Ala Gly
 370 375 380
 Val Tyr Gln Pro Thr Ile Gly Thr Ile Ser Thr Asn Gln Arg Asp Leu
 385 390 395 400
 Asn Ile Gly Ile Leu Ser Gln Gln Pro Tyr Ile Phe Ser Ala Ser Ile
 405 410 415
 Lys Glu Asn Ile Thr Met Phe Lys Asp Ile Glu Asn Asn Thr Ile Glu
 420 425 430
 Glu Val Leu Asp Glu Val Gly Leu Leu Asp Lys Val Gln Ser Phe Thr
 435 440 445
 Lys Gly Ile Asn Thr Ile Ile Gly Glu Gly Gly Glu Met Leu Ser Gly
 450 455 460
 Gly Gln Met Arg Arg Ile Glu Leu Glys Arg Leu Leu Val Met Lys Pro
 465 470 475 480
 Asp Leu Val Ile Phe Asp Glu Pro Ala Thr Gly Leu Asp Ile Gln Thr
 485 490 495
 Glu His Met Ile Gln Asn Val Leu Phe Gln His Phe Lys Asp Thr Thr
 500 505 510
 Met Ile Val Ile Ala His Arg Asp Asn Thr Ile Arg His Leu Gln Arg
 515 520 525
 Arg Leu Tyr Ile Glu Asn Gly Arg Leu Ile Ala Asp Asp Arg Asn Ile
 530 535 540
 Ser Val Asn Ile Thr Glu Asn Gly Asp Asp Leu
 545 550 555

(2) INFORMATION FOR SEQ ID NO:5248:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 393 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5248:

Val Trp Lys Leu Lys Met Arg Trp Ile Lys Arg Lys Lys Lys Asn Phe
1 5 10 15

Leu Asn Ser Lys Phe Asn Phe Asn Asn Gly Lys Ile Ala Thr Tyr Leu
20 25 30

Tyr Lys Glu Arg Thr Ala Met Trp Asn Lys Asn Arg Leu Thr Gln Met
35 40 45

Leu Ser Ile Glu Tyr Pro Ile Ile Gln Ala Gly MetAla Gly Ser Thr
50 55 60

Thr Pro Lys Leu Val Ala Ser Val Ser Asn Ser Gly Gly Leu Gly Thr
65 70 75 80

Ile Gly Ala Gly Tyr Phe Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp
85 90 95

Tyr Val Arg Gln Leu Thr Ser Asn Ser Phe Gly Val Asn Val Phe Val
100 105 110

Pro Ser Gln Gln Ser Tyr Thr Ser Ser Gln Ile Glu Asn Met Asn Ala
115 120 125

Trp Leu Lys Pro Tyr Arg Arg Ala Leu His Leu Glu Glu Pro Val Val
130 135 140

Lys Ile Thr Glu Glu Gln Gln Phe Lys Cys His Ile Asp Thr Ile Ile
145 150 155 160

Lys Lys Gln Val Pro Val Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu
165 170 175

Gln Ile Ile Ser Arg Leu Lys Ala Ala Asn Val Lys Leu Ile Gly Thr
180 185 190

Ala Thr Ser Val Asp Glu Ala Ile Ala Asn Glu Lys Ala Gly MetAsp
195 200 205

Ala Ile Val Ala Gln Gly Ser Glu Ala Gly Gly His Arg Gly Ser Phe
210 215 220

Leu Lys Pro Lys Asn Gln Leu Pro Met Val Gly Thr Ile Ser Leu Val
225 230 235 240

Pro Gln Ile Val Asp Val Val Ser Ile Pro Val Ile Ala Ala Gly Gly
245 250 255

Ile Met Asp Gly Arg Gly Val Leu Ala Ser Ile Val Leu Gly Ala Glu
260 265 270

Gly Val Gln Met Gly Thr Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala

275

280

285

Ser Glu Leu Leu Arg Asp Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr
290 295 300

Val Ile Thr Lys Ala Phe Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn
305 310 315 320

Arg Phe Ile Glu Glu Met Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr
325 330 335

Pro Ile Gln Asn Glu Leu Thr Ser Ser Ile Arg Lys Ala Ala Asn
340 345 350

Ile Gly Asp Lys Glu Leu Ile His Met Trp Ser Gly Gln Ser Pro Arg
355 360 365

Leu Ala Thr Thr His Pro Ala Asn Thr Ile MetSer Asn Ile Ile Asn
370 375 380

Gln Ile Asn Gln Ile Met Gln Tyr Lys
385 390

(2) INFORMATION FOR SEQ ID NO:5249:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 936 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5249:

Asn Asp Phe Leu Lys Arg Gly Asn Lys Met Asn Met Lys Lys Lys Glu
1 5 10 15

Lys His Ala Ile Arg Lys Lys Ser Ile Gly Val Ala Ser Val Leu Val
20 25 30

Gly Thr Leu Ile Gly Phe Gly Leu Leu Ser Ser Lys Glu Ala Asp Ala
35 40 45

Ser Glu Asn Ser Val Thr Gln Ser Asp Ser Ala Ser Asn Glu Ser Lys
50 55 60

Ser Asn Asp Ser Ser Ser Val Ser Ala Ala Pro Lys Thr Asp Asp Thr
65 70 75 80

Asn Val Ser Asp Thr Lys Thr Ser Ser Asn Thr Asn Asn Gly Glu Thr
85 90 95

Ser Val Ala Gln Asn Pro Ala Gln Gln Glu Thr Thr Gln Ser Ser Ser
100 105 110

Thr Asn Ala Thr Thr Glu Glu Thr Pro Val Thr Gly Glu Ala Thr Thr
115 120 125

Thr Thr Thr Asn Gln Ala Asn Thr Pro Ala Thr Thr Gln Ser Ser Asn
 130 135 140

Thr Asn Ala Glu Glu Leu Val Asn Gln Thr Ser Asn Glu Thr Thr Ser
 145 150 155 160

Asn Asp Thr Asn Thr Val Ser Ser Val Asn Ser Pro Gln Asn Ser Thr
 165 170 175

Asn Ala Glu Asn Val Ser Thr Thr Gln Asp Thr Ser Thr Glu Ala Thr
 180 185 190

Pro Ser Asn Asn Glu Ser Ala Pro Gln Ser Thr Asp Ala Ser Asn Lys
 195 200 205

Asp Val Val Asn Gln Ala Val Asn Thr Ser Ala Pro Arg Met Arg Ala
 210 215 220

Phe Ser Leu Ala Ala Val Ala Ala Asp Ala Pro Val Ala Gly Thr Asp
 225 230 235 240

Ile Thr Asn Gln Leu Thr Asn Val Thr Val Gly Ile Asp Ser Gly Thr
 245 250 255

Thr Val Tyr Pro His Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe
 260 265 270

Ser Val Pro Asn Ser Ala Val Lys Gly Asp Thr Phe Lys Ile Thr Val
 275 280 285

Pro Lys Glu Leu Asn Leu Asn Gly Val Thr Ser Thr Ala Lys Val Pro
 290 295 300

Pro Ile Met Ala Gly Asp Gln Val Leu Ala Asn Gly Val Ile Asp Ser
 305 310 315 320

Asp Gly Asn Val Ile Tyr Thr Phe Thr Asp Tyr Val Asn Thr Lys Asp
 325 330 335

Asp Val Lys Ala Thr Leu Thr Met Pro Ala Tyr Ile Asp Pro Glu Asn
 340 345 350

Val Lys Lys Thr Gly Asn Val Thr Leu Ala Thr Gly Ile Gly Ser Thr
 355 360 365

Thr Ala Asn Lys Thr Val Leu Val Asp Tyr Glu Lys Tyr Gly Lys Phe
 370 375 380

Tyr Asn Leu Ser Ile Lys Gly Thr Ile Asp Gln Ile Asp Lys Thr Asn
 385 390 395 400

Asn Thr Tyr Arg Gln Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val
 405 410 415

Ile Ala Pro Val Leu Thr Gly Asn Leu Lys Pro Asn Thr Asp Ser Asn
 420 425 430

Ala Leu Ile Asp Gln Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp
 435 440 445

Asn Ala Ala Asp Leu Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe
450 455 460

Glu Asp Val Thr Asn Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln
465 470 475 480

Tyr Lys Val Glu Phe Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr
485 490 495

Ile Val Val Val Asn Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu
500 505 510

Ala Leu Arg Ser Thr Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg
515 520 525

Ser Met Ser Trp Asp Asn Glu Val Ala Phe Asn Asn Gly Ser Gly Ser
530 535 540

Gly Asp Gly Ile Asp Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro
545 550 555 560

Gly Glu Ile Glu Pro Ile Pro Glu Asp Ser Asp Ser Asp Pro Gly Ser
565 570 575

Asp Ser Gly Ser Asp Ser Asn Ser Asp Ser Gly Ser Asp Ser Gly Ser
580 585 590

Asp Ser Thr Ser Asp Ser Gly Ser Asp Ser Ala Ser Asp Ser Asp Ser
595 600 605

Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser
610 615 620

Asp Ser Ala Ser Asp Ser Asp Ser Asp Asn Asp Ser Asp Ser Asp Ser
625 630 635 640

Asp Ser
645 650 655

Asp Ser
660 665 670

Asp Ser
675 680 685

Asp Ser
690 695 700

Asp Ser
705 710 715 720

Asp Ser
725 730 735

Asp Ser
740 745 750

Asp Ser
755 760 765

Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Asp Ser
770 775 780

770	775	780
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser		
785	790	795
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser		
805	810	815
Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser		
820	825	830
Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Gly Ser		
835	840	845
Asp Ser Asp Ser Ser Asp Ser Asp Ser Glu Ser Asp Ser Asn Ser		
850	855	860
Asp Ser Glu Ser Val Ser Asn Asn Asn Val Val Pro Pro Asn Ser Pro		
865	870	875
Lys Asn Gly Thr Asn Ala Ser Asn Lys Asn Glu Ala Lys Asp Ser Lys		
885	890	895
Glu Pro Leu Pro Asp Thr Gly Ser Glu Asp Glu Ala Asn Thr Ser Leu		
900	905	910
Ile Trp Gly Leu Leu Ala Ser Ile Gly Ser Leu Leu Leu Phe Arg Arg		
915	920	925
Lys Lys Glu Asn Lys Asp Lys Lys		
930	935	

(2) INFORMATION FOR SEQ ID NO:5250:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 194 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5250:

Val Ser Lys Leu Lys Lys Glu Ile Leu Glu Trp Ile Ile Ser Ile Ala		
1	5	10
Val Ala Phe Val Ile Leu Phe Ile Val Gly Lys Phe Ile Val Thr Pro		
20	25	30
Tyr Thr Ile Lys Gly Glu Ser Met Asp Pro Thr Leu Lys Asp Gly Glu		
35	40	45
Arg Val Ala Val Asn Ile Val Gly Tyr Lys Thr Gly Gly Leu Glu Lys		
50	55	60
Gly Asn Val Val Val Phe His Ala Asn Lys Asn Asp Asp Tyr Val Lys		
65	70	75
80		

Arg Val Ile Gly Val Pro Gly Asp Lys Val Glu Tyr Lys Asn Asp Thr
85 90 95

Leu Tyr Val Asn Gly Lys Lys Gln Asp Glu Pro Tyr Leu Asn Tyr Asn
100 105 110

Leu Lys His Lys Gln Gly Asp Tyr Ile Thr Gly Thr Phe Gln Val Lys
115 120 125

Asp Leu Pro Asn Ala Asn Pro Lys Ser Asn Val Ile Pro Lys Gly Lys
130 135 140

Tyr Leu Val Leu Gly Asp Asn Arg Glu Val Ser Lys Asp Ser Arg Ala
145 150 155 160

Phe Gly Leu Ile Asp Glu Asp Gln Ile Val Gly Lys Val Ser Phe Gln
165 170 175

Val Leu Ala His Phe Ser Glu Phe Gln Thr Ser Ile Ser Xaa Leu Lys
180 185 190

Ile Leu

(2) INFORMATION FOR SEQ ID NO:5251:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 559 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5251:

Leu Lys Ala Xaa Tyr Ala Lys Leu Asp Asp Val Ser Lys Phe Glu Asp
1 5 10 15

Val Thr Asp Asn Met Ser Leu Asp Phe Asp Thr Asn Gly Gly Tyr Ser
20 25 30

Leu Asn Phe Asn Asn Leu Asp Gln Ser Lys Asn Tyr Val Ile Lys Tyr
35 40 45

Glu Gly Tyr Tyr Asp Ser Asn Ala Ser Asn Leu Glu Phe Gln Thr His
50 55 60

Leu Phe Gly Tyr Tyr Asn Tyr Tyr Thr Ser Asn Leu Thr Trp Lys
65 70 75 80

Asn Gly Val Ala Phe Tyr Ser Asn Asn Aa Gln Gly Asp Gly Lys Asp
85 90 95

Lys Leu Lys Glu Pro Ile Ile Glu His Ser Thr Pro Ile Glu Leu Glu
100 105 110

Phe Lys Ser Glu Pro Pro Val Glu Lys His Glu Leu Thr Gly Thr Ile
115 120 125

Glu Glu Ser Asn Asp Ser Lys Pro Ile Asp Phe Glu Tyr His Thr Ala
130 135 140

Val Glu Gly Ala Glu Gly His Ala Glu Gly Thr Ile Glu Thr Glu Glu
145 150 155 160

Asp Ser Ile His Val Asp Phe Glu Glu Ser Thr His Glu Asn Ser Lys
165 170 175

His His Ala Asp Val Val Glu Tyr Glu Glu Asp Thr Asn Pro Gly Gly
180 185 190

Gly Gln Val Thr Thr Glu Ser Asn Leu Val Glu Phe Asp Glu Asp Ser
195 200 205

Thr Lys Gly Ile Val Thr Gly Ala Val Ser Asp His Thr Thr Ile Glu
210 215 220

Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn Leu IleGlu Leu Val Asp
225 230 235 240

Glu Leu Pro Glu Glu His Gly Gln Ala Gln Gly Pro Ile Glu Glu Ile
245 250 255

Thr Glu Asn Asn His His Ile Ser His Ser Gly Leu Gly Thr Glu Asn
260 265 270

Gly His Gly Asn Tyr Gly Val Ile Glu Glu Ile Glu Glu Asn Ser His
275 280 285

Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu Gly Gly Gln Asn Ser Gly
290 295 300

Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu Asp Lys Pro Lys Tyr Glu
305 310 315 320

Gln Gly Gly Asn Ile Val Asp Ile Asp Phe Asp Ser Val Pro Gln Ile
325 330 335

His Gly Gln Asn Asn Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Lys
340 345 350

Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Ile Asp Ile Asp Phe
355 360 365

Asp Ser Val Pro His Ile His Gly Phe Asn Lys His Thr Glu IleIle
370 375 380

Glu Glu Asp Thr Asn Lys Asp Lys Pro Asn Tyr Gln Phe Gly Gly His
385 390 395 400

Asn Ser Val Asp Phe Glu Glu Asp Thr Leu Pro Gln Val Ser Gly His
405 410 415

Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro Ile Val
420 425 430

Pro Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro

435	440	445
Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro Thr Pro		
450	455	460
Pro Thr Pro Glu Val Pro Thr Glu Pro Gly Lys Pro Ile Pro Pro Ala		
465	470	475
Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu Gln Gly Lys Val		
485	490	495
Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys Ala Val Val Pro		
500	505	510
Thr Lys Lys Ala Gln Ser Lys Lys Ser Glu Leu Pro Glu Thr Gly Gly		
515	520	525
Glu Glu Ser Thr Asn Asn Gly Met Leu Phe Gly Gly Leu Phe Ser Ile		
530	535	540
Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys LysAsn His Lys Ala		
545	550	555

(2) INFORMATION FOR SEQ ID NO:5252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 251 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5252:

Thr Lys Asn Glu Lys Ile Asn Asp Val Thr Ala Val Ala Glu Lys Glu		
1	5	10
Val Val Glu Glu Thr Lys Ala Thr Gly Thr Asp Val Thr Asn Lys Val		
20	25	30
Glu Val Glu Glu Gly Ser Glu Ile Val Gly His Lys Gln Asp Thr Asn		
35	40	45
Val Val Asn Pro His Asn Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp		
50	55	60
Lys Phe Gly Glu Gly Ile Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu		
65	70	75
80		
Ser Asp Asn Val Glu Thr His Gly Ile Ser Thr Leu Arg Lys Val Pro		
85	90	95
Glu Ile Lys Ser Thr Asp Gly Gln Val Met Ala Thr Gly Gu Ile Ile		
100	105	110
Gly Glu Arg Lys Val Arg Tyr Thr Phe Lys Glu Tyr Val Gln Glu Lys		
115	120	125

Lys Asp Leu Thr Ala Glu Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr
 130 135 140
 Thr Val Thr Gln Lys Gly Asn Gln Asn Val Glu Val Lys Leu Gly Glu
 145 150 155 160
 Thr Thr Val Ser Lys Ile Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg
 165 170 175
 Asp Asn Trp Gly Val Thr Ala Asn Gly Arg Ile Asp Thr Leu Asn Lys
 180 185 190
 Val Asp Gly Lys Phe Ser His Phe Ala Tyr Met Lys Pro Asn Asn Gln
 195 200 205
 Ser Leu Ser Ser Val Thr Val Thr Gly Gln Val Thr Lys Gly Asn Lys
 210 215 220
 Pro Gly Val Asn Asn Pro Thr Val Lys Val Tyr Lys His Ile Gly Ser
 225 230 235 240
 Asp Asp Leu Ala Glu Ser Xaa Xaa Cys Lys Ala
 245 250

(2) INFORMATION FOR SEQ ID NO:5253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5253:

Ile Leu His Leu Arg Glu Asn Ile Ile Val Lys Ser Asn Leu Arg Tyr
 1 5 10 15
 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Se Val Phe Leu Gly Thr
 20 25 30
 Met Ile Val Val Gly Met Gly Gln Glu Lys Glu Ala Ala Ala Ser Glu
 35 40 45
 Gln Asn Asn Thr Thr Val Glu Glu Ser Gly Ser Ser Ala Thr Glu Ser
 50 55 60
 Lys Ala Ser Glu Thr Gln Thr Thr Asn Asn Val Asn Thr Ile Asp
 65 70 75 80
 Glu Thr Gln Ser Tyr Ser Ala Thr Ser Thr Glu Gln Pro Ser Gln Ser
 85 90 95
 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Thr Val Gln Ala Pro Lys
 100 105 110

Val	Glu	Thr	Ser	Arg	Val	Asp	Leu	Pro	Ser	Glu	Lys	Val	Ala	Asp	Lys
115							120				125				
Glu	Thr	Thr	Gly	Thr	Gln	Val	Asp	Ile	Ala	Gln	Pro	Ser	Asn	Val	Ser
130						135					140				
Glu	Ile	Lys	Pro	Arg	Met	Lys	Arg	Ser	Met	Thr	Leu	Gln	Gln	Leu	Gln
145						150					155			160	
Arg	Lys	Lys													

(2) INFORMATION FOR SEQ ID NO:5254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1027 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5254:

Ile	Leu	His	Leu	Lys	Gly	Asp	Ile	Ile	Val	Lys	Asn	Asn	Leu	Arg	Tyr
1				5					10					15	
Gly	Ile	Arg	Lys	His	Lys	Leu	Gly	Ala	Ala	Ser	Val	Phe	Leu	Gly	Thr
						20			25				30		
Met	Ile	Val	Val	Gly	Met	Gly	Gln	Asp	Lys	Glu	Ala	Ala	Ser	Glu	
					35			40			45				
Gln	Lys	Thr	Thr	Thr	Val	Glu	Glu	Asn	Gly	Asn	Ser	Ala	Thr	Asp	Asn
					50			55			60				
Lys	Thr	Ser	Glu	Thr	Gln	Thr	Thr	Ala	Thr	Asn	Val	Asn	His	Ile	Glu
					65			70			75			80	
Glu	Thr	Gln	Ser	Tyr	Asn	Ala	Thr	Val	Thr	Gly	Gln	Pro	Ser	Asn	Ala
					85				90			95			
Thr	Gln	Val	Thr	Thr	Glu	Glu	Ala	Pro	Lys	Ala	Val	Gln	Ala	Pro	Gln
					100			105				110			
Thr	Ala	Gln	Pro	Ala	Asn	Ile	Glu	Thr	Val	Lys	Glu	Glu	Val	Val	Lys
					115				120			125			
Glu	Glu	Ala	Lys	Pro	Gln	Val	Lys	Glu	Thr	Thr	Gln	Ser	Gln	Asp	Asn
					130			135			140				
Ser	Gly	Asp	Gln	Arg	Gln	Val	Asp	Leu	Thr	Pro	Lys	Lys	Ala	Thr	Gln
					145			150			155			160	
Asn	Gln	Val	Ala	Glu	Thr	Gln	Val	Glu	Val	Ala	Gln	Pro	Arg	Thr	Ala
					165				170			175			
Ser	Glu	Ser	Lys	Pro	Arg	Val	Thr	Arg	Ser	Ala	Asp	Val	Ala	Glu	Ala

180	185	190
Lys Glu Ala Ser Asn Ala Lys Val Glu Thr Gly Thr Asp Val Thr Ser		
195	200	205
Lys Val Thr Val Glu Ile Gly Ser Ile Glu Gly His Asn Asn Thr Asn		
210	215	220
Lys Val Glu Pro His Ala Gly Gln Arg Ala Val Leu Lys Tyr Lys Leu		
225	230	235
Lys Phe Glu Asn Gly Leu His Gln Gly Asp Tyr Phe Asp Phe Thr Leu		
245	250	255
Ser Asn Asn Val Asn Thr His Gly Val Ser Thr Ala Arg Lys Val Pro		
260	265	270
Glu Ile Lys Asn Gly Ser Val Val Met Ala Thr Gly Glu Val Leu Glu		
275	280	285
Gly Gly Lys Ile Arg Tyr Thr Phe Thr Asn Asp Ile Glu Asp Lys Val		
290	295	300
Asp Val Thr Ala Glu Leu Glu Ile Asn Leu Phe Ile Asp Pro Lys Thr		
305	310	315
Val Gln Thr Asn Gly Asn Gln Thr Ile Thr Ser Thr Leu Asn Glu Glu		
325	330	335
Gln Thr Ser Lys Glu Leu Asp Val Lys Tyr Lys Asp Gly Ile Gly Asn		
340	345	350
Tyr Tyr Ala Asn Leu Asn Gly Ser Ile Glu Thr Phe Asn Lys Ala Asn		
355	360	365
Asn Arg Phe Ser His Val Ala Phe Ile Lys Pro Asn Asn Gly Lys Thr		
370	375	380
Thr Ser Val Thr Val Thr Gly Thr Leu Met Lys Gly Ser Asn Gln Asn		
385	390	400
Gly Asn Gln Pro Lys Val Arg Ile Phe Gl Tyr Leu Gly Asn Asn Glu		
405	410	415
Asp Ile Ala Lys Ser Val Tyr Ala Asn Thr Thr Asp Thr Ser Lys Phe		
420	425	430
Lys Glu Val Thr Ser Asn Met Ser Gly Asn Leu Asn Leu Gln Asn Asn		
435	440	445
Gly Ser Tyr Ser Leu Asn Ile Glu Asn Leu Asp Lys Thr Tyr Val Val		
450	455	460
His Tyr Asp Gly Glu Tyr Leu Asn Gly Thr Asp Glu Val Asp Phe Arg		
465	470	480
Thr Gln Met Val Gly His Pro Glu Gln Leu Tyr Lys Tyr Tyr Asp		
485	490	495
Arg Gly Tyr Thr Leu Thr Trp Asp Asn Gly Leu Val Leu Tyr Ser Asn		
500	505	510

Lys Ala Asn Gly Asn Glu Lys Asn Gly Pro Ile Ile Gln Asn Asn Lys
 515 520 525
 Phe Glu Tyr Lys Glu Asp Thr Ile Lys Glu Thr Leu Thr Gly Gln Tyr
 530 535 540
 Asp Lys Asn Leu Val Thr Thr Val Glu Glu Tyr Ap Ser Ser Thr
 545 550 555 560
 Leu Asp Ile Asp Tyr His Thr Ala Ile Asp Gly Gly Gly Tyr Val
 565 570 575
 Asp Gly Tyr Ile Glu Thr Ile Glu Glu Thr Asp Ser Ser Ala Ile Asp
 580 585 590
 Ile Asp Tyr His Thr Ala Val Asp Ser Glu Ala Gly His Val Gly Gly
 595 600 605
 Tyr Thr Glu Ser Ser Glu Glu Ser Asn Pro Ile Asp Phe Glu Glu Ser
 610 615 620
 Thr His Glu Asn Ser Lys His His Ala Asp Val Val Glu Tyr Glu Glu
 625 630 635 640
 Asp Thr Asn Pro Gly Gly Gln Val Thr Thr Glu Ser Asn Leu Val
 645 650 655
 Glu Phe Asp Glu Glu Ser Thr Lys Gly Ile Val Thr Gly Ala Val Ser
 660 665 670
 Asp His Thr Thr Val Glu Asp Thr Lys Glu Tyr Thr Glu Ser Asn
 675 680 685
 Leu Ile Glu Leu Val Asp Glu Leu Pro Glu Glu His Gly Gln AlaGln
 690 695 700
 Gly Pro Val Glu Glu Ile Thr Lys Asn Asn His His Ile Ser His Ser
 705 710 715 720
 Gly Leu Gly Thr Glu Asn Gly His Gly Asn Tyr Asp Val Ile Glu Glu
 725 730 735
 Ile Glu Glu Asn Ser His Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu
 740 745 750
 Gly Gly Gln Asn Ser Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu
 755 760 765
 Asp Lys Pro Lys Tyr Glu Gln Gly Asn Ile Val Asp Ile Asp Phe
 770 775 780
 Asp Ser Val Pro Gln Ile His Gly Gln Asn Lys Gly Asn Gln Ser Phe
 785 790 795 800
 Glu Glu Asp Thr Glu Lys Asp Lys Pro Lys Tyr Glu His Gly Gly Asn
 805 810 815
 Ile Ile Asp Ile Asp Phe Asp Ser Val Pro His Ile His Gly Phe Asn
 820 825 830

Lys His Thr Glu Ile Ile Glu Glu Asp Thr Asn Lys Asp Lys Pro Ser
 835 840 845
 Tyr Gln Phe Gly Gly His Asn Ser Val Asp Phe Glu Glu Asp Thr Leu
 850 855 860
 Pro Lys Val Ser Gly Gln Asn Glu Gly Gln Mr Ile Glu Glu Asp
 865 870 875 880
 Thr Thr Pro Pro Ile Val Pro Pro Thr Pro Pro Thr Pro Glu Val Pro
 885 890 895
 Ser Glu Pro Glu Thr Pro Thr Pro Pro Glu Val Pro Ser Glu
 900 905 910
 Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu
 915 920 925
 Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ala Glu Pro Gly Lys Pro
 930 935 940
 Val Pro Pro Ala Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu
 945 950 955 960
 Gln Gly Lys Val Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys
 965 970 975
 Ala Val Ala Pro Thr Lys Lys Pro Gln Ser Lys Lys Ser Glu Leu Pro
 980 985 990
 Glu Thr Gly Gly Glu Glu Ser Thr Asn Lys Gly Met Leu Phe Gly Gly
 995 1000 1005
 Leu Phe Ser Ile Leu Gly Leu Ala Leu Leu Arg Arg Asn LysLys Asn
 1010 1015 1020
 His Lys Ala
 1025

(2) INFORMATION FOR SEQ ID NO:5255:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 155 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5255:

Gly Glu Lys Cys Met Phe Leu Ala Trp Asn Glu Ile Arg Arg Asn Lys
 1 5 10 15
 Leu Lys Phe Gly Leu Ile Ile Gly Val Leu Thr Met Ile Ser Tyr Leu
 20 25 30
 Leu Phe Leu Leu Ser Gly Leu Ala Asn Gly Leu Ile Asn Met Asn Lys

35

40

45

Glu Gly Ile Asp Lys Trp Gln Ala Asp Ala Ile Val Leu Asn Lys Asp
50 55 60

Ala Asn Gln Thr Val Gln Gln Ser Val Phe Asn Lys Lys Asp Ile Glu
65 70 75 80

Asn Lys Tyr Lys Lys Gln Ala Thr Leu Lys Gln Thr Gly Glu Ile Val
85 90 95

Ser Asn Gly His Gln Lys Asp Asn Val Leu Val Phe Gly Val Glu Lys
100 105 110

Ser Ser Phe Leu Val Pro Ser Leu Ile Glu Gly His Lys Ala Thr Lys
115 120 125

Asp Asn Glu Val Leu Ala Asp Glu Thr Leu Lys Asn Lys Gly Leu Lys
130 135 140

Leu Gly Asp Thr Leu Ser Leu Ser Xaa Xaa Arg
145 150 155